

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2005, 16:30:41 ; Search time 20847.7 Seconds
(without alignments)
5315.550 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPBRVPRCVRTPPLRGAR.....KKDTLSLSGLSSDPTDMPZ 2287

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12024	100.0	7540	6	AX068898 Sequence
2	11980	99.6	6942	10	AF290212 Rattus no
3	11980	99.6	7542	10	RNCAALG AF027984 Rattus no
4	11829	98.3	7285	6	BD224079 T-type ca

5	11829	98.3	7286	10	AF125161	AF125161 Rattus no
6	11673	97.0	7129	6	BD224078	BD224078 T-type ca
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8	11489	95.5	7527	10	BC057399	BC057399 Mus muscu
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10	11088	92.2	7349	9	AF190860	AF190860 Homo sapi
11	11066.5	92.0	7741	6	AR201015	AR201015 Sequence
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13	10948.5	91.0	6822	6	AR201014	AR201014 Sequence
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17	10914.5	90.7	6966	9	AF227749	AF227749 Homo sapi
18	10902	90.6	6855	9	AF227751	AF227751 Homo sapi
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28	6248	51.9	8447	6	BD087035	BD087035 Calcium c
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37	5596.5	46.5	6924	6	CO730788	AF086827 Rattus no
38	5441	45.2	6911	10	AF086827	AF142567 Homo sapi
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ALIGNMENTS

RESULT 1
AX068898 LOCUS AX068898 7540 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 23 from Patent WO0102561.
ACCESSION AX068898
VERSION AX068898.1 GI:12578748
KEYWORDS
SOURCE
ORGANISM Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Snutch,T.P. and Baillie,D.L.
TITLE Mammalian calcium channels and related probes, cell lines and methods
JOURNAL Patent: WO 0102561-A 23 11-JAN-2001;
FEATURES
source location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:10118"
ORIGIN
Alignment Scores:
Pred. No.: 0
Score: 12024.00 Length: 7540
Matches: 2286

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.97% Indels: 0
DB: 6 Gaps: 0

US-09-611-257A-24 (1-2287) x AX068898 (1-7540)

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DB	385	ATGCTCCCCACCAGGTCCTCCGTGCGTAGAGACACTCTCTGAGGGCTCCGCTCGC	444
QY	21	ProSerSerAspProProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGlu	40
DB	445	CCCTCTTCGGACCCCCCGGGCCCCGGCTGGCCAGAGATGGACGAGAGAGATGAG	504
QY	41	ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCysProGly	60
DB	505	CGGGCCCGGAGAGTCGGGACAGCCCCGTAGCTTCAAGCTCAACGACTGTCCGGGG	564
QY	61	ProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGluAla	80
DB	565	CCGGGGCCGGCAGGGGGCCGGGTGACGGAAAGAACCCGGGCAGCGCGGACTCCGAGGCG	624
QY	81	GluGlyLeuProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSer	100
DB	625	GAGGGCTGCCGTACCCCGCGCTAGCCCCGGTGGTTTCTTACTTGAGCCAGAGACAGC	684
QY	101	ArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMet	120
DB	685	CGCCCGCGAGACTGTGTCTCCGACAGGTCTGTAAACCGGTGTTGAGGAGTCAATATG	744
QY	121	LeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAla	140
DB	745	CTGGTATTCTTCTCAACTGTGTGACTCTGGGTATGTTCAGGCCGTGTGAGACATTGGC	804
QY	141	CysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePhe	160
DB	805	TGTGACTCCAGCGCTGCCGGATCTGCAGAGCCCTTGATGACTTCACTCTTGCCCTTT	864
QY	161	AlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeu	180
DB	865	GCTGTGAAATGTGTGAAGATGGTGGCTTGCGCATCTTTGGGAAGAAATGTTACCTG	924
QY	181	GlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer	200
DB	925	GGAAGACCTTGGAACCGGCTGACTTTTTCATTGTGATTCAGGGATGTGAGTATTGG	984
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DB	985	CTGGACTGCAGAACGTCACTTCTCCGACAGTCAGACAGTCCGTGTGTCGCAACCGCTC	1044
QY	221	ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrLeu	240
DB	1045	AGGGCCATTAAACGGGTGCCAGCATGCGCATTTCTGTCACTTACTGTGGAACACTTG	1104
QY	241	ProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVal	260
DB	1105	CCTATGCTGGGCAACGTCCTGCTGTCTGTTCGTTCCTTTTTCATCTTTGGCATCGTG	1164
QY	261	GlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer	280
DB	1165	GGCGTCAAGCTGTGGCAGAGACTGCTTCGCAACCGGTGCTTCTCCCGAGAACTTCAGC	1224
QY	281	LeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPro	300
DB	1225	CTCCCCCTGAGCGGTGACCTGAGCCCTTATTACCAAGACAGAATGAGACGAGAGCCCC	1284
QY	301	PheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeu	320
DB	1285	TTCACTGTGCTCAGCCTCGGAGAAATGGCATGAGATCTGCAGAGAGTGTGCCACACTG	1344
QY	321	ArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSer	340

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QY	381	GlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHisSer	400
DB	1525	CAGGTCACTACACTGGAGGGCTGGGTGCACATCATGTACTTCGTATAGACGCTCACTCC	1584
QY	401	PheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsn	420
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QY	421	LeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeu	440
DB	1645	CTGTGCCTGTGTGATGCCACAGCAGATTCTCCGAGACCAACAGCGGAGAGTCACTTG	1704
QY	441	MetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGlu	460
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QY	461	ProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAla	480
DB	1765	CCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTGTGTACATCTCCGAAAGCAGCC	1824
QY	481	ArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerPro	500
DB	1825	CGAAGCTGGCCCAAGTCTCTAGGGCTATAGGCGTGGCGGCTGGGCTGCTCAGCAGCCCA	1884
QY	501	ValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArg	520
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QY	541	AsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGly	560
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QY	561	SerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArg	580
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QY	581	GlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCys	600
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QY	601	GlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLys	620
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QY	641	GluValAlaProSerProGlyProProProThrLeuThrSerPheAsnIleProProGlyPro	660
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QY	661	PheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCys	680
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REFERENCE		1 (bases 1 to 6942)		
AUTHORS		McRoy,J.E., Santl,C.M., Hamming,K.S., Mezeyova,J., Sutton,K.G., Baillie,D.L., Stea,A. and Snutch,T.P. Molecular and functional characterization of a family of rat brain T-type calcium channels J. Biol. Chem. 276 (6), 3999-4011 (2001) JOURNAL MEDLINE 21264893 PUBMED 11073957		
JOURNAL TITLE		2 (bases 1 to 6942)		
REFERENCE AUTHORS		Snutch,T.P., McRoy,J.E. and Hamming,K.S. Direct Submission Submitted (27-JUL-2000) Biotechnology Laboratory, University of British Columbia, 6174 University Blvd., Vancouver, BC V6T1Z3, Canada		
JOURNAL TITLE		3 (bases 1 to 6942)		
REFERENCE AUTHORS		Snutch,T.P., McRoy,J.E. and Hamming,K.S. Direct Submission Submitted (29-NOV-2000) Biotechnology Laboratory, University of British Columbia, 6174 University Blvd., Vancouver, BC V6T1Z3,		
JOURNAL COMMENT FEATURES		REMARK On Nov 29, 2000 this sequence version replaced gi:11415015.		
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QY 780 rGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluG 800
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QY	820	laleuGlumetLeuleuLysleuLeuValTyrGlyProPheGlyTyrIleLysAsnProt	840
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QY	840	yrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnGlnG	860
Db	2536	ACACATCTTTGATGGTGTCTATGTGTGTCATCATGTGTGGAGATTGTGGCCACGACGG	2595
QY	860	lyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgP	880
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QY	880	heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaT	900
Db	2656	TCCTGCCGGCCCTGCAGCGCCAGCTCGTGTGTCTCATGAAGACCATTGACACGTGGCCA	2715
QY	900	hrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeup	920
Db	2716	CCTTCTGCATGCTCCTCATGTGCTGTTTCATCTTACATCTTACAGCATCCTGGGCATGCTCT	2775
QY	920	heGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheA	940
Db	2776	TTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACGTTGCCAGACCCGAGAAATTTCG	2835
QY	940	spSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnL	960
Db	2836	ACTCCCTGCTCTGGGCCATTCGTCACTGCTTTCAGATTCTGACTCAGGAAGACTGGAATA	2895
QY	960	ysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaL	980
Db	2896	AACTCCTCTACACACGGCATGGCCTCCACATCGTCTTGGGCTGCTCTTACTTCATCGCCC	2955
QY	980	eumetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyP	1000
Db	2956	TCATGACTTTTGGCAACTATGTGCTCTTAACTGCTGTGGCCATTCTTGTGAAGGAT	3015
QY	1000	heGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerV	1020
Db	3016	TCCAGGCAGAGGAGATGCCAACCAAGTCTGAGTCAGACCTGATTCTTTTCGCCACGTG	3075
QY	1020	alAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaG	1040
Db	3076	TGGATGGTGATGGGACAGAAAGAGCGCTTGCGCTGTGGCTTTGGAGAACACGCGG	3135
QY	1040	IuleuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerH	1060
Db	3136	AACTACGAAGAGCCTTTTGCACCCCTCATCATCCATACGGCTGCAGACCAATGTCAAC	3195
QY	1060	isProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrs	1080
Db	3196	ACCCCAAGAGCTCCAGACACAGGTGTGGGGGAGACATGGGCTCTGGCTCTGCAGCTTACA	3255
QY	1080	erSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSera	1100
Db	3256	GTAAGCAGTGGGTCCGCTGAGCTGGAGCTGCCACCAATGATGAATGTCCGCCAAGTG	3315
QY	1100	laArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSers	1120
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Db	3976	TCCTGACCTCTCCAACTACTCATCTTCACGGCAGTCTTTCTAGCTGAATGACGTGAAGG	4035
Qy	1340	alValAlaLeuGlyTyrCysPheGlyGlyGlnAlaTyrLeuArgSerSerTrpAsnValL	1360
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Qy	1440	eugLyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGlyAspThrArgAsnI	1460
Db	4336	TCCGGGTGCACTCTTCAAAAGGGAATTCTTCTGTGTTCAGGGTGAGACACCAAGAAACA	4395
Qy	1460	leThrAsnLysSerAspCysAlaGlnAlaSerTyrArgTrpValArgHisLysTyrAsnP	1480
Db	4396	TCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGATGGGTCCGGCACAAGTCAACT	4455
Qy	1480	heAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpV	1500
Db	4456	TTGACAAACCTGGGCCAGGCTCTGATGTCCCTGTTGTGTGCGCTCCAAAGATGGTTGGG	4515
Qy	1500	alAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnH	1520
Db	4516	TTGACATCATGTATGATGGGTGATGCTGTGGGTGTGATCAGCAGCCCATCATGAACC	4575
Qy	1520	isAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValL	1540
Db	4576	ACAAACCCCTGATGCTGCTATACTCATCTCTCTCTCATCGTGCCCTTCTTGTGCC	4635
Qy	1540	euAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnGluG	1560

Db 4636 TGAACATGTTTGTGGCGGTGTGTGTGAGAACTTCCATAAGTGACAGACACCAGAGG 4695
QY 1560 l uGluGluAlAArgAArgGluGluLysArgLeuArgArgLeuGluLysIlySArgArgS 1580
Db 4696 AGGAGGAGCGGAGCGCGGTGAGAGAACGACTACGGAGGCTGGAGAAAAGAGAAGA 4755
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QY 1820 h rC y s T y r A s n T h r V a l l e S e r P r o l e T y r P h e V a l S e r P h e V a l l e u T h r A l a G l n P 1840
Db 5476 C C T G C T A C A A C A C T G T C A T C T C C C T A T C T A C T T G T C C T T C G T G A C G G C C A G T 5535
QY 1840 h e V a l l e u V a l A s n V a l V a l l e a V a l l e u M e t L y s H i s l e u G l n G l u S e r A s n l y s G 1860
Db 5536 T T G T G C T G T C A A C G T G C A T A G C T G T G C T G A T G A A G C A C C T G G A A A G C A A C A A G 5595
QY 1860 l u a l a l y s G l u G l u a l a g l u l e u G l u a l a g l u l e u G l u l e u G l u M e t l y s T h r l e u S e r P 1880
Db 5596 A G G C C A A G A G A G A G G C C G A G C T C G A G G C C G A G C T G G A G A T G A A C A C G C T C A G C C 5655
QY 1880 r o G l n P r o H i s e r P r o l e u G l y S e r P r o P h e l e u T r p P r o G l y V a l G l u l y V a l A s n S 1900
Db 5656 C G A G C C C C A C T C C C C G C T G G G C A G C C C C T T C T C T G G C C C G G G G T G A G G G T C A A C A 5715
QY 1900 e r T h r A s p S e r P r o l y s P r o G l y A l a P r o H i s T h r T h r A l a H i s l e G l y A l a l a S e r G 1920
Db 5716 G T A C T G A C A G C C C T A A G C C T G G G G C T C C A C A C A C A C T G C C C A C A T T G A G C A G C C T C G G 5775

QY 1920 l y P h e S e r l e u G l u H i s P r o T h r M e t V a l P r o H i s P r o G l n G l u V a l P r o V a l P r o l e u G 1940
Db 5776 G C T T C T C C T T G A G C A C C C C A C G A T G T A C C C C A C C C C G A G A G G T G C C A G T C C C C T A G 5835
QY 1940 l y P r o A s p l e u l e u T h r V a l A r g l y S e r G l y V a l S e r A r g T h r H i s S e r l e u P r o A s n A 1960
Db 5836 G A C C A G A C C T G A C T G T G A G G A A G T C T G G T G C A G C C G G A C G C A C T C T C T G C C C A A T G 5895
QY 1960 s p S e r T y r M e t C y s A r g A s n G l y S e r T h r A l a G l u A r g S e r l e u G l y H i s A r g l y T r p G 1980
Db 5896 A C A G C T A C A T G T C C G C A A T G G A G C A C T G C T G A G A T C C C T A G A C A C A G A G G G C T G G 5955
QY 1980 l y l e u P r o l y s A l a G l n S e r G l y S e r l e u S e r V a l H i s S e r G l n P r o A l a A s p T h r S 2000
Db 5956 G G C T C C C C A A G C C C A G T C A G G C T C C A T C T T G T C C G T T C A C T C C C A A C C A G C A G A C C A 6015
QY 2000 e r C y s I l e l e u G l n l e u P r o l y s A s p V a l H i s T y r l e u l e u G l n P r o H i s G l y A l a P r o T 2020
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QY 2180 l a V a l S e r C y s l e u A s p S e r G l y S e r G l n P r o A r g l e u C y s P r o S e r P r o S e r S e r l e u G 2200
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Db 6676 T C T C T A T A G A C C C C C G A G A G C A G G G C T C T G G C C C C A T G C A G T C C T G T G T C T G C C 6735
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RESULT 3
RNCNA1G 7542 bp mRNA linear ROD 24-OCT-1998
LOCUS Rattus norvegicus low voltage-activated, T-type calcium channel
DEFINITION alpha subunit (CACNA1G) mRNA, complete cds.
ACCESSION AF027984
VERSION AF027984.1 GI:3786350
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 7542)
Perez-Reyes,E., Cribbs,L.L., Daud,A., Lacerda,A.E., Barclay,J.,
AUTHORS Williamson,M.P., Fox,M., Rees,M. and Lee,J.H.
TITLE Molecular characterization of a neuronal low-voltage-activated
T-type calcium channel
JOURNAL Nature 391 (6670), 896-900 (1998)
MEDLINE 98154730
PUBMED 9495342

REFERENCE 2 (bases 1 to 7542)
Cribbs,L.L., Yang,J., Daud,A., Lee,J.-H. and Perez-Reyes,E.
AUTHORS Direct Submission
TITLE Submitted (02-OCT-1997) Physiology, Loyola University Medical
JOURNAL Center, 2160 South First Avenue, Maywood, IL 60153, USA
3 (bases 1 to 7542)
Cribbs,L.L., Yang,J., Daud,A., Lee,J.-H. and Perez-Reyes,E.
REFERENCE Direct Submission
TITLE Submitted (22-OCT-1998) Physiology, Loyola University Medical
AUTHORS Center, 2160 South First Avenue, Maywood, IL 60153, USA
JOURNAL
REMARK Sequence update by submitter
COMMENT On Oct 24, 1998 this sequence version replaced gi:2921748.
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GPFGYIKNPYNI FDGVI VVISWEIVGQGGGLSVLRTERLMRVLKLVRFLPALQRL
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DATKSESSEDPFSPSVDGDRKKRLALVALGEBALRKSLPLPLIHTAATPMSPHK
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VIFPLNCITIAMERPKIDPHSAERIFLTLSNYIFTAVFLEMTVKVALGWCFFEQAY
LRSSMNVL DGLVLISVIDILVSWVSDSGTKILGMLRVALLRTLRLRVISRAQGL
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ASYRWVRHKYNDNLGOALMSLFVLASKDGVNDIMYDGLDVGVDQOPI MNHNPML
YFISFLIYAFVFLNMFVGVVVENFHKCRQHOEEEARRREKRLRLEKRRSRKEQ
MABAQCKPYSDYSRFLNHLCTSHYLDLFTGVIGLNVVTMAMEHYQOPOILDEA
LKICNYIFVI FVEESVFKLVAFGFRFFQDRMNOLDLAILVISIMGITLEEIVNLS
LPINPTIIRIMRVLIARVXLKMAVGMRALHTVMQALPOGNLGLLFMLLPFIFA
ALGVELFGDLECDETHPCCEGLGRHATFRNFGMAFLTILFRVSTGDNWNGIMKDTLRDCD
QESTCYNTVISPIYFVSFVLTAQFVLVNVIAVLMKHEESNKEAKEBALEALELE
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ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 7542
Score: 11980.00 Matches: 2283
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 3
Query Match: 99.60% Indels: 2
DB: 10 Gaps: 0

US-09-611-257A-24 (1-2287) x RNCNA1G (1-7542)

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Db 445 CCCTCTTCGACCCCCCGGGGCCCCGCTGCGCCAGAGATGACGAGAGAGATGGAG 504

Qy 41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrTyrCysProGly 60
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Qy 140 laCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPheP 160
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Db 805 CCTGTGACTCCACGCGCTGCCGATCTTGACAGGCTTCGATGACTTCATCTTGCCCTTCT 864

Qy 160 heAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrL 180
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Db 865 TTGCTGTGAATAGTGTGAAGATGTTGCTTGCGCATCTTTGGAGAAATGTTACC 924

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Db 3385 TCCAGGCGAGAGGAGATGCCACCAAGCTGAGTCAGAGCCTGATTTCTTTCCGCCAGTG 3444
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QY 1040 luleuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrPrometSerH 1060
Db 3505 AACTACGAAGAGCCTTTTCCACCCCTCATCATCAGCTGCGACACCAATGTCAC 3564
QY 1060 iSProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrs 1080
Db 3565 ACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAAGCACTGGGCTCTGGCTTCGACGTACCA 3624
QY 1080 erSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSera 1100
Db 3625 GTAGCAGTGGGTCCGCTGAGCCTGAGCTGCCACCATGAGATGAATGTCCGCCAAGTG 3684
QY 1100 laArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSers 1120
Db 3685 CCGCGAGCTCCCCGACAGTCCCTGAGGTGGGCAAGCAGCTGGACCAAGAGCGCGCTCCA 3744
QY 1120 eArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArga 1140
Db 3745 GCAGGAACAGCTGGGGCCGGGCCCCCAACCTAAAGCGAGAGCCCGAGCGGGAGCGGA 3804
QY 1140 rGSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluA 1160
Db 3805 GGTCCTGCTGTGGAAGAGGCCAGGAGAGTCAGGATGAGGAGGAAAGTTCAAGAGAGG 3864
QY 1160 sPARGAlaserProAlaGlySerAspHisArgHisArgLysSerLeuGluArgGluAlaL 1180
Db 3865 ACCGGGCCAGCCCAAGCAGAGCAGTGAACCATGCCACAGGGGTTCTTGGAACGTAGGCCA 3924
QY 1180 ySerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerG 1200
Db 3925 AGAGTTCCTTTGACTCTGACACTGTGACACTCTGCAAGGTGCCGGGGCTGCAACCGCACGCCGCG 3984
QY 1200 lYArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA 1220
Db 3985 GCCGGAGCTCTGCTCTGAGCACCAAGACTGTAATGGCAAGTCGGCTTCAGGGCGTTTGG 4044
QY 1220 laArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyA 1240
Db 4045 CCGCACCCCTGAGGACTGATGACCCCACTGATGGGATGATGACAATGATGAGGAA 4104
QY 1240 snLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysA 1260
Db 4105 ATCTGAGCAAAAGGGGAACGATACAAAGCCTGGGTCAAGATCCGGCTTCCTGCTGTGGC 4164
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QY 1300 snCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIleP 1320
Db 4285 ACTGTATCACCATGCTTAAGAGCGCCCCCAAAATTGACCCCCACAGCGCTGAGCGCATCT 4344
QY 1320 heLeuThrLeuSerAsnTyrllePheThrAlaValPheLeuAlaGluMetThrValLysV 1340
Db 4345 TCCTGACCCCTCTCCAACATCATCTTCACGGCAGCTTTCTAGCTGAATGACAGTGAAG 4404
QY 1340 aIValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyraArgSerSerTrpAsnValL 1360
Db 4405 TGGTGCACTGGGCTGTGCTTTGGGAGCAGGCTTACCTGCGCAGCAGCTGGAATGTGC 4464
QY 1360 euAspGlyLeuLeuValleuIleSerValIleAspIleLeuValSerMetValSerAsps 1380
Db 4465 TGGACGGCTTGCTGTGTCTCATCTCCGTATCGACATCCTGCTCCATGTGCTCCGACA 4524
QY 1380 erGlyThrLysIleLeuGlyMetLeuArgValleuArgLeuLeuArgTrpThrLeuArgProL 1400
Db 4525 GCGGACCAAGATCCTTGGCATGTCTGAGGGTGTCTGGCTGCTGCGGACCTGCGCTCAC 4584
QY 1400 euArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerL 1420
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QY 1420 euLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleL 1440
Db 4645 TCAAACCATTTGGCAACATTTGTGTCATTTGCTGTGCTTCTTCATCATTTTGGAAATC 4704
QY 1440 euGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnI 1460
Db 4705 TCGGGGTGACGCTCTTCAAAGGAAGTTCTTGCTGTGTCAGGGTGAGGACCAAGAAACA 4764
QY 1460 leThrAsnLysSerAspCysAlaGluAlaSerTyraArgTrpValArgHisLysTyraSnP 1480
Db 4765 TCACCTAACAAATCCGACTGCGCTGAGGCCAGCTACCGATGGGTCCGGCACAACTAACACT 4824
QY 1480 heAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValleuAlaSerLysAspGlyTrpV 1500
Db 4825 TTGACAACCTGGGCCAGGCTGTGATGTCCCTGTGTGTGCTGCTCCAAAGGATGGTTGGG 4884
QY 1500 aLAspIleMetTyraAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnH 1520
Db 4885 TTGACATCATGTATGATGGGCTGATGCTGTGGTGTGATCAGCAGCCCATCATGAACC 4944
QY 1520 iSAsnProTrpMetLeuLeuTyrlleSerPheLeuLeuIleValAlaPhePheValL 1540
Db 4945 ACAACCCCTGATGCTGCTTAATCTTCATCTCTCTCCTCATCGTGGCTTTGTGCC 5004
QY 1540 euAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluG 1560
Db 5005 TGAACATGTTTGTGGCGCTGTGTGTGAGAACTTCCATAAGTCAGACAGCACAGAGAGG 5064
QY 1560 lGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgS 1580
Db 5065 AGAGAGGCGAGGCGCGGTGAGAGAAAGCACTACGAGGGCTGGAGAAAAGAGAAAGGA 5124
QY 1580 erLysGluLysGlnMetaLagluAlaGlnCysLysProTyrlleSerAspTyrlleSerArgP 1600
Db 5125 GTAAAGAGAACAGATGCGCGAAGCCAGTGCAAGCCCTACTACTGACTACTCGAGAT 5184
QY 1600 heArgLeuLeuValHisHisLysCysThrSerHisTyrlleAspLeuPheIleThrGlyV 1620
Db 5185 TCCGGCTCTTGTCCACCACTGTGTACCAAGCACACTGGAACCTTTCATTCACCTGTGTG 5244
QY 1620 aIleGlyLeuAsnValValThrMetaLametGluHisTyrlleGlnProGlnIleLeuA 1640
Db 5245 TCATCGGGGTGAACGTGTCTACTATGCGCATGGAACATTACCAAGACAGCCCGAGATCCTGG 5304
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QY	1640	spGIuAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValP	1660
Db	5305	ACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGCATCTTTGTCTTTGAGTCAGTTT	5364
QY	1660	hellysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspL	1680
Db	5365	TCAAACCTGTGCGCTTTGGCTCCGCCGTTTCTTCCAGACAGGTGGAACCACTGACCC	5424
QY	1680	eulAlaIleValIleLeuSerIleMetGlyIleThrLeuGluIleGluValAsnLeus	1700
Db	5425	TGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGAGAGAGATTGAGGTCAATCTGT	5484
QY	1700	erLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValL	1720
Db	5485	CGCTGCCCATCAACCCACCATCATCCGTATCATGAGGGTGCTCCGCATTGCTCGATTTC	5544
QY	1720	eulLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaL	1740
Db	5545	TGAAGCTGTTGAAGATGGCTGTGGGCATGCGGCACCTGCTGCACACGGTGATGCAGGCC	5604
QY	1740	eupProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaL	1760
Db	5605	TGCCCCAGGTGGGAACCTGGGACTTCTCTCATGTATTGTTTTCATCTTTGCAGCTTC	5664
QY	1760	eugLysValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuG	1780
Db	5665	TGGCGGTGAGCTCTTTGGAGACCTGGAGTGATGAGACACACCCTTGAGAGGCTTGG	5724
QY	1780	lyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerT	1800
Db	5725	GTCGCATGCCACCTTTAGGAACCTTGATAGCCTTTCTGACCTCTTCCGAGTCTCCA	5784
QY	1800	hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerT	1820
Db	5785	CTGTGACAACTGGAATGATATTATGAAGACACACCTCCGGCACTGTGACCAGAGTCCA	5844
QY	1820	hrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnP	1840
Db	5845	CCTGCTACACACTGTCTCTCCCTATCTACTTGTGTCTTCTGCTGACGGCCCACT	5904
QY	1840	heValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluSerAsnLysG	1860
Db	5905	TTGTCTGTGTCACGCTGTCTCATAGCTGTGCTGATGAGCACCTGGAAGAACCAACAG	5964
QY	1860	luAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerP	1880
Db	5965	AGGCCAAGGAGGAGGCCGAGCTCGAGCGGAGCTGAGATGAAGACGCTCAGCC	6024
QY	1880	roGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnS	1900
Db	6025	CGCAGCCCCACTCCCGCTGGGGCAGCCCTTCTCTGCGCCGGGGTGGAGGTTGTAACA	6084
QY	1900	erThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerG	1920
Db	6085	GTACTGACAGCCCTAAGCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCCTCGG	6144
QY	1920	lyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuG	1940
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QY	1940	lyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnA	1960
Db	6205	GACCAGACCTGCTGACTGTGAAGAACTGTGTGTACGCCGAGCACTCTGCCCCAATG	6264
QY	1960	spSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpG	1980
Db	6265	ACAGCTACATGTGCCGCAATGGAGCACTGCTGAGAGATCCCTAAGACACAGGGGCTGGG	6324
QY	1980	lyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrS	2000
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Db	6385	GCTGATCCTACAGCTTCCCAAGATGTGACTATCTGCTCCAGCCTCATGGGGCTCCCA	6444
QY	2020	hrrTpglyAlaileProLysleuProProGlyArgSerProleuAlaGlnArgProL	2040
Db	6445	CCTGGGGCGCCATCCCTAAACTACCCTGAGCCGCTCCCTCTGGCTCAGAGGCCTC	6504
QY	2040	euarGArgGlnAlaAlaileArgThrAspSerleuaspValGlnGlyleuGlySerArg	2060
Db	6505	TCAGGCGCCAGGACCAATAAGACTGACTCCCTGATGTGACAGGCGCTGGGTAGCCGG	6564
QY	2060	luaspIleuSerGlnValSerGlyProSerCysProleuThrArgSerSerPheT	2080
Db	6565	AAGACCTGTGTGACAGGTGAGTGGCCCTCTGACCCTGACACCCGGTCTCATCTTCT	6624
QY	2080	rrpGlyGlySerSerileGlnValGlnGlnArgSerGlyileGlnSerlyValSerlySH	2100
Db	6625	GGGGCGGGTCGACATCCAGGTGACAGCAGCGTTCCGGCATCCAGAGCAAGTCTCCAAG	6684
QY	2100	isileargleuProAlaProCysProGlyleuGlnProSerTrpAlaLysaspProProG	2120
Db	6685	ACATCCGCTGCGACGCCCTTGCCAGGCGCTGGAACCCAGCTGGGCCAAGACCTCCAG	6744
QY	2120	luThrArgSerSerleuGlnleuaspThrGlnleuSerTrpIleSerGlyaspIleuLeuP	2140
Db	6745	AGACCAGAAGCAGCTTAGAGCTGACACAGGAGCTGAGTGGATTTCAGGAGACCTCCTTC	6804
QY	2140	roSerSerGlnGlnGluProleuPheProArgaspIleuLysLysCysTyrSerValGlnT	2160
Db	6805	CCAGCAGCCAGGAAGAACCCCTGTGCCACGGAACCTGAAGAAGTGCTACAGTGAAGA	6864
QY	2160	hrGlnSerCysargArgArgProGlyPheTrpIleuaspGlnGlnArgHisSerIleA	2180
Db	6865	CCGAGAGCTGCGAGCGCGCCTGGGTTTGCTAGATGAACAGCGGAGCACTCCATTG	6924
QY	2180	lavalSerCysleuaspSerGlySerGlnProArgleuCysProSerProSerSerleuG	2200
Db	6925	CTGTCAAGTGTGTGACACGCGGCTCCCAACCCGCTATGTCCAAGCCCTCAAGCCTCG	6984
QY	2200	lyGlyGlnProleuGlyGlyProGlySerArgProLysLysLysleuSerProProSerI	2220
Db	6985	GGGGCCAACTCTTGGGGGCTCTGGAGCGCGCTTAAGAAAAACTCAGCCCAACCACTA	7044
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Db	7045	TCTCTATAGACCCCCCGGAGAGACGAGGCTCTCGGCCCCCATGACAGTCTGTGCTGCC	7104
QY	2240	euarGArgArgAlaProAlaSerAspSerlyaspProSerValSerSerProleuaspS	2260
Db	7105	TCAGGAGGAGGGCGCGCCGAGTAGTACTTAAGATCCCTCGGTCCAGCCCCCTTGACA	7164
QY	2260	erThrAlaAlaSerProSerProLysLysaspThrleuSerleuSerGlyleuSerSera	2280
Db	7165	GCAAGGCTGCTACCTCCCAAGAAAGAACACGCTGAGTCTCTGTGTTGTCTTCTG	7224
QY	2280	spProThrAspMetaspPro	2286
Db	7225	ACCCAAACAGACATGACCCC	7244
RESULT 4			
LOCUS	BD224079	7285 bp	DNA linear
DEFINITION	T-type calcium channel.		
ACCESSION	BD224079		
VERSION	BD224079.1	GI:33033849	
KEYWORDS	JP 2002525077-A/2.		
SOURCE	Rattus sp.		
ORGANISM	Rattus sp.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
REFERENCE	1 (bases 1 to 7285)		

AUTHORS Li,M.
TITLE T-type calcium channel
JOURNAL Patent: JP 2002525077-A 2 13-AUG-2002;
SOUTH ALABAMA MEDICAL SCIENCE FOUNDATION
COMMENT OS Rattus sp. (rat)
PN JP 2002525077-A/2
PD 13-AUG-2002
PF 26-AUG-1999 JP 2000570372
PR 26-AUG-1998 US 60/098004,27-JAN-1999 US 60/117399 PI

PC C12N15/09,A61K31/711,A61K45/00,A61K48/00,A61P3/10,C07K14/47,
PC C07K16/18,
PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12Q1/68,G01N33/
PC 15,G01N33/50,
PC G01N33/53,G01N33/53,G01N33/566,G01N33/577,G01N33/58,G01N33/68// PC
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CC T-type calcium channel
FH Key Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 7285
Score: 11829.00 Matches: 2270
Percent Similarity: 97.72% Conservative: 1
Best Local Similarity: 97.68% Mismatches: 15
Query Match: 98.35% Indels: 38
DB: 6 Gaps: 2

US-09-611-257A-24 (1-2287) x BD224079 (1-7285)

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DB 57 ATGCTCCCCACCGGGGTCCCCCGGTTCGTGAGACACCTCTCTGAGGGGCTCCGCTC 116
QY 20 rGProSerSerSPPProProGlyProArgLeuAlaArgGlyTyrThrArgArgMetG 40
DB 117 GCCCCCTCTCGGACCCCCCGGGGCTGGCCAGAGATGACGAGAGAGATGG 176
QY 40 lUaRgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCysProG 60
DB 177 AGCGGGCGCGGAGAGTCCGGACAGCCCCGCTTAGCTTCAACGACTCAACGACTGTCGG 236
QY 60 lYProGlyAla-AlaGlyAla-GlySerThrGlyLysAspProGlySerAlaAspSerG 79
DB 237 GCGCGGGGGCCGGCAGGGGCGGGGTTCGACGAAAGAACCCGGGCAAGCGGACTCCGA 296
QY 79 uAlaGlyLysLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAs 99
DB 297 GCGGAGGGGCTGCCTACCCGGCGCTAGCCCCGGTGTTCCTTCTTACTTGAGCCAGGA 356
QY 99 pSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGlyuArgValSe 119
DB 357 CAGCGCGCCGCGAGCTGGTGTCTCCGACGCTGTGAACCCGCTGTTGAGCGAGTCAG 416
QY 119 rMetLeuValIleuLeuAsnCysValThrLeuGlyMetPheArgProCysGlyuAspI 139
DB 417 TATGCTGTGATCTTCTCACTGTGACTCTGGGTATGTTCAGGCCGTGTGAGGACAT 476
QY 139 eAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPh 159
DB 477 TGCCTGTGACTCCACGCGCTGCCGATCCTGACAGCCCTTCGATGACTTCATCTTGCCCT 536
QY 159 ePheAlaValGlyMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyr 179

DB 537 CTTTGCTGTGAATGTGTGAGATGTGTGCGCTTGCGCATCTTTGGGAAGAAATGTTA 596
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DB 597 CTTGGAGACACTTGGAACCGGCTTGACTTTTCATTGTTCATTGACGGATGCTGGAGTA 656
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DB 717 GCTCAGGGCCATTAAACGGGTGCCAGCATGGCATTCGTACACATTACTGCTGAGACAC 776
QY 239 rLeuProMetLeuGlyAsnValIleuLeuLeuCysPhePheValPhePheIlePheGlyI 259
DB 777 CTTGCTATGCTGGGCAACGTCTGCTGCTCTGTTCTTTCGTTTCATTCTTTGGCAT 836
QY 259 eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGlyuAsnPh 279
DB 837 CGTGGCGCTCCAGCTGTGGGCAAGACTGTTCGCAACCGATGCTTCCTCCCGAGAACTT 896
QY 279 eSerLeuProLeuSerValAspLeuGlyProTyrTyrGlnThrGluAsnGlyuAspGlySe 299
DB 897 CAGCTTCCCCCTGAGCGGTGACCTGAGCCTTAATTAACAGACAGAAATGACGACGAGAG 956
QY 299 rProPheIleCysSerGlnProArgGlyuAsnGlyMetArgSerCysArgSerValProTh 319
DB 957 CCCCTTCATCTGCTCTCAGCCTCGGAGAAATGGCATGAGATCCTGCAGGAGTGTGCCAC 1016
QY 319 rLeuArgGlyGlyGlyGlyGlyGlyProProCysSerLeuAspTyrGlyuThrTyrAsnSe 339
DB 1017 ACTGCGTGGGGAAGCGGTGTGGCCACCCTGCACTCTGACTATGAGACTTAACAG 1076
QY 339 rSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyG 359
DB 1077 TTCCAGCAACACCCTGTGTCACTGGAACCACTACTATACCAACTGTCTGCGGGCGGA 1136
QY 359 uHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTyrIleAlaI 379
DB 1137 GCACAACCCCTTCAAGGCGGCATCACTTTGACAACATTGGCTATGCTTGATCGCCAT 1196
QY 379 ePheGlnValIleThrLeuGlyGlyTyrValAspIleMetTyrPheValMetAspAlaHi 399
DB 1197 CTTCCAGTCATCACACTGGAGGGCTGGGTGCACATCATGTACTTCGTAATGACGCTCA 1256
QY 399 sSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetI 419
DB 1257 CTCTTTCACAACTTCATCTTCACTTCTTCTCATCATCGTGGCTCTTTCATGAT 1316
QY 419 eAsnLeuCysLeuValValIleAlaThrGlnPheSerGlyuThrLysGlnArgGlyuSerG 439
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QY 439 nLeuMetArgGlyGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe 459
DB 1377 GCTGATGCGGAGCAGCGTGTACGATTCCTGTCCAATGCTAGCACCTGGCAAGCTTCTC 1436
QY 459 rGlyuProGlySerCysTyrGlyGlyLeuLeuLeuLysTyrLeuValTyrIleLeuArgLy 479
DB 1437 TGAGCCAGGACAGTGTATGAGGACTACTCAAGTACTGTGTACATCCTCGAAAAAGC 1496
QY 479 aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe 499
DB 1497 AGCCCGAAGGCTGGCCAGGCTCTAGGGCTATAGGCGTGGCGGTGCTGCAGCAG 1556
QY 499 rProValAlaArgSerGlyGlnGlyuProGlnProSerGlySerCysThrArgSerHisAr 519
DB 1557 CCAAGTGGCCGTAAGTGGGACAGACCCCAAGCGCAGCTGCACCTCGCTCACACCG 1616
QY 519 gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyrHisIle 539
DB 1617 TCGTGTGTGTCCACCACTGTGTCCACCACTATCACCAACCATCACCACTACCACT 1676

QY	539	UGLYASNGLYThrLEuARgValPProARgAlaSerProGluILEGlnASPARGAsPAlaAs	559
Db	1677	GGGTAAATGGGACGCTCAGAGATTCCCCGGGCCAGGCCAGAGATCCAGGACAGGGATGCCAA	1736
QY	559	NGLYSerARgARgLeuMetLeuProProProSerThrPProThrProSerGLYGLYProPr	579
Db	1737	TGGGTCTCGCCGGCTCATGTCTACCACCACCCCTTACACCACCTCCCTTGGGGGCCCTCC	1796
QY	579	OARGGLYAlaGLuSerValHisSerPheTYrHisAlaSPCYSHISLeuGluProValAr	599
Db	1797	GAGGGTGCGAGTCTGTACACACACTTCTTACCATGCTGACTGCCACTTGAGCCAGTCCG	1856
QY	599	GCYSGlnAlaProProProARgCysProSerGlnAlaSerGLYARgThrValGLYSerGL	619
Db	1857	TTGCCAGGCACCCCCCTCCAGATGCCCATCGGAGGCATCTGGTAGGACTGTGGGTAGTGG	1916
QY	619	YLYSValTYrProThrValHisThrSerProProProGluILEuLysASPlySAlaLe	639
Db	1917	GAAAGTGTAACCCCACTGTGCAATACAGCCCTCCACCAAGATACTGAAGATAAAGCACT	1976
QY	639	UValGLuValAlaProSerProGLYProProProThrLeuThrSerPheASNILEProProGL	659
Db	1977	AGTGAGGTGGCCCCCAGCCCTGGGGCCCCCACCCTCAACAGCTTCAACATCCCACTGG	2036
QY	659	YProPheSerSerMetHisLYSLeuLeuGluuThrGlnSerThrGLYAlaCYSHISerSe	679
Db	2037	GCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGATACGGAGCCTGCCATAGCTC	2096
QY	679	RCYSLYSILESerSerProCYSerLYSAlaASPserGLYAlaCYSGLYProASPserCY	699
Db	2097	CTGCAAAATCTCCAGCCCTTGCTCCAAGGACAGACAGTGAAGCTTGGCGGCCGACAGTTG	2156
QY	699	SPROTYrCYsAlaARgThrGLYAlaGLYGLuProGluSerAlaASPHisValMetProAs	719
Db	2157	TCCCTACTGTGCCCGGACAGGACAGAGAGCCAGAGTCCGCTGACCATGTCTAGCTCTGA	2216
QY	719	PSERASPserGLuAlaValTYrGLuPheThrGlnASPAlaGlnHisSerASPLeuARgAs	739
Db	2217	CTCAGACAGCGAGGCTGTGTATGATTACACACAGGACGCTTCAGCACAGTGACCTCCGGGA	2276
QY	739	PProHISserARgARgARgGlnARgSerLeuGLYProASPAlaGLuProSerSerValLe	759
Db	2277	TCCCCACAGCCGGCGGCGACAGCGAGCCTGGGCCAGATGCAGAGCCTAGTTCTGTGCT	2336
QY	759	UAlaPheTYrARgLeuILECYsASPThrPheARgLYSILEValASPserLYSTyrPheGL	779
Db	2337	GGCTTTCTGAGGCTGATCTGTACACATTCGGAGAGATCGTAGATAGCAAAATACTTTGG	2396
QY	779	YARGGLYILEMetILEAlaILEuValASNThrLeuSerMetGLYILEGluTYrHisGL	799
Db	2397	CCGGGGAATCATGATCCCATCTCTGTCATATACACTCGCATGGGCATCGAGTACCACGA	2456
QY	799	UGlnProGLuGLuLeuThrASNAlaLeuGluuILESerASNILEValPheThrSerLeuPh	819
Db	2457	GCAGCCCGAGGAGCTCACCAACGCCCTGGAATCAGCAACATCGTCTTCAACCAAGCCTCTT	2516
QY	819	EAlaLeuGLuMetLeuLeuLysLeuLeuValTYrGLYProPheGLYTYrILELysASNPr	839
Db	2517	CGCCTTGAGATGCTGCTGAAACTGCTTGTCTACGGTCCCTTGGCTACATTAAAGAAATCC	2576
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Db	2577	CTACAACATCTTTGATGCTGTCAATTGTGTATCATCAGTGTGTGGAGATTGTGGGCCACA	2636
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Db	2637	GGGAGGTGGCCTGTGCGGTGCTGCCGACCTTCCGCGCTGATGCCGGTCTGAAGCTGTGCG	2696
QY	879	GPheLeuProAlaLeuGlnARgGlnLeuValValLeuMetLYSThrMetASPASNValAl	899
Db	2697	CTTCCCTGCCGCCCTGTGACGCCACAGCTCGTGTGTCTCATGAAGACCATGGACAAACGTGGC	2756

QY	899	aThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLe	919
Db	2757	CACCTTCTGCATGCTCTCCTCATGCTGTTCATCTTCATCTTCAGCATCTTGCGCATGCA	2816
QY	919	uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPh	939
Db	2817	CTTTGGTTGCCAAGTTTCGCATCTGCAACGGGATGGGGACAGCTTGCCAGACC	2876
QY	939	eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAs	959
Db	2877	CGACTCCCTGCTCTGGGGCATGCTTCACCTGCTTTCAAGTTCTGACTCAGAGACTGGAA	2936
QY	959	nLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaIleLeuTyrPheIleAl	979
Db	2937	TAAAGTCTCTACAAACGGCATGGCTCCACATCGTCTTGGGCTGCTCTTACTTCATCGC	2996
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QY	999	yPheGlnAlaGlu-----	1003
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QY	1016	eSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuG	1036
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Db	3237	AGAACACGGGGAACACTACGAAGAAGCCTTTTGCCACCCTCATCATCAGGCTGCGAC	3296
QY	1056	rPrometSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySe	1076
Db	3297	ACCAATGTCACTACCCAGAGCTTCCAGCACAGGTGTGGGGGAAGCACTGGGCTCTGCTC	3356
QY	1076	rArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCy	1096
Db	3357	TGCACGTACCAAGTAGCAGTGGGTCCGTGAGCCTGAGCTGCCACCATGAGATGAATC	3416
QY	1096	sProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe	1116
Db	3417	TCCGCCAAGTCCCGCAGCTCCCCGCACAGTCCCTGAGTGGCGCAAGCAGCTGGACCA	3476
QY	1116	rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysBArgArgSerProSe	1136
Db	3477	CAGGCGCTCCAGCAGGAACAGCCTGGGCGGGCCCCAGCCTTAAAGCGAGGAGCCCGAG	3536
QY	1136	rGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluSe	1156
Db	3537	CGGGGAGCGGAGGTCCCTGCTGTCTGAGAGGGGCCAGAGAGTCAGATGAGGAGAAAG	3596
QY	1156	rSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuG	1176
Db	3597	TTCAAGAGAGGACCGGGCCAGCCAGCAGCAGTGAACATCGCCACAGGGGTCTCTTGA	3656
QY	1176	uArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisAr	1196
Db	3657	ACGTGAGCCCAAGAGTTCCTTGAACCTGCTGACACTCTGCAGGTGCCGGGCTGCACCG	3716
QY	1196	gThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSe	1216
Db	3717	CACAGCCAGCGCCGAGCTTCTGCTGTGAGCACCAAGACTGTATGGCAAGTCGGCTTC	3776
QY	1216	rGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAs	1236
Db	3777	AGGCGGTTGGCCCCGACACCTGAGGACTGATGACCCCAACTGATGGGAGATGACAA	3836
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Db 4557 CAAGTACAACCTTGACAACCTGGGCGAGCTCTGATGTCCTGTTGTGCTGGCTGCCAA 4616
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Db 4677 CATCATGAACCAACCCCTGGATGCTGTATACTTCATCTCTCTCCTCATCGTGCC 4736
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Db 4737 CTTCCTTGTCTGAACATGTTTGTGGGCGTGTGTTGAGAACTTCCATAAGTGACAGACA 4796
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Qy	2025	o	LysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaI	2045
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Qy	2105	a	ProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLe	2125
Db	6477	CCCTGCCAGGCTTGAAACCAGCTGGGCCAAGGACCTCCAGAGACCAAGAAGCATT		6536
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Db	6537	AGAGCTGCACACGAGCTGAGCTGATTTCAGAGACCTCCTCCAGACGCCAGAAGA		6596
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RESULT 5				
AF125161				
LOCUS AF125161 7286 bp mRNA linear ROD 19-OCT-2001				
DEFINITION Rattus norvegicus T-type calcium channel isoform mRNA, complete				

ACCESSION	AF125161	cds.
VERSION	AF125161.1	GI:4633669
KEYWORDS		
SOURCE		
ORGANISM	Rattus norvegicus (Norway rat)	
REFERENCE	1 (bases 1 to 7286)	
AUTHORS	Zhuang,H., Bhattacharjee,A., Hu,F., Zhang,M., Goswami,T., Wang,L., Wu,S., Berggren,P.O. and Li,M.	
TITLE	Cloning of a T-type Ca2+ channel isoform in insulin-secreting cells	
JOURNAL	Diabetes 49 (1), 59-64 (2000)	
MEDLINE	20081696	
PUBMED	10615950	
REFERENCE	2 (bases 1 to 7286)	
AUTHORS	Zhuang,H., Hu,F., Bhattacharjee,A., Zhang,M., Wu,S., Berggren,P. and Li,M.	
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ORIGIN

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US-09-611-257A-24 (1-2287) x AF125161 (1-7286)

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Qy	1845	IValIleAlaValIleuMeTlysHisLeuGIuGIuSerAsnLysGIuAlaIaLysGIuGIuAl	1865
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Qy	1865	aGIuLeuGIuAlaGIuLeuGIuLeuGIuMeTlysThrIleuSerProGlnProHisSerPr	1885
Db	5758	CGAGCTCGAGGCCGAGCTGAGCTGAGATGAAGACGCTCAGCCCGACCCCACTCCCC	5817
Qy	1885	oLeuGIySerProPheLeuTrpProGIyValGIuGIyValAsnSerThrAsPSerProLy	1905
Db	5818	GCTGGGAGCCCTTCTCTCTGCGCCGGGGTGAGGGTGTCAACAGTCTGACAGCCCTAA	5877
Qy	1905	sProGIyAlaProHisThrThrAlaHisIleGIyAlaIaSerGIyPheSerLeuGIuHi	1925
Db	5878	GCCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCTCGGGCTTCTCCCTTGAGCA	5937
Qy	1925	sProThrMeTValProHisProGIuGIuValProValProLeuGIyProAsPLeuLeuTh	1945
Db	5938	CCCCACGATGTAACCCACCCCGAGGAGGTGCCAGTCCCCCTTAGACACAGACTGTCTAC	5997
Qy	1945	rValArGIySerGIyValSerArGTThrHisSerLeuProAsnAsPSerTyrMeCyAsr	1965
Db	5998	TGTGAGGAAGTCTGGTGTACGCCGAGCACTCTCTGCCCAATGACAGCTACATGTGCCG	6057
Qy	1965	gAsnGIySerThrAlaGIuArGSerLeuGIyHisArGIyTTrpGIyLeuProLysAlaGI	1985
Db	6058	CAATGGAGCACTGTGAGAGATCCCTAGACACAGGGGCTGGGGGCTCCCCAAAGGCCA	6117
Qy	1985	nSerGIySerIleLeuSerValHisSerGlnProAlaAsPThrSerCysIleLeuGlnLe	2005
Db	6118	GTCAGGCTCCATCTTGTCCGTTCACTCCCAACGACAGACACCACTGCATCCTACAGCT	6177
Qy	2005	uProLyAsPValHisTyrLeuLeuGlnProHisGIyAlaProThrTrpGIyAlaIlePr	2025
Db	6178	TCCCAAGATGTGCACTATCTGCTCAGCCTCATGGGGCCCACTGGGGCGGCATCCC	6237
Qy	2025	oLySLeuProPProPProGIyArGSerProLeuAlaGIuArGProLeuArGArGIuAlaAl	2045
Db	6238	TAAACTACCCCACTGGCCGCTCCCTCTGGCTCAGAGGCTCTCAGGCGCCAGGACG	6297
Qy	2045	aIleArGTThrAsPSerLeuAsPValGIuGIyLeuGIySerArGIuAsPLeuLeuSerGI	2065
Db	6298	AATAAGGACTGACTCCCTGATGTGACGGGCTGGGTAGCCGGGAAGACCTGTGTTCAGA	6357
Qy	2065	uValSerGIyProSerCysProLeuThrArGSerSerSerPheTrpGIyGIySerIle	2085

Db	6358	GGTAGTGGG	CCCTCCTG	CCCTCTG	ACC	CGG	CTCAT	CTTCTG	GGGG	GGGTG	AGCAT	6411
QY	2085	eglnValgln	glnArgSerglyl	leglnSerLysValSerLysHisIle	ArgLeuProAl							2105
Db	6418	CCAGGTG	CAGCAGCG	TTCCGG	CATCC	AGACAA	AGTCTC	CAAG	CACATC	CGCCTG	CCAGC	6477
QY	2105	apProCys	ProGlyLeu	GluProSer	TrpAlaLys	AspProProGlu	ThrArgSer	SerLe				2125
Db	6478	CCCTTG	CCCAAG	CGCTG	GAAC	CCAG	CTGG	CCAA	GGACC	CTCC	AGAC	6537
QY	2125	uglLeu	AspThrGlu	LeuSerTrpIle	SerGlyAsp	LeuLeuPro	SerSergln	GluGl				2145
Db	6538	AGAGCTG	ACACGAG	CTGAGCT	GATTTC	AGAGAC	CTCCTT	CCAG	ACCG	CAAG	AAGA	6597
QY	2145	uProLeu	PheProArg	AspLeuLysCys	TyrSerVal	GluThrGln	SerCysArg	Ar				2165
Db	6598	ACCCCTG	TCCCC	CACGG	GA	CTGA	AGAG	TGCTA	CAGT	AGAC	CCAG	6657
QY	2165	gArg	ProGlyPhe	TrpLeuAsp	GluGlnArg	ArgHis	SerIleAla	ValSer	CysLeu	As		2185
Db	6658	CAGGCCT	GGGTCT	CGCTA	GATGA	ACAC	GGGAG	ACACT	CCATTG	CTGT	CA	6717
QY	2185	pSerg	LysSerGln	ProArgLeu	CysProSer	ProSerSer	LeuGlyGly	GlnPro	LeuGl			2205
Db	6718	CAGCGG	CTCCCA	CCGCC	CTATG	TCCA	AGCC	CTCA	AGC	CTCG	GGGCC	6777
QY	2205	Ygly	ProGlySer	ArgProLys	LysLysLeu	SerProPro	SerIleSer	IleAsp	ProPr			2225
Db	6778	GGGTCTG	GAGCGCG	CTAAG	AAAAA	ACTCA	GGCC	ACCA	GTAT	CTTA	TAG	6837
QY	2225	ogLys	erGlnLys	erArgPro	ProCysSer	ProGlyVal	CysLeuArg	ArgAla	Pr			2245
Db	6838	GGAGAG	CCAGG	CGCTCT	CGCCCC	ATGAG	TCTG	TGCTG	CTC	AGAG	AGGCG	6897
QY	2245	oAla	SerAspSer	LysAspPro	SerValSerSer	ProLeuAsp	SerThrAla	AlaSer	Pr			2265
Db	6898	GGCCAG	TGACTCT	AAGAT	CCCTCG	GTCTC	AGCCCC	CTTG	AC	AGC	AGC	6957
QY	2265	oSer	ProLysLys	AspThrLeu	SerLeuSer	GlyLeuSer	SerAspPro	ThrAsp	MetAs			2285
Db	6958	CTCCCC	AAAGAA	GACAC	GC	TGAG	TCTCT	GTG	TTG	TTCT	TG	7017
QY	2285	pPro	2286									
Db	7018	CCCC	7021									
RESULT 6												
LOCUS	BD224078	BD224078 7129 bp DNA linear PAT 17-JUL-2003										
DEFINITION	T-type calcium channel.											
ACCESSION	BD224078											
VERSION	BD224078.1 GI:33033848											
KEYWORDS	JP 2002525077-A/1.											
SOURCE	Rattus sp.											
ORGANISM	Rattus sp. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.											
REFERENCE	1 (bases 1 to 7129)											
AUTHORS	Li,M.											
TITLE	T-type calcium channel											
JOURNAL	Patent: JP 2002525077-A 1 13-AUG-2002; SOUTH ALABAMA MEDICAL SCIENCE FOUNDATION											
COMMENT	OS Rattus sp. (rat) PN JP 2002525077-A/1 PD 13-AUG-2002 PF 26-AUG-1999 JP 2000570372 PR 26-AUG-1998 US 60/098004, 27-JAN-1999 US 60/117399 PI MING LI PC C12N15/09, A61K31/711, A61K45/00, A61K48/00, A61P3/10, C07K14/47, PC C07K16/18, PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12Q1/68, G01N33/15, G01N33/50,											

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G01N33/53, G01N33/53, G01N33/566, G01N33/577, G01N33/58, G01N33/68// PC												
C12P21/08,												
PC C12N15/00, C12N5/00												
CC T-type calcium channel												
FH Key Location/Qualifiers												
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1. .7129												
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ORIGIN												
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Score: 11673.00												
Percent Similarity: 97.77%												
Best Local Similarity: 97.73%												
Query Match: 97.05%												
DB: 6												
Gaps: 2												
US-09-611-257A-24 (1-2287) x BD224078 (1-7129)												
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Db	2	TGAC	CGAG	GAGAG	AGATG	AGCGG	CCGAG	AGTCC	GGAC	AGCCCG	TGACTT	61
QY	54	SerSer	ThrThr	CysPro	GlyPro	GlyAla	AlaGly	AlaGly	SerThr	GluLys	Asp	73
Db	62	AGCT	CAAC	GACTGT	CCGGG	CGCGG	CGCGG	CGGAG	GGCGG	GTCG	ACGAA	121
QY	73	roGly	SerAla	AspSer	GluAla	GluGly	LeuPro	TyrPro	AlaLeu	AlaPro	ValAla	93
Db	122	CGGG	CAGCG	CGGACT	CCGAG	CGGAG	GGGCTG	CCGTAC	CCGGCT	AGCCCG	GTGTT	181
QY	93	hePhe	TyrLeu	SerGln	AspSer	ArgPro	ArgSer	TrpCys	LeuArg	ThrVal	CysAsp	113
Db	182	TCTT	CTACTT	GGACCA	GAGAC	AGCCCG	CGGAG	CTGTGT	CTCCG	ACGCT	GTATACC	241
QY	113	roTrp	PheGlu	ArgVal	SerMet	LeuVal	IleLeu	LeuAsn	CysVal	ThrLeu	GlyMet	133
Db	242	CGTG	TTGAG	CGAGT	CAGTAT	GTGTG	TATTT	CTTCA	CTGTG	TGACT	CTGGTATGT	301
QY	133	heArg	ProCys	GluAsp	IleAla	CysAsp	SerGln	ArgCys	ArgIle	LeuGln	AlaPhe	153
Db	302	TCAG	CGCGT	GTAGAC	ATTGCC	CTGTG	ACTCC	CAGCG	CTGCG	ATCTG	CAGGCTTCG	361
QY	153	spAsp	PheIle	PheAla	PhePhe	AlaVal	GluMet	ValIle	YsMet	ValAla	LeuGly	173
Db	362	ATGA	CTTCAT	CTTTG	CCCTT	CTTGT	GTG	GAATG	TGTG	TAAAG	ATGTTG	421
QY	173	lePhe	GlyLys	LysCys	TyrLeu	GlyAsp	ThrTrp	AsnArg	LeuAsp	PhePhe	IleVal	193
Db	422	TCTT	TGGGA	GAATG	TTACT	TGGG	AGAC	ACTT	GGAA	CCGGCT	TGACTTT	481
QY	193	leAla	GlyMet	LeuGlu	TyrSer	LeuAsp	LeuGln	AsnVal	SerPhe	SerAla	ValArg	213
Db	482	TTG	CAGG	ATGCT	GAGAT	GTATTC	GTGAC	CTGC	AGAAC	GTGAC	TTCTCC	541
QY	213	hrVal	ArgVal	LeuArg	ProLeu	ArgAla	IleAsn	ArgVal	ProSer	MetArg	IleLeu	233
Db	542	CAGT	CCGTGT	GTGCG	ACCG	CTCAG	GGCC	ATTAA	CCGGG	TGCC	AGCATG	601
QY	233	alThr	LeuLeu	LeuAsp	ThrLeu	ProMet	LeuGly	AsnVal	IleLeu	LeuCys	PhePhe	253
Db	602	TCA	CATTACT	GTGGA	CACCTT	GTGCT	ATGCT	GGCA	ACGTCT	GCTGT	CTGTTCTTCG	661
QY	253	alPhe	PheIle	PheGly	IleVal	GlyVal	GlnLeu	TrpAla	GlyLeu	LeuArg	AsnArg	273
Db	662	TCTT	TTTCAT	CTTTG	GCATC	GTGG	GGTCC	ACAG	CTGTG	GGGAG	ACTGCTT	721

Qy	273	ysPheLeuProGluAsnPheserLeuProLeuSerValAspLeuGluProTyrTyrGlnT	293
Db	722	GCTTCCTCCCGAAGCTTCAAGCTCTCCCTGAGCGTGGAAGCTGAGCTTATTAACAGA	781
Qy	293	hrGluAsnGluAspGluSerProPheileCysSerGlnProArgGluAsnGluMetArgS	313
Db	782	CAGAGAATGAGACGAGAGCCCTTCATCTGCTCTGAGCCTCGGAGAATGGCATGAGAT	841
Qy	313	ercYsaArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA	333
Db	842	CCTGACGAGAGTGTGCCCACTGCGTGGGAGAGCGGTGGGCCACCTGCAGTCTGG	901
Qy	333	sPTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT	353
Db	902	ACTATGAGACCTATTAACAGTTCCAGCAACACCACCTGTGTCAACTGGAAACCACTATA	961
Qy	353	hrAsnCysSerAlaGlyGluHisAsnProPheIleGlyAlaIleAsnPhesAspAsnIleG	373
Db	962	CCAACCTGCTCTGGCGGCGAGACAACCCCTTCAAGGCGCCATCACTTGACAAACATTG	1021
Qy	373	lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	393
Db	1022	GCTATGCCCTGATCGCCATCTTCCAGTGCATCACACTGAGAGGGCTGGTGCAATCATGT	1081
Qy	393	yrPheValMetAspAlaHisSerPheTyrAsnPhelIeTyrPheIleLeuLeuIleIleV	413
Db	1082	ACTTCGTAATGAGCGCTCACTCTTCTACAACTTCATCTCATCTTCTCTCATTCG	1141
Qy	413	alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT	433
Db	1142	TGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGTGATTGCCACGAGTTCTCCAGA	1201
Qy	433	hrLySGlnArgGluSerGlnLeuMetCArgGluGlnArgValAlArgPheLeuSerAsnAlaS	453
Db	1202	CCAAACAGCGGAGAGTCACTGATGCGGAGAGCAGCGTGTACGATTCCTGTCCAATGCTA	1261
Qy	453	erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLySTyrLeuV	473
Db	1262	GCACCTGGCAAGCTTCTGTGAGCCAGGAGCTGCTATGAGAGACTACTCAAGTACCTGG	1321
Qy	473	alTyrIleLeuArgLySAIAlaAArgArgLeuAlaGlnValSerArgAlaIleGlyValA	493
Db	1322	TGTACATCTCCGAAAAGCAGCCGGAAGCTGGCCAGGTTCTTAAGGCTATAGCGCTGC	1381
Qy	493	rgAlaGlyLeuLeuSerSerProValAlaAArgSerGlyGlnGluProGlnProSerGlyS	513
Db	1382	GGGCTGGGCTGCTCAGCAGCCGAGTGGCCCGTAGTGGGCGAGAGCCCAAGTGGCA	1441
Qy	513	ercYsThrArgSerHisArgArgLeuSerValHisHisIleValHisHisHisHisSH	533
Db	1442	GCTGCACTCGCTCACACCCGTGCTGTCTGTCCACCACCTGTGTCCACCACCATCACACC	1501
Qy	533	ishishishistYrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI	553
Db	1502	ACCATCACCACTACCACTGGGTATGGGAGCGTCAAGATTCCCGGGCCAGCCAGAGGA	1561
Qy	553	leglnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProt	573
Db	1562	TTCAGGACAGGAGTGCCAATGGGTCTGCGCGGCTCATGTACCAACACCTCTACACCCA	1621
Qy	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC	593
Db	1622	CTCCCTCTGGGGGCCCTCCGAGGGGTGGGAGTGTGTACACAGCTTCTTACCATGTGACT	1681
Qy	593	ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG	613
Db	1682	GCCACTTGAGCCAGTCCGTTGCCAGGCAACCCCTCCAGATGCCATCGGAGGATCTG	1741
Qy	613	lyArgThrValGlySerGlyLyValTyrProThrValHisThrSerProProProGluI	633
Db	1742	GTAGACTGTGGGTAGTGGAGAGGTGTACCCCACTGTGCATACCAAGCCCTCCACACAGAGA	1801
Qy	633	leLeuLyAsbPLySAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs	653

Db	1802	TACTGAAGGATTAAGCACTAGTGAAGTGCCCCCAGCCCTGGCCCCCACCCTCACCA	1861
Qy	653	erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT	673
Db	1862	GCTTCAACATCCACACTGGGCCCTTACGCTCCATGCACAAAGCTCCTGGAGACACAGATA	1921
Qy	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
Db	1922	CGGAGCCCTGCCATAGCTCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCACAGTGAAG	1981
Qy	693	laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA	713
Db	1982	CCTGGGGCCGGACAGTTGTCTCCCTACTGTGTCCCGACAGAGCAGAGCAGAGTCCG	2041
Qy	713	laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733
Db	2042	CTGACCATGTATGCTGCTGACTCAGACAGCGAGGCTGTGTATGATTACACAGGACGCTC	2101
Qy	733	lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA	753
Db	2102	AGCACAGTGAACCTCCGGATCCCCACAGCCGCGGAGCAGACAGCGAGCCTGGGCCAGATG	2161
Qy	753	laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV	773
Db	2162	CAGAGCCTAGTTCTGTGCTGGCTTCTGAGGCTGATCTGTACACATTCGGGAAGATCG	2221
Qy	773	alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM	793
Db	2222	TAGATAGCAAAATACTTTGGCCCGGGAATCATGATCCCATCTCGTCAATACACTCAGCA	2281
Qy	793	etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
Db	2282	TGGGCATCGAGTACCACGAGCAGCCGAGAGCTCAACAAGCCCTGGAATCAGCAACA	2341
Qy	813	leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp	833
Db	2342	TGCTCTTACACCAAGCCTTTCGCCCTTGAGATGCTGTGAACCTGTTGTACGCTCCCT	2401
Qy	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT	853
Db	2402	TTGGCTACATTAAGATCCCTACACATCTTGAATGTGTCTATTGTGTCATCAGTGTGT	2461
Qy	853	rpGluIleValGlyGlnGlnGlyGlyLysSerValLeuArgThrPheArgLeuMetA	873
Db	2462	GGGAGATTGTGGGCCAGCAGGAGGTGGCTGTGGTCTGCGACCTTCGCTGATGC	2521
Qy	873	rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893
Db	2522	GGGTGCTGAAGCTGTGTGCGCTTCTGCGCGCCCTGCGACGCCAGCTCGTGTGCTCATGA	2581
Qy	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheHis	913
Db	2582	AGACCATGACAAACGTGGCCACCTTCTGCATGCTCTCATGTGCTTCACTTCACTTCA	2641
Qy	913	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL	933
Db	2642	GCATCCTGGGCATGCATCTCTTGTGTGAAGTTGCATCTGAACGGAGTGGGACAGT	2701
Qy	933	euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953
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Qy	953	euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA	973
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Qy	993	alAlaIleLeuValGluGlyPheGlnAlaGlu-----	1003

Db 2882 TGGCCATTCTTGTGAAGGATTCCAGGCAGAGAAATCGCAACGGAGAGATGCGAGTG 2941
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ORIGIN

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COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buettow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Boufard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2238257
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2 (bases 1 to 7527)
Strausberg,R.
Direct Submission
Submitted (03-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305

web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAK Plate: 114 Row: p Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

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In some sub-families (e.g. Na channels) the domain is
repeated four times, whereas in others (e.g. K channels)
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ORIGIN

Alignment Scores:

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ORIGIN

Best Local Similarity:	96.05%	Mismatches:	43
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US-09-611-257A-24 (1-2287) x BC057399 (1-7527)

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QY	419	eAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlnSerGly	439
Db	1561	-----TTCTCTGAGACCAAGCAACGGAGAGTCA	1589
QY	439	nLeuMetArgGlnGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe	459
Db	1590	GCTGATGCGGAGCAGCGGTGATGATTCCTGTCCAATGCTAGCACCTGGCAAGCTTCTC	1649
QY	459	rGluProGlySerCysTyrGlnGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAl	479
Db	1650	TGAGCCAGGCAGCTGCTATGAGAGCTTCTCAAGTACTGTGTACATCCTCCGCAAGC	1709
QY	479	aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe	499
Db	1710	AGCCCGCAGGCTGGCCAGGCTCTAGGGCTGTAAGCGTGGCGGCTGGTGTCAAGCAG	1769
QY	499	rProValAlaArgSerGlyGlnGlnProGlnProSerGlySerCysThrArgSerHisAr	519
Db	1770	CCCAAGTGTCCGTGGTGGGCGAGAGCCCAAGCCAGCGAGTGGCAGCTGCTCTGTTCAACCG	1829
QY	519	gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisTyrHisLe	539
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QY	539	uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs	559
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QY	559	nGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPr	579
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QY	599	gCysGlnAlaProProProArgCysProSerGlyAlaSerGlyArgThrValGlySerGly	619
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QY	619	YLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe	639
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QY	639	uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGly	659
Db	2190	AGTGAAGGTGCCCCCGCCCTGGGCCCCCACCCTTCAACAGCTTCAACATCCCACTTGG	2249
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Db 3447 ACTGCCCAAGAGCTTCAGACACAGGTGTGGGGGAAGCACTGGGCTCTGGCTCTGCCCGCAC 3506
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Db 3507 CAGTAGCAGTGGGTCCGTGAGCCTGGAATGCTTCATCATGAGATGAATAACCGCCAAG 3566
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Qy	2267	oLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro	2286
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DEFINITION	AF126966	isoform (CACNA1G) mRNA, complete cds.	
ACCESSION	AF126966		
VERSION	AF126966.1	GI:4761540	
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SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
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AUTHORS		1 (bases 1 to 7274)	
TITLE		Monteil,A., Chennin,J., Bourinet,E., Mennesier,G., Lory,P. and Nargeot,J.	
JOURNAL		Molecular and functional properties of the human alpha(1g) subunit	
MEDLINE		that forms T-type calcium channels	
PUBMED		J. Biol. Chem. 275 (9), 6090-6100 (2000)	
REFERENCE		2 (bases 1 to 7274)	
AUTHORS		Monteil,A., Mennesier,G., Bourinet,E., Lory,P. and Nargeot,J.	
TITLE		Direct Submission	
JOURNAL		Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R.	
FEATURES		1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France	
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Qy	82	lyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP	102
Db	324	GGCTGCCGTACCCCGCGCTGGCCCGGTGTTTCTTCTACTTGAGCCAGACAGCCGCC	383
Qy	102	roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV	122
Db	384	CGCGGAGCTGTGTCTCCGACACGGTCTGTAAACCCCTGTGAGCGCATCAGCATGTTGG	443
Qy	122	allleuleuasnCysValThrleuGlyMetPheArgProCysGluAspIleAlaCysA	142

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Pred. No.: 0

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Percent Similarity: 94.75%

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Query Match: 92.18%

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ORIGIN

Db	444	TCATCCTTCTCAACTGCGGTGACCCCTGGGCATGTTCCGGCCATGCGAGGACATCGCCTGTG	503
Oy	142	spSerGlnArgCysArgGileuGlnAlaPheAspSppheilePheAlaPhePheAlaV	162
Db	504	ACTCCAGCGCTGCCGGAATCTGCAGGCGCTTGATGACTTCATCTTGCCCTTTTGCCG	563
Oy	162	alGluMetValValLysMetValAlaleuGlyilePheGlyLysLysCysTyrLeuGlyA	182
Db	564	TGGAGATGGTGTGAAGATGGTGGCCTTGGCATCTTTGGGAAAAAGTGTACCTGGAG	623
Oy	182	spThrTyrAsnArgLeuAspPhePheileValilealaglyMetLeuGluTyrSerLeuA	202
Db	624	ACACTTGGAAACCGGCTTGACTTTTTCATCGTCATCGCAGGAGATGCTGGAGTACTCGCTGG	683
Oy	202	spleuGlnasnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA	222
Db	684	ACCTGCAGAACGTACGCTTCTCAGCTGTGAGACAGATCCGTGTGCTGCCAGCCGCTCAGGG	743
Oy	222	laileAsnArgValProSerMetArgileLeuValThrLeuLeuLeuAspThrLeuProm	242
Db	744	CCATTAAACGGGGTGCCACGCAATGCCATCTTGTCACGTTGCTGCTGATACGCTGCCCA	803
Oy	242	etLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheilePheGlyileValGlyV	262
Db	804	TGCTGGGGCAACGTCCTGCTGCTCTGCTTCTGCTCTTCTCATCTTCGACATCGTCGGCG	863
Oy	262	alGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP	282
Db	864	TCCACGCTGTGGGCAGGCGCTGCTTCGGAACCGATGCTTCTACCTGAGATTTCAGCCTCC	923
Oy	282	roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI	302
Db	924	CCCTGAGCGTGGACCTGGACCGCTATTACAGACAGAGAAGAGATGAGAGCCCTTCA	983
Oy	302	leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG	322
Db	984	TCGTCTCCACGCCACGCGAGAACGCGCATGCGGTCTGCAGAAAGCGTGCCACGCTGCGCG	1043
Oy	322	lyGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSera	342
Db	1044	GGGACGGGGGCGGTGGCCCACTTGCGGTCTGACTATGAGGCTCAACAACAGCTCCAGCA	1103
Oy	342	snThrThrCysValAsnTyrAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnP	362
Db	1104	ACACCACCTGTGTCACTGGAACCACTACTACACCACTGCTCAGCGGGAGACACAACC	1163
Oy	362	roPheLysGlyAlaileAsnPheAspAsnileGlyTyrAlaTsrPileAlailePheGlnV	382
Db	1164	CCTTCAAGGGCGCCATCACTTTGACAACATTGGCTATGCTCGATCGCCATCTTCCAGG	1223
Oy	382	alileThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHisSerPheT	402
Db	1224	TCATCAGCTGAGGGCTGGGTGCATCATGTACTTTGTGATGATGCTCATTTCTTCT	1283
Oy	402	yrAsnPheileTyrPheileLeuLeuileileValGlySerPhePheMetileAsnLeuC	422
Db	1284	ACAAATTTCATCTACTCTCATCTCTTCATCATCATCGTGGCTCCTTCTTCATGATCAACTGT	1343
Oy	422	ysLeuValValileAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMetA	442
Db	1344	GCGTGGGTGATTGCCACGCACTTCTCAGAGACCAAGCAGCGGGGAAAAAGCAGCTGATGC	1403
Oy	442	rgGlnGlnArgValArgPheLeuSerAsnAlaserThrLeuAlaserPheSerGluProG	462
Db	1404	GGGAGCAGCGTGTGCGGTTCTCTGTCCAACGCCAGCACCCGTGGCTAGCTTCTGTAGCCCG	1463
Oy	462	lySerCysTyrGluGluLeuLeuLysTyrLeuValTyrileLeuArgLysAlalaArgA	482
Db	1464	GCAGCTGTATGAGGAGCTGCTCAAGTACCTGCTGATCATCTTCTGTAAGGACGCCGCA	1523
Oy	482	rgLeuAlaGlnValSerArgAlaileGlyValArgAlaGlyLeuLeuSerSerProValA	502
Db	1524	GGCTGGCTCAGGTCCTCTCGGGCAGACGCTGTGCGGTTGGGCTGCTCAGCAGCCACGAC	1583

[illegible]

QY	862	LYLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP	882
DB	2661	GCCTGTGGGTGCTGCGGACCTTCCGCTGATGCGTGTCTGAAGCTGTGCGCTTCTGC	2720
QY	882	roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC	902
DB	2721	CGGCGCTGCAGCGGACGCTGGTGTGCTCATGAAGACCATGACAACGTTGCCACCTTCT	2780
QY	902	YSMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC	922
DB	2781	GCATGCTGCTTATGCTCTTCACTTTCATCTTCAGCATCTCGGGCATGCATCTTGGCT	2840
QY	922	YSLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL	942
DB	2841	GCAAGTTTGCTCTGAGCGGGATGGGGACACCCTGCCAGACCGAAGAATTTGACTTCT	2900
QY	942	euleuTPAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL	962
DB	2901	TGCTCTGGGCCATCGTCACTGTCTTTCAGATCCTGACCAGAGGAGCACTGGAACAAGTCC	2960
QY	962	eUTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT	982
DB	2961	TCTACAATGATAGCGCTCCACGTCGTCCTGGCGGCCCTTATTTCAATGCCCTCAATGA	3020
QY	982	hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA	1002
DB	3021	CCTTCGGCAACTACGTGCTTTCATATTGCTGTGCGCAATTCTGTGAGGGCTTCCAGG	3080
QY	1002	laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG	1022
DB	3081	CGAGGGAGATGCCAACAGTCCGAATCAGAGCCCGATTCTTCAACCCAGCCTGGATG	3140
QY	1022	LYAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA	1042
DB	3141	GTGATGGGGACAGGAAGAGTGTGGCCTTGCTGTGCTTCCCTGGAGAGCACCCGGAGTGC	3200
QY	1042	rgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrPrometSerHisProL	1062
DB	3201	GGAAGAGCCTGTGCGCTTCTTCATCACCACGCGGCCACACCATGTGCTGCCCA	3260
QY	1062	YSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSerS	1082
DB	3261	AGAGCACCGACGCGGCTGGGCGAGGCGCTGGGCGCTGCGCTGCGCCGACCGACGACA	3320
QY	1082	erGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgS	1102
DB	3321	GCGGCTCGGCAGAGCCTGGGCGGGCC--CACAGATGAAGTCAACGCCAGCGCCGCA	3377
QY	1102	erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgA	1122
DB	3378	GCTCTCCGCACAGCCCCCTGGAGCGCTGCAGACGACTGACACGACGAGCGCTCCAGCCGGA	3437
QY	1122	snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL	1142
DB	3438	ACAGCCTCGGCGCTGCACCCACCTGAAGCGGAGAGACCAGTGAAGAGCGCGGTCCC	3497
QY	1142	euleuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluAspArgA	1162
DB	3498	TGTTGTGGGAGAGGCCAGAGAGCCAGGATGAAGAGAGAGACTCAGAAAGAGAGCGGG	3557
QY	1162	laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerS	1182
DB	3558	CCAGCCCTGCGGCACTGACCATCGCCACAGGGGGTCCCTCGAGCGGAGGCCAAGAGTTT	3617
QY	1182	erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS	1202
DB	3618	CCTTTGACCTGCAGACACACTGCAGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAG	3677
QY	1202	erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT	1222
DB	3678	GGTCTGCTTCTGAGCACCGAGACTGCAATGGCAAGTCCGGCTTCAAGGGCGCTGCGCGGG	3737
QY	1222	hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeuS	1242

Db	3738	CCCTGCGCCTGATGACCCCCCACTGGATGGGGATGACGCCGATGACGAGGCAACTGA	3797
QY	1242	erlySGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArgGluA	1262
Db	3798	GCAAGGGGAACGGGTCGGCGGTGATCCGAGCCGCACTCCCTGCTGCTCGAGC	3857
QY	1262	rgASpSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuCysHisA	1282
Db	3858	GAGACTCCTGGTCAGCCTACATCTTCCCTCCTCAGTCCAGGTCCGCGCTGTGTCAAC	3917
QY	1282	rgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysI	1302
Db	3918	GGATCATCACCACAAGATGTTCCAGCACGTGTCTTGTATCATCATCTTCTTAAC	3977
QY	1302	IeThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuT	1322
Db	3978	TCACCATCGCCATGGAGCGCCCAAAATTGACCCACAGCGCTGAACGCACTTCTGA	4037
QY	1322	hrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysValAla	1342
Db	4038	CCCTCTCCAATACATCTTCAACGCACTCTTCTGGCTGAATGACAGTGAAGTGTGG	4097
QY	1342	IaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspG	1362
Db	4098	CACTGGGCTGTGCTTCCGGGAGCAGGCGTACCTGCGAGCAGTTGGAAGCTGTGAGC	4157
QY	1362	IlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyT	1382
Db	4158	GGCTGTGTGCTCATCTCCGTATCGACATTTCTGGTTCATAGTCTCTGACAGCGCA	4217
QY	1382	hrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgV	1402
Db	4218	CCAAGATCTGGGCATGCTGAGGGTGTGCGCTGCTGCGAACCTTGCGCCGCTCAGGG	4277
QY	1402	alIleSerArgAlaGlnGlyLeuLysLeuValAlaGluThrLeuMetSerSerLeuLysP	1422
Db	4278	TGATCAGCCGGCGCAGGGGCTGAAGCTGTGTGGAGACGCTGATGCTTCACTGAAC	4337
QY	1422	roIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyV	1442
Db	4338	CCATCGCAACATGTAGTCATCTGCTGTGCTTCTTCATCATTTCCGCACTTGGGGG	4397
QY	1442	alGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThra	1462
Db	4398	TGCAGCTCTTCAAGGAAGTTTTCGTGTGCCAGGGCGAGATACCAAGAACATCACCA	4457
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LOCUS Homo sapiens low voltage-activated T-type calcium channel alpha 1G
DEFINITION

ACCESSION AFI90860 splice variant CavT.1a (CACNA1G) mRNA, complete cds.
VERSION AFI90860.1 GI:7021332
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Cribbs,L.L., Gomora,J.C., Daud,A.N., Lee,J.H. and Perez-Reyes,E.
TITLE 1 (bases 1 to 7349)
JOURNAL Molecular cloning and functional expression of Ca(v)3.1c, a T-type
MEDLINE calcium channel from human brain
PUBMED FEBS Lett. 466 (1), 54-58 (2000)
10648811
REFERENCE
AUTHORS 2 (bases 1 to 7349)
Cribbs,L.L., Gomora,J.C., Lee,J.-H., Daud,A.N. and Perez-Reyes,E.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-1999) Physiology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA
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ORIGIN
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Best Local Similarity: 93.31% Mismatches: 112
Query Match: 92.18% Indels: 8
DB: 9 Gaps: 4
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Db	3122	CGAGGGAGATGCCAACAAAGTCCGAATCAGAGCCCGATTCTTCTCACCCAGCCTGGATG	3181
QY	1022	lYAspGIYAspArgIySArgIySArgIyAlaLeuValAlaLeuGIyGluHisAlaGluLeuA	1042
Db	3182	GTGATGGGACAGGAAGAGTGTTCCTGGCTTGTTGTCCTGGAGAGACACCCGAGCTGC	3241
QY	1042	rgIySerLeuLeuProProLeuIleIleHisThrAlaAlaThrPrometSerHisProL	1062
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QY	1062	ySSerSerSerThrGIyValGIyGluAlaLeuGIySerGIySerArgArgThrSerSers	1082
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QY	1082	erGIySerAlaGluProGIyAlaAlaHisHisGIuMetIySArgProProSerAlaArgS	1102
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QY	1102	erSerProHisSerProITrpSerAlaAlaAserSerITrpThrSerArgArgSerArgA	1122
Db	3419	GCTCTCCGACAGCCCTTGAGCGCTGCAAGCAGCTGACCAAGCGCTCCAGCCGA	3478
QY	1122	anSerleuGIYArgAlaProSerLeuIySArgArgSerProSerGIyGIyArgArgSerL	1142
Db	3479	ACAGCCTCGCGCTGCACCCAGCCTGAAGCGGAGAGGCCAAAGTGAGAGCGCGGTCC	3538
QY	1142	euleuSerGIyGIyGIyGluSerGIyAspGIyGluGluSerSerGIyGluAspArgA	1162
Db	3539	TGTTGTGGAGAAAGCCAGAGAGAGCCAGATGAAGAGAGAGCTCAGAAGAGAGCGGG	3598
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Db	3599	CCAGCCCTGCGGGCAGTACCATCGCCACAGGGGCTCCTGGAGCGGAGGCCAAGATT	3658
QY	1182	erPheAspLeuProAspIThrleuGluValProGIyLeuHisArgThrAlaSerGIyArgS	1202
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QY	1222	hrLeuArgIThrAspAspProGluLeuAspGIyAspAspAsnAspGIyGluIyAsnLeuS	1242
Db	3779	CCCTGCGGCTGATGACCCCACTGGATGGGATGACGCCGATGACGAGGGCAACTGA	3838
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QY	1262	rgAspSerITrpSerAlaITyrllePheProProGluInsarGArgLeuLeuCysHisA	1282
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QY	1342	laLeuGIyITrpCysPheGIyGIyGluGluAlaITyrlleuArgSerSerITrpAsnValLeuAspG	1362
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QY	1422	roIleGIyAsnIleValIleCysCysAlaPhePheIleIlePheGIyIleuGIyV	1442
Db	4379	CCATCGCAACATTTAGTATCATCTGTGCTGTGCTTCTTATCATTTTCGGCATCTTGGGGG	4438
QY	1442	alGIuLeuPheLysGIyLysPhePheValCysGIuGIyGIuAspThrArgAsnIleThra	1462
Db	4439	TGCAGCTCTTCAAGGGAAGTTTTCGTGTGCCAGGGCGAGGATACCAAGAACATCACCA	4498
QY	1462	snLYsSerAspCysAlaGIuAlaSerTyrArgTrpValArgHisLYeTYrAsnPheAspa	1482
Db	4499	ATAATCGACTGTGCCGAGGCCAGTTACCGTGGGTCCGGCACAACTACACTTTGACA	4558
QY	1482	snLeuGIyGIuAlaLeuMetSerLeuPheValLeuAlaSerLYsAspGIyTrpValAspI	1502
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QY	1642	IaLeuLYsIleCysAsnTyrIlePheThrValIlePheValPheGIuSerValPheLYsL	1662
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QY	1682	IeValLeuLeuSerIleMetGIyIleThrLeuGIuGIuIleGIuValAsnLeuSerLeuP	1702
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QY	1702	roIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLYsL	1722
Db	5219	CCATCAACCCCAACCATCATCCGCATCATGAGGGTGTGGCATTTGCCGAGTGTGAAGC	5278
QY	1722	euleuLYsMetAlaValGIyMetArgAlaLeuLeuHisThrValMetGIuAlaLeuProG	1742

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DEFINITION AR201015
ACCESSION AR201015
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7741)
AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.
TITLE DNA encoding human alpha1G-C T-Type calcium channel
JOURNAL Patent: US 6358706-A 4 19-MAR-2002;
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Score: 11066.50 Matches: 2134
Percent Similarity: 93.81% Conservative: 33
Best Local Similarity: 92.38% Mismatches: 112
Query Match: 92.01% Indels: 31
DB: 6 Gaps: 5
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Db 491 CCGGATCGCCCGGGCCCGGGTGGCCAGAGGATGACGAGAGGAGATGAGCGGGCG 550
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AF126965			
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DEFINITION	Homo sapiens voltage-dependent calcium channel alpha 1g subunit b isoform (CACNA1G) mRNA, complete cds.		
ACCESSION	AF126965		
VERSION	AF126965.1	GI:4761538	
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Monteil,A., Cheman,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.		
TITLE	Molecular and functional properties of the human alpha(1g) subunit that forms T-type calcium channels		
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)		
MEDLINE	20158909		
PUBMED	10692398		
REFERENCE	2 (bases 1 to 7253)		
AUTHORS	Monteil,A., Menessier,G., Bourinet,E., Lory,P. and Nargeot,J.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R. 1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France		
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ORIGIN

Alignment Scores:

Score:	11037.50	Matches:	212
Percent Similarity:	94.45%	Conservative:	34
Best Local Similarity:	92.96%	Mismatches:	112
Query Match:	91.77%	Indels:	15
DB:	9	Gaps:	5

US-09-611-257A-24 (1-2287) x AF126965 (1-7253)

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QY	63	Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGlu	82
DB	264	GCCGGCCGGGGCCGGGGTCAGCAGAAAGAACCCGGGACGGCGGACTCCGAGCGGAGG	323
QY	82	LYLeuProTYrProAlaLeuAlaProValValPhePheTYrLeuSerGlnAspSerArgP	102
DB	324	GGCTGCCGTAACCGGCGCTGGCCCCGGTGTCTTCTTAAGCCAGACAGACCGCC	383
QY	102	roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV	122
DB	384	CGCGGAGCTGTGTCTCCGCACGGCTGTAAACCCCTGGTTGAGCGCATCAGCATGTGG	443
QY	122	AlIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA	142
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QY	142	spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaV	162

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QY	1062	ysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSers	1082
Db	3261	AGAGCACACGACGCGGCTGGGCGAGCGCTGGGCCCTGCGTCGCGCCGACCAAGACA	3320
QY	1082	erGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgS	1102
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QY	1102	erSerProHisSerProTyrSerAlaAlaSerSerTrpThrSerArgArgSerSerArgA	1122
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QY	1122	snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL	1142
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QY	1142	euleuSerGlyGluGlyGlnGluSerGlnAspGluGluLysSerSerGluLysAspArgA	1162
Db	3498	TGTTGTCCGGAGAGGCCAGGAGAGCCAGGATGAAGAGAGAGACTCAGAAGAGAGCGGG	3557
QY	1162	laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSers	1182
Db	3558	CAAGCCTGCGGCGAGTGACCATTCGCCACAGGGGTCCTTGAGCGGGAGGCCAAGACTT	3617
QY	1182	erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS	1202
Db	3618	CCTTTGACCTGCAGACACACTGCAAGTGCAGGGCTGCATCGCACTGCAGTGGCCGAG	3677
QY	1202	erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT	1222
Db	3678	GGTCTGCTTCTGAGCACACGAGACTGCAATGGCAAGTGGCTTCAAGGCGCTGGCCGGG	3737
QY	1222	hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeuS	1242
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QY	1242	erLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArgGluA	1262

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Qy	1382	hrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgV	1402
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Db	4278	TGATCAGCCGGGCGAGGGCTGAAGCTGTGTGTGAGACGCTGATGTCCTCACTGAAC	4337
Qy	1422	roIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyV	1442
Db	4338	CCATCGCAACATGTAGTCATCTGCTGTGCTTCTTCATCATTTTCGCATCTTGGGG	4397
Qy	1442	alGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThra	1462
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Qy	1462	snLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspA	1482
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ACCESSION AR201014
VERSION AR201014.1 GI:20251902
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 6822)
AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.
TITLE DNA encoding human alpha1G-C T-Type calcium channel
JOURNAL Patent: US 6358706-A 3 19-MAR-2002;
FEATURES Location/Qualifiers
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/organism="unknown"
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ORIGIN

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Best Local Similarity: 92.63% Mismatches: 105
Query Match: 91.03% Indels: 31
DB: 6 Gaps: 5

US-09-611-257A-24 (1-2287) x AR201014 (1-6822)

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QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
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QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
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Qy	1070	IuaLaleuGlySerGlySerArgArgThrSerSer	SerGlySerAlaGluProGlyAla	1090
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Qy	1090	laHisHISgluMetLysCysProProSerAla	ArgSerSerProHisSerProTrpSera	1110
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RESULT 14
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LOCUS AF227744 6822 bp mRNA linear PRI 06-MAR-2000
DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1g subunit
isoform ae (CACNA1G) mRNA, complete cds.
ACCESSION AF227744
VERSION AF227744.1 GI:7159260
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 6822) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Montell,A., Chemlin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.
TITLE Molecular and functional properties of the human alpha(1g) subunit that forms T-type calcium channels
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE 20158909
PUBMED 10692398
REFERENCE 2 (bases 1 to 6822)
AUTHORS Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France
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ORIGIN
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QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
|||
Db 1142 TGGGCTCCTTCTTCAATGATCAACCTGTGCTGGTGGTGAATGCCAGCATTCAGAGA 1201
QY 433 hrLySGlnArgGlnSerGlnLeuMetArgGlnGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGGAAGCCAGCTGATGCGGGAGCAGCGTGTGCGGTCTGTCCAACGCCA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
|||

Db 1262 GCACCCCTGGTAGCTTCTTGAGCCCGGACAGCTGTATGAGAGCTGTCAAGTACTGG 1321
QY 473 alTyrIleLeuArgIlyValAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
|||
Db 1322 TGTATCATCCTTCTGTAGGAGCCCGCAGGCTGTGCTCAGTCTCTCGGGCAGCAGTGTGC 1381
QY 493 rGAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
|||
Db 1382 GGGTTGGGCTGCTCAGAGCCCAAGACCCCTCGGGGGCCAGAGAGACCAGCCAGCAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisIleValHisHisHisHisHisH 533
|||
Db 1442 GCTGCTCTGCTCCACCGCGCCTATCGTCCACCACTGTGTGACCAACCACCAACCACC 1501
QY 533 IHisHisHisIstYrHisIleuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
|||
Db 1502 ATCACCACTACTACCACTGGGCAATGGAGCGCTCAGGGCCCCCGGGCCAGCCGAGAGA 1561
QY 553 IeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProT 573
|||
Db 1562 TCCAGACAGAGGATGCCATGGGTCCCGCGGCTCATGTGCCACCACTCGACGCTG 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
|||
Db 1622 CCTCTCCGGGGCCCCCCTGTGTGGCGCAGAGTGTGTGCACAGCTTCTTACATGCCGACT 1681
QY 593 yHisIleuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
|||
Db 1682 GCCATTAGAGCCAGTCCGCTGCGCAGGCGCCCTCCCAAGTCCCATGTGAAGGCATCCG 1741
QY 613 IyArgThrValGlySerGlyLyValTyrProThrValHisThrSerProProGluI 633
|||
Db 1742 GCAGACTGTGGCAGCGGGAAGTGTATCCACCGTGCACACCAAGCCTTCCACCGAGA 1801
QY 633 IeLeuLyAspLyAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
|||
Db 1802 CGCTGAAGAGAAGCAGCATAGAGGTGCTGCCAGCTTGCGCCCCCAACCTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisIlySleuLeuGluThrGlnSert 673
|||
Db 1862 GCCTCAACATCCACCCGGGCCCTTACAGTCCATGCACAAGCTGTGAGACACAGAGTA 1921
QY 673 hrGlyAlaCysHisSerSerCysIlyIleSerSerProCysSerLyAlaAspSerGlyA 693
|||
Db 1922 CAGTGTCTGCCAAAGCTTTCGAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGGAG 1981
QY 693 IaCySGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera 713
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Db 1982 CCTGTGTCCAGACAGAGCTGCCCTACTGTGCCGGCGGGGCGAGGGAGGTGAGCTCG 2041
QY 713 IaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
|||
Db 2042 CCGACCGTGAATGCTGACTGACAGACAGGAGCACTTATGAGTTACACAGGATGCC 2101
QY 733 IHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
|||
Db 2102 AGCACAGCAACTCCGGGAGCCCAACAGC--CGCGGCAACGAGCCTGGGCCAAGATG 2158
QY 753 IaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLySileV 773
|||
Db 2159 CAGAGCCCAAGCTGTGTGCTGGCCTTCTGAGGCTAATCTGTGACACCTTCCGAAGAATTG 2218
QY 773 alAspSerLySTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerm 793
|||
Db 2219 TGGACAGCAAGTACTTGGCCGGGAATCATGATGCCATCTGTGTCAACACACTCAGCA 2278
QY 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
|||
Db 2279 TGGGCATGAATACACAGAGAGCCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACA 2338
QY 813 IeValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
|||
Db 2339 TCGTCTTCAACAGCCTCTTGTGCTGGAAGATGTGCTGAAGCTGTGTGTATGTGTCCT 2398

QY	833	heGLYTrILeLYsAsnProTYrAsnIlePheAspGIValIleValIleSerValT	853
Db	2399	TTGGCTACATCAAGAAATCCCTACAACATCTTCGATGGTGTCAATTGTGTATCATCAGCGTGT	2458
QY	853	rPGluIleValGIgInGIgLYGLyLeuSerValIleuArgThrPheArgLeuMetA	873
Db	2459	GGGAGATCGTGGGCCAGAGAGGGGGCGGCTGTTCGGTGTCTGGACCTTCGCGCTGATGC	2518
QY	873	rgValLeuLYsLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893
Db	2519	GTGTGCTGAAGCTGTGTGCTTCTCTGCGGCGCTGCAGCGGACGCTGGTGTGTCTATGA	2578
QY	893	YsThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
Db	2579	AGACCATGACAACGTGGCCACTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTTCA	2638
QY	913	erIleLeuGLYMetHisLeuPheGLYCYsLYsPheAlaSerGluArgAspGLYAspThrL	933
Db	2639	GCATCCCTGGGCATGCATCTCTCGGCTGCAGATTGGCTCTGAGCGGGATGGGACACCC	2698
QY	933	eUProAspArgLYsAsnPheAspSerLeuLeuTrrPalaIleValThrValPheGlnIleL	953
Db	2699	TGCCAGACCGGAAGATTGTGACTCTTGCTCTGGGCCATGTCTACTGTCTTTCAGATCC	2758
QY	953	eUTHrGlnGLYAspTrpAsnLYsValLeuTYrAsnGLYMetAlaSerThrSerSerTrpA	973
Db	2759	TGACCAGAGAGACTGGACAAGTCCCTTACAATGGTATGGCTCCACGTCGTCTGGG	2818
QY	973	lAAlaLeuTYrPheIleAlaLeuMetThrPheGLYAsnTYrValLeuPheAsnLeuLeuV	993
Db	2819	CGGCCCTTATTATTCATGCGCTCATGACCTTCGCAACTACGTGCTCTTCAATTGTCTGG	2878
QY	993	aLAlaIleLeuValGluGLYpHeGlnAlaGlu-----	1003
Db	2879	TGCGCATTCTGTGTGAGGGCTTCCAGCGGAGAAATCAGCAACGGGAGATGCGAGTG	2938
QY	1004	-----GlyAspAlaThrLYsSerG	1010
Db	2939	GACAGTTAAGCTGTATTACAGCTGCCTGTGCACTCCAGGGGGGAGATGCCAACAAAGTCCG	2998
QY	1010	lUsErGluProAspPhePheSerProSerValAspGLYAspGLYAspArgLYsLYsArgL	1030
Db	2999	AATCAGAGCCCGATTCTTCTTCAACCAGCCTGGATGGTATGGGGAACAGAAAGATGCT	3058
QY	1030	eUAlaLeuValAlaLeuGLYGLYHisAlaGluLeuArgLYsSerLeuLeuProProLeuI	1050
Db	3059	TGGCCTTGGTGTCCCTGGGAGACACCCGAGCTGCGGAAGAGCTGTGCGCGCTTCA	3118
QY	1050	IeIleHisThrAlaIaThrProMetSerHisProLYsSerSerSerThrGLYValGLYG	1070
Db	3119	TCATCCACACGCGCCGCCACACCCATGTGCTGCCCCAAGAGCACACGACGCGCTGGGCG	3178
QY	1070	lUAlaLeuGLYSerGLYSerArgArgThrSerSerSerGLYSerAlaGluProGlyAlaA	1090
Db	3179	AGGCGCTGGGCCCTGCGTCCGCCGCCGACACAGCAGCAGCGGGTCCGACAGAGCTGGGCGG	3238
QY	1090	lAhIshISGLuMetLYsCysProProSerAlaArgSerSerProHisSerProTrpSerA	1110
Db	3239	CC--CACGAGATGAATGACCGCCGACGCGCCGACGCTTCCGACACAGCCCTTGAGCG	3295
QY	1110	lAAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGLYArgAlaProSerL	1130
Db	3296	CTGCAAGCAGCTGGACCAAGCGCTCCAGCCGGAACAGCTTGGCCGTGCACCCAGCC	3355
QY	1130	eULYsArgArgSerProSerGLYGLYArgArgSerLeuLeuSerGLYGLYGLYGLYus	1150
Db	3356	TGAAGCGGAGAGCCCAAGTGGAGAGCGCGGTCCCTGTGTCCGGAGAGGCCAGAGA	3415
QY	1150	erGlnAspGLYGLYGLYSerGLYGLYAspArgAlaSerProAlaGLYSerAspHisA	1170
Db	3416	GCCAGGATGAAGAGGAGCTCAGAAGAGGAGCGGGCCAGCCCTTGGGGCAGTGACCATC	3475

QY	1170	IGHISARGLYSERLEUGLWARGGLUALALYSERSERPHEASPLEUPROASPThrLeug	1190
Db	3476	GCCACAGGGGGTCCCTGGAGCGGGAGGCCAAGATTCTTTGACCTGCCAGACACACTGC	3535
QY	1190	INVALPROGLYLeuHISARGThrAlaSERGLYArgSERSERAlaSERGLuHISGLInaSPC	1210
Db	3536	AGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCAGAGGTCTGCTTCTGAGCACAGGACT	3595
QY	1210	YSASNGLYLysSERAlaSERGLYArgLeuAlaARGThrLeuArgThrAspAspPROGLInL	1230
Db	3596	GCAATGGCAAGTCGGCTTCAGGGCGCCCTGGCCCCGCCCTGCAGCTGATGACCCCCAC	3655
QY	1230	EUASPGLYAspAspAspAsnAspGLUGLYAsnLeuSERLysGLYGLUArgILEGLInaLAT	1250
Db	3656	TGGATGGGATGACGCCGATGACGAGGGCAACTGAGCAAAAGGGGAACGGGTCCGCGCT	3715
QY	1250	TPVALArgSERArgLeuPROAlaCysCysArgGLUArgAspSERTrpSERAlaTYRILEP	1270
Db	3716	GGATCCGAGCCCGACTCCCTGCTGCTGCTGAGCGAGACTCCGTGTCAGCTTACATCT	3775
QY	1270	HEPROPROGLInSERArgPHEArgLeuLeuCYSHISArgILEIleThrHISLysMetPHEA	1290
Db	3776	TCCCTCCTCAGTCCAGGTTCCGCTCCTGTGTACACCGATCATCACCCACAGATGTTGG	3835
QY	1290	SPHISValValLeuValILEIlePHELeuAsnCYsILEThrILEAlaMetGLUArgPROL	1310
Db	3836	ACCACGTGGTCTTGTTCATCATCTTCTTACTGATCACCATCGCCATGAGCGCCCA	3895
QY	1310	YSILEAspPROHISSERAlaGLUArgILEPHELeuThrLeuSERAsnTYRILEPETHRA	1330
Db	3896	AAATGACCCCCACAGCGCTGAACGATCTTCTGACCCTCCAAATTACATCTTCACCG	3955
QY	1330	LAVALPHELeuAlaGLUMETThrValLysValAlaLeuGLYTRPCysPHEGLYGLUG	1350
Db	3956	CAGTCTTTCTGGCTGAATGACAGTGAAGTGGTGGCACTGGGCTGGTGCCTTCGGGAGC	4015
QY	1350	INAlaTYRLeuArgSERSErTrpAsnValLeuAspGLYLeuLeuValLeuIleSERValI	1370
Db	4016	AGGCGTACCTGGGAGACAGTTGGAACGTGCTGACGCGGCTGTGGTGCATCTCCGTCA	4075
QY	1370	LEASPIleLeuValSERMetValSERAspSERGLYThrLysILELeuGLYMETLeuArgV	1390
Db	4076	TCGACATTCTGGTGTCCATGTTCTGTGACAGCGGCACCAAGATCTGGGCGATGCTGAGGG	4135
QY	1390	ALLEuArgLeuLeuArgThrLeuArgPROLeuArgValIleSERArgAlaGLINGLYLeuL	1410
Db	4136	TGCTGCGGCTGCTGGGACCCCTGCGCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGA	4195
QY	1410	YSLeuValValGLUThrLeuMETSERSerLeuLysPROIleGLYAsnILEValValIleC	1430
Db	4196	AGCTGTGTGTGAGACGCTGATGTCTCTACTGAACCATCGGCACATTGTAGTCATCT	4255
QY	1430	YSCysAlaPHEPHEILEIlePHEGLYILEuGLYValGLInLeuPHELysGLYLysPHEP	1450
Db	4256	GCTGTGCCCTTCTTCATCATTTTTCGCACTTTGGGGGTGCAGCTCTTCAAGGGAAGTTT	4315
QY	1450	HEVALCysGLINGLYGuAspThrArgAsnILEThrAsnLysSERAspCysAlaGLUALAS	1470
Db	4316	TCGTGTGCCAGGCGAGGATACCAAGAACATCAACCAATAATCGACTGTGCCAGGCCA	4375
QY	1470	ERTYrArgTrpValARGHISLysTYRAsnPHEAspAsnLeuGLYGLInaLeuMETSerL	1490
Db	4376	GTTACCGGTGGTCCGGCACAAGTACACTTTGACCAACCTTGGCCAGGCCCTGATGTCC	4435
QY	1490	EUPHEValLeuAlaSERLysAspGLYTrpValAspILEMETTYRAspGLYLeuAspAlaV	1510
Db	4436	TGTTGTTTGGCTTCCAAGATGTTGGTGACATCATGTACGATGGGCTGGATGCTG	4495
QY	1510	ALGLYValAspGLINGInPROIleMETAsnHISAsnPROTrpMETLeuLeuTYRPHelLES	1530
Db	4496	TGGCGTGCAGCAGCAGCCCATCATGAACCAACCCCTGATGCTGCTGTACTTCATCT	4555
QY	1530	ERPHELeuLeuILEValAlaPHEPHEValLeuAsnMETPHEValGLYValValGLUa	1550

Db	4556	CGTTCGCTCATTTGGCCCTTCTTGTCTCCTGAACATGTTGTGGGTGTGGTGGAGA	4615
Qy	1550	snPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluLysA	1570
Db	4616	ACTTCCACAAGTGTGGCAGCACACGAGAGGAAGAGGCCCGCGCGGAGAGAAAGC	4675
Qy	1570	rgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnC	1590
Db	4676	GCCTACGAAGACTGGAGAAAGAAGAGAGTAAGAGAAAGCATGGCTGAAGCCAGT	4735
Qy	1590	ysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrs	1610
Db	4736	GCAAACTTACTACTCCGACTACTCCCGCTTCCGGCTCTCGTCCACCACCTGTGCACCA	4795
Qy	1610	erHisTyrLeuAspLeuPheIleThrglyValIleGlyLeuAsnValValThrMetAlam	1630
Db	4796	GCCACTACCTGGACCTTTCATCACAGGTGTCACTGGGCTGAACGTGGTCACCATGGCCA	4855
Qy	1630	etGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIleP	1650
Db	4856	TGGAGCACTACCAGACGCCCCAGATTCTGATGAGGCTCGAAGATCTGCAACTACATCT	4915
Qy	1650	heThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgP	1670
Db	4916	TCACTGTCACTTGTGTCTTGAGTCACTGTTTCAACTGTGGCCTTGTGTTCCGTCCGT	4975
Qy	1670	hePheGlnAspArgTTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyI	1690
Db	4976	TCTTCCAGACAGGTGAACCAAGCTGGACCTGGCCATTGTGCTGTCTCATCATATGGCA	5035
Qy	1690	IeThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgI	1710
Db	5036	TCACGCTGGAGGAATCGAGGTCAACGCTCGTGGCCCATCAACCCACCATCATCCGA	5095
Qy	1710	IeMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetA	1730
Db	5096	TCATGAGGGTGTGCGCATTTGCCAGTGTGAAGCTGCTGAAGATGGCTGTGGGCATGC	5155
Qy	1730	rgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuP	1750
Db	5156	GGGCGCTGTGACACGCGTATGACAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCT	5215
Qy	1750	heMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluC	1770
Db	5216	TCATGTTGTTGTTTTCATCTTTGCAGCTCTGGCGTGAAGCTCTTTGGAGACCTGGAGT	5275
Qy	1770	ysAspGluThrHisProCysGluGluGlyArgHisAlaThrPheArgAsnPheGlyM	1790
Db	5276	GTCAGCAGACACACCCCTGTGAGGGCTGGGCCGTATGCCACCTTCGAACTTTGGCA	5335
Qy	1790	erAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysA	1810
Db	5336	TGGCCTTCTTAACCTCTTCCGAGTCTCCACAGGTGACAAATTGGCAATTATGAAGG	5395
Qy	1810	spProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleT	1830
Db	5396	ACAACCTCCGGGACTGTGACCAGGAGTCCACCTGTACAACACGGTCAATCTCGCCTATCT	5455
Qy	1830	yrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValL	1850
Db	5456	ACTTTGTGTCTTGTGTGTCGACGGCCAGTTCGTGTAAGTCAAGTGTGATCGCCGTGC	5515
Qy	1850	eumetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaG	1870
Db	5516	TGATGAAGCACTGGAGAGAGCAACAAGAGGCCAAGAGAGGCCGAGCTAGAGGCTG	5575
Qy	1870	IuLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProP	1890
Db	5576	AGCTGAGCTGAGATGAAGACCTCAGCCCCCAGCCCCACTTCGCCACTGGGCAGCCCT	5635
Qy	1890	heLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProH	1910

Db	5636	TCCTCTGGCCTGGGGTCGAGGGCCCCGACAGCCCCCGACAGCCCCCAAGCCTGGGGCTCTGC	5695
Qy	1910	iSthrThralaHisIleGIyalaalaSerGIyPheSerIeuGIuHisProThMetValP	1930
Db	5696	ACCCAGCGGCCACCGGAGATCAgCCTCCCACTTTCTCGGAGCACCCCAAGATGCAGC	5755
Qy	1930	roHisProGIuGIuValProValProIeuGIyProAspIeuIeuThrValArgIySerG	1950
Db	5756	CCCAACCCACGAGCTGCCA-----GGACCAAGACTTAAGTGTGTGCGGAAGTCTG	5806
Qy	1950	lyValSerArgThrHisSerIeuProAsnAspSerTyMetCysArgAsnGIySerThra	1970
Db	5807	GGGTGACCGCAACGCACTCTCTGCCAATGACAGCTACATGTGTGCGCATGGAGCACTG	5866
Qy	1970	laGIuArgSerIeuGIyHisArgGIyTrpGIyIeuProIySaIaGIuSerGIySerIleL	1990
Db	5867	CCGAGGGGGCCCTGGGACACAGGGGCTGGGGCTCCCAAGCTCAGTCAGGCTCGCTCT	5926
Qy	1990	euservalHisSerGIuProAlaAspThrSerCysIleIeuGIuIeuProIySaPValH	2010
Db	5927	TGTCGGTTCACCTCCAGCCAGCAGATACAGTACATCCTGCAGCTTCCCAAGATGCAC	5986
Qy	2010	iSTyrIeuIeuGIuProHisGIyAlaProThrTrpGIyAlaIleProIySleuProProp	2030
Db	5987	CTCATCTGTCTCAGCCCCACAGCGGCCCAACTGGGGCACCATCCCAACTGCCCCCAC	6046
Qy	2030	roGIyArgSerProIeuAlaGIuArgProIeuArgArgGIuAlaIleArgThrAsps	2050
Db	6047	CAGAGCGTCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGCGCAATAAGACTGACT	6106
Qy	2050	erIeuAspValGIuGIyIeuGIySerArgGIuAspIeuIeuSerGIuValSerGIyPros	2070
Db	6107	CCTTGAGCGTCAAGGGTCTGGGACGGGGAAAGACCTGCTGGCAGAGGTGAGTGGCCCT	6166
Qy	2070	erCysProIeuThrArgSerSerSerPheTrpGIyIySerSerIleGIuValGIuIuAla	2090
Db	6167	CCCCGGCCCTGGCCCCGGCCTACTCTTTCTGGGGCCAGTCAAGTACCAGGACAGCAGC	6226
Qy	2090	rgSerGIyIleGIuSerIyValSerIyHisIleArgIeuProAlaProCysProGIyL	2110
Db	6227	ACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCCAGCCCTTGCCAGGCC	6286
Qy	2110	eugIuProSerTrpAlaIyAspProProGIuThrArgSerSerIeuGIuIeuAspThrG	2130
Db	6287	CAGAACCACCACTGGGGCAAGGGCCCTCCAGAGACCAGAAGCAgCTTAAGTTGACACGG	6346
Qy	2130	IuIeuSerTrpIleSerGIyAspIeuIeu---ProSerSerGIuGIuProIeuPheP	2149
Db	6347	AGCTGAGCTGGATTTCAGGAGACCTCTGCCCCCTGGCGGCCAGAGGAGGCCCATCCC	6406
Qy	2149	roArgAspIeuIySlyCysTyrSerValGIuThrGIuSerCysArgArgArgProGIyP	2169
Db	6407	CACGGACCTGAAGAAGTGCTACAGCGGTGAGGGCCACAGAGCTGCCAGCGCCGCCACGT	6466
Qy	2169	heTrpIeuAspGIuGIuArgArgHisSerIleAlaValSerCysIeuAspSerGIySerG	2189
Db	6467	CCTGGCTGATGAGCAGAGAGACACTATGCGCGTCAAGTGCCTGGACAGCGGCTCCC	6526
Qy	2189	IuProArgIeuCysProSerProSerSerIeuGIyGIyGIuProIeuGIyGIyProGIyS	2209
Db	6527	AACCCACCTGGGCAAGACCCCTTAACCTTGGGGGCCAGCCTTGGGGGGCCTGGGA	6586
Qy	2209	erArgProIySlySlyIeuSerProProSerIleSerIleAspProProGIuSerGIuG	2229
Db	6587	GCTGGCCCAAGAAAAAATCAGCCCGCCTAGTATCACCATAGACCCCCCGAGAGCCAAG	6646
Qy	2229	IySerArgProProCysSerProGIyValCysIeuArgArgArgAlaProAlaSerAsps	2249
Db	6647	GTCCTCGACCCCGCCAGCCCTGTATCTGCTCCGAGAGGGGCTCCGTCCAGGACT	6706
Qy	2249	erIyAspProSerValSerSerProIeuAspSerThrAlaIaSerProSerProIySlyL	2269
Db	6707	CCAAGATCCCTTGGCCTTGGCCCCCTGACAGCATGCGTGCCTGCCCTCCCAAGA	6766

[illegible]

EA0CKPYSYDSRFRLLVHHLCTSHYLDFTIGVIGLNVYTMAMEHYQ0PQILDEALK
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INPTIRIMRVLIRARVLLKLAQVGRALDLTVMQALPV0GNI0GLLPMLLPFI PAAL
GVELFGDCEDETHPC0EGLRHFTRFN0GMAFILTFRVSTGDNNGIMKDTLRDCE0E
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I0V0SCD0G0PHL0GT0DPSN0LG0P0G0P0R0PKK0L0SP0S0IT0D0P0ES0G0R0TP0P0SP
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ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	6897
Score:	10936.00	Matches:	2111
Percent Similarity:	93.01%	Conservative:	32
Best Local Similarity:	91.62%	Mismatches:	105
Query Match:	90.92%	Indels:	56
DB:	9	Gaps:	5

US-09-611-257A-24 (1-2287) X AF227746 (1-68977)

34 TTTThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53

2 TGGACGAGGAGGATGGAGCGGCGCGGAGGATCGGACAGCCCGGAGCTTCAAGC 61

Qy 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 62 GGCTCAACGACTGTGGGGGCCGGGGCCGGCCGGGGCGTCAGCAGAAAAAGACC 121

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Qy      73 roGlyserAlaaspSerGluaglGlyLeuProIyrProAlaLeuAlaProValValP 93
Db      122 CGGGCAAGCCGACTCCGAGGCGGAGGGGCTGCCGTACCCGCGCTGGCCCCGGTGT 181
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QY 93 hePheTYrLeuSerGIAspSeraArgProARgSerTTPCySleuAArgThrValCysAsnP 113
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Db 182 TCtTTCTACTTGAGCCAGGACAGCCGCCCGGAGCTGGTGTCTCCGCACGGTCTGTAAc 241

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Qy      113  roTPheGLuArqValSerMetLeuValIleLeuLeuAbnCyValThrLeuGLyMeCP 133
      |||||::|||
Db      242  CCTGTTTGAGCGCATCAGCATGTGGTCATCCTTCTCACTGCGTGACCCGCGCATGT 301
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Oy      133 hearProCysGluAspIleAlaCysaspSerGlnArgCysArgIleLeuGlnAlaPhea 153
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Db       302 TCCGCCATGCAGACATCGCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCTTTG 361
```

Qy	153	spaspPheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGlyI	173
Db	362	ATGACTTCATCTTTGGCTTCITTTGCCGTGAGATGCTGTGTCAGATGCTGGCCTTGGGCA	421

[illegible]

QY 193 lealaglymetleuglutyrsersleuaspplenglansvalserpheseralavalargt 213

Db 482 TCGCAGGATGCTGCAGTACTCGCTGGAACCTGCAGACTTCTCAGCTGCAGA 541

QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233

QY 233 a lThrIeuLeuLeuAspThrIeuProMetLeuGlyasnValIeuLeuLeuCysPhePheV 2533

Qy 253 a l P h e p e i l e p h e g l y l e v a l g l n l e u t r p a l a g l y l e u l e u a r g a s n a r g c 273
 |||||
 Db 662 T C T T C T T C A T C T T C G G C A T C G T C G C C G T C C A G C T G T G G C A G G C T G C T T C G G A C C G A T 721

QY	273	ysPheLeuProGluAsnPheserLeuSerValaspLeuGluProTyrTyrGlnT	293
Db	722	GCTTCCTACCTGAGATTTCAGCCTCCCCCTGAGCGTGAGCCTGAGCGCTATTACAGA	781
QY	293	hrcGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS	313
Db	782	CAGAGAACGAGGATGAGAGCCCTTCATCTGTCTCCAGCCACGCGAGAACGGCATGCCGT	841
QY	313	erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA	333
Db	842	CCTGCAGAAGCGTCCACCGCTGCGCGGGAGCGGGCGGTGGCCACCTTGCGGTCTGG	901
QY	333	spTyrgLutThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT	353
Db	902	ACTATGAGGCCTACAAACAGCTCCAGCAACACCACCTGTGTCAACTGGAACCACTACA	961
QY	353	hrAsnCysSerAlaGlyGlyHisAsnProPheLysGlyAlaIleAsnPhesAspAsnIleG	373
Db	962	CCAACCTGCTCAGCGGGGAGCACAAACCTTCAGAGGGCCCATCACTTGACACACATTG	1021
QY	373	lyTyraIatRPIleAlaIlePheGlnValIleThrLeuGlnGlyTrpValAspIleMetT	393
Db	1022	GCTATGCCCTGATCGCCATCTTCCAGGTATCAGCTGAGGGCTGGTGACATCATGT	1081
QY	393	yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIleV	413
Db	1082	ACTTGTGATGATGCTCATCTCTTCTACAAATTTCATCTACTCATCTCCTCATCATCG	1141
QY	413	alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheserGluT	433
Db	1142	TGGGCTCTTCTTCATGATCAACCTGTGCTGTGTGATGCCACGCAGTTCTCAGAGA	1201
QY	433	hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS	453
Db	1202	CCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGGTGCGGTTCTGTCCAACGCCA	1261
QY	453	erThrLeuAlaSerPheSerGluProGlySerCysTyrGlnGluLeuLeuLysTyrLeuV	473
Db	1262	GCAACCTGGCTAGCTTCTGTAGCCCGGCAGCTGCTATGAGAGCTGCTCAAGTACCTGG	1321
QY	473	alTyrIleLeuArgLysAlaAlaArgLeuAlaGlnValSerArgAlaIleGlyValA	493
Db	1322	TGTATCATCTTCTGTAAGCAGCCCGCAGCTGGCTCAGGTCTTCGGGCAGCAGGTGTGC	1381
QY	493	rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS	513
Db	1382	GGGTTGGGCTGCTCAGCAGCCCAAGCAACCTCGGGGCCAGAGAACCCAGCCAGCAGCA	1441
QY	513	erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH	533
Db	1442	GCTGCTCTCGCTCCACCGCGCCTATCCGTCACCAACCTGTCACCAACCAACCAACC	1501
QY	533	leHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI	553
Db	1502	ATCACCAACCACTACCACTGGGCATGGGACGCTCAGGGCCCCCGGGGCCAGCCCGAGA	1561
QY	553	leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProt	573
Db	1562	TCCAGGACAGGATGCCAATGGTCCCGCGGCTCATGTGCCAACCCCTGACGCGCTTG	1621
QY	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC	593
Db	1622	CCCTCTCCGGGGCCCCCCTGTGGCGCAGAGTGTGTGACACAGCTTTCACCATGCCGACT	1681
QY	593	ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG	613
Db	1682	GCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCATCTGAGGCATCCG	1741
QY	613	lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI	633
Db	1742	GCAGGACTGTGGGCAGCGGGAAGGTATTCACCGTGACACACCAACCTCCACCGGAGA	1801
QY	633	leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThS	653

Db	1802	CGCTGAAGAGAGACGACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACCA	1861
Qy	653	erPheAsnIleProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSert	673
Db	1862	GCCTCAACATCCACCCTGGGCCCTACAGCTCCATGCACAAGCTGCTGGAGACACAGATA	1921
Qy	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
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Qy	693	IaCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera	713
Db	1982	CCTGTGTGCCAGACAGCTGCCCTACTGTGTGCCGGGCCGGGGCAGGAGGTGGAGCTCG	2041
Qy	713	IaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733
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Qy	733	IhHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA	753
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Qy	793	etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
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Db	2819	CGGCCCTTATTATTCATGCTCTCATGACCTTCGGCACTACGTGCTCTTCAATTGCTGG	2878
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-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09611257@cgn.1.1_3609@runat.15092005_134300_25163 -NCPU=6 -ICPU=3
-NO_MMWP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12024	100.0	7540	5	AAF31677 Rat alpha
2	11980	99.6	6942	13	ADSI16295 Rat volta
3	11829	98.3	7286	3	AAZ52309 Rat pancr
4	11798	98.1	6762	2	AAx83485 Rat T-typ
5	11767	97.8	6816	2	AAx83487 Rat T-typ

6	11751.5	97.7	6795	2	AAx83486 Rat T-typ
7	11747.5	97.7	6741	2	AAx83488 Rat T-typ
8	11066.5	92.0	7741	4	AAD04756 Human T-t
9	10970	91.2	6750	2	AAx83481 Human T-t
10	10946	91.0	6804	2	AAx83483 Human T-t
11	10923.5	90.8	6783	2	AAx83482 Human T-t
12	10919.5	90.8	6729	2	AAx83484 Human T-t
13	10916	90.8	6892	5	AAF31684 Human alp
14	10845.5	90.2	7648	13	ADQ89063 Human uro
15	10845.5	90.2	7648	13	ADSI16298 Human vol
16	10843.5	90.2	8002	4	AAH98402 Human EST
17	6248	51.9	8447	5	AAF31678 Rat alpha
18	6243	51.9	7898	2	AAx59081 Human act
19	6242	51.9	7898	8	ABZ58365 Human T-t
20	6241	51.9	7898	2	AAx59080 Human act
21	6103	50.7	3993	4	AA501624 Human T-t
22	5895	49.0	6132	2	AAx83489 Human T-t
23	5886	48.9	6114	2	AAx83490 Human T-t
24	5738.5	47.7	6941	2	AAx59082 Human act
25	5432.5	45.2	6990	13	ADSI16296 Human vol
26	5420	45.1	6816	6	AA516826 Human T-t
27	5420	45.1	6816	8	ABX93560 Human CDN
28	5420	45.1	6816	12	ADH69264 Human TCC
29	5420	45.1	6855	6	AA516827 Human T-t
30	5420	45.1	6855	8	ABX93561 Human CDN
31	5420	45.1	6855	12	ADH69266 Human TCC
32	5407	45.0	6503	12	ADH69275 Human T-t
33	5346.5	44.5	5469	2	AAx83491 Human T-t
34	5345	44.4	5505	2	AAx83492 Rat T-typ
35	5200.5	43.2	5735	5	AAf31679 Rat brain
36	3950	32.8	5562	2	AAV57542 Human cal
37	3950	32.8	5562	5	AAf31674 Human alp
38	3937.5	32.7	7969	4	ABL07263 Drosophila
39	3861.5	32.1	6073	13	ADSI16299 C. elegans
40	3399.5	28.3	6933	5	AA575141 DNA encod
41	3356	27.9	2212	5	AAf31681 Human alp
42	2091.5	17.4	3464	4	AAx94358 Human ful
43	2091.5	17.4	3464	12	ADL31040 Full leng
44	1974	16.4	1669	2	AAx59083 Human act
45	1751.5	14.6	7362	2	AAQ37817 sequence

ALIGNMENTS

RESULT 1	AAf31677	standard; cDNA; 7540 BP.
ID	AAf31677	
XX	AAf31677;	
AC	XX	
DT	09-APR-2001	(first entry)
XX	XX	
DE	Rat alpha-IG calcium channel cDNA.	
XX	XX	
KW	Rat; expressed sequence tag; EST; antiarrhythmic; anticonvulsant;	
KW	hypotensive; cardiant; nootropic; T-type calcium channel subunit;	
KW	cardiac hypertrophy; cardiac arrhythmia; hypertension; sleep disorder;	
KW	epilepsy; alpha-IG calcium channel; ss.	
XX	XX	
OS	Rattus sp.	
XX	XX	
PN	W0200102561-A2.	
XX	XX	
PD	11-JAN-2001.	
XX	XX	
PF	04-JUL-2000; 2000WO-CA000794.	
XX	XX	
PR	02-JUL-1999; 99US-00346794.	
XX	XX	
PA	(NEUR-) NEUROMED TECHNOLOGIES INC.	
XX	XX	
PI	Snutch TP, Baillie DL;	
XX	XX	

DR WPI: 2001-123111/13.
DR P-PSDB; AAB66475.
XX Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.
XX
PS Example 2; Page 61-63; 103pp; English.
XX
CC The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha-1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy

XX SQ Sequence 7540 BP; 1502 A; 2313 C; 2161 G; 1564 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 7540
Score: 12024.00 Matches: 2286
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.97% Indels: 0
DB: Gaps: 0

US-09-611-257A-24 (1-2287) x AAF31677 (1-7540)

QY 1 MetIeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg 20
DB ATGCTCCCCACCGGGTCCCGGTGGTGAGACACCTCTGTAGGGGCTCCGCTCGC 444
QY 21 ProSerSerAspProProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGlu 40
DB CCTCTTCGGACCCCGGGGCCCCGGCTGGCCAGAGATGGACGAGGAGGATGGAG 504
QY 41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCysProGly 60
DB CGGGGCGCGAGGAGTGGGACAGCCCGTAGCTTCA CGAGCTCAACGACTGTCCGGGG 564
QY 61 ProGlyAlaAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGluAla 80
DB CCGGGGGCGGCGAGGGCCGGGTGACGAAAGGACCCGGGCGAGCGGGA CTCCGAGCGG 624
QY 81 GluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSer 100
DB GAGGGGCTGCCGTACCCGGGCTAGCCCGGTGTTTCTTCTACTTGAGCCAGAGACG 684
QY 101 ArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGlnArgValSerMet 120
DB CGCCCGCGGAGCTGTGTCTCCGACGCTGTGTAA CCGTGTTCGAGGAGTCAGTATG 744
QY 121 LeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGlnAspIleAla 140
DB CTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATGTTCA GGCCTGTGAGACATTGCC 804
QY 141 CysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePhe 160
DB TGTGACTCCAGCGCTGCCGATCTGTGAGGCTTTCATGACTTCATCTTTCCTTT 864
QY 161 AlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeu 180
DB GGTGTGAAATGTGTGTGAAGTGTGCTTGGCATCTTTGGGAAATGTTACCTG 924
QY 181 GlyAspThrTyrAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer 200
DB GGAGACACTTGGAACCGGCTTGACTTTTTCATTGCA TTGACAGGATGCTGAGTATTCG 984
QY 201 LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu 220

DB 985 CTGACCTGCAGAACGTACGTTCTCCGCACTCAGACAGAGTCGCTGCGACCGCTC 1044
QY 221 ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrLeu 240
DB AGGGCATTAACGGGGTGCCCGAGCATGGCATTTCTGTCA CATTACTGTGACACCTTG 1104
QY 241 ProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVal 260
DB CCTATGCTGGGCAAGTCTGCTGTCTGTCTTCTTTCATCTT TGCAATCGT 1164
QY 261 GlyValGlnLeuTyrPalaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer 280
DB GGCGTCCAGCTGTGGGCAAGACTGCTTCCCAACCGGTCTTCTCCCGAGAACTTCAGC 1224
QY 281 LeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPro 300
DB CTCCCTGAGCGTGAGACCTGAGCCTTATTACAGACAGAGATGAGAGAGAGCCCC 1284
QY 301 PheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeu 320
DB TTCATCTGCTCTGACCTCGGAGAAATGCGATGATCCTGCA GAGTGTGCCACACTG 1344
QY 321 ArgGlyGluGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSer 340
DB CGTGGGGAAGCGGTGTGGCCCAACCTGCAGTCTGACTATGAGACCTATAACAGTTCC 1404
QY 341 SerAsnThrThrCysValAsnTyrAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHis 360
DB AGCAACACCACCTGTGTCACTGGAACCACTACTATACCA CACTGCTCGCGGCGAGCAC 1464
QY 361 AsnProPheIleGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTyrIleAlaIlePhe 380
DB AACCCTTCAAGGCGCCATCACTTGCACAACATTGGCTATG CCGATCGCATCTTC 1524
QY 381 GlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHisSer 400
DB CAGGTATCACACTGAGGCGTGGGTGCAATCATGTACTTGT AATGACGCTCACTCC 1584
QY 401 PheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsn 420
DB TTCTACAACCTTACTTCACTTCTTCATCATCGTGGCTCTT CTTCATGATCAAC 1644
QY 421 LeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeu 440
DB CTGTGCTGTGTGTGATGGCCACGCACTTCTCCGAGACCA AAGCGGAGAGTCACTG 1704
QY 441 MetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGlu 460
DB ATCGGGAGCAGCGTGTACGATTCTGTCCAATGCTTAGCA CCGCTGGCAAGCTTCTTGAG 1764
QY 461 ProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAla 480
DB CCAGCAGCTGTATGAGAGCTACTCAAGTACCTGTGTACAT CTTCCGAAAAGCAGCC 1824
QY 481 ArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerPro 500
DB CGAAGCTGGCCAGGTCTCTAGGGCTATAGGCGTGGGCTG GCTGCTCAGCAGCCCA 1884
QY 501 ValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArg 520
DB GTGGCCGTA GTGGGCAAGAGCCCAAGTGGCAGCTGCACT CGCTCACACCGTGTGT 1944
QY 521 LeuSerValHisIleLeuValHisHisHisHisHisHisHisHisTyrHisLeuGly 540
DB CTGTCTGTCCACCACTGTGTCCACCACTACCAACCACTAC CACTACCACTGCGGT 2004
QY 541 AsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGly 560
DB AATGGAGCGCTCAGATTCCCGGGCCAGCCCAAGATCCAG AACAAGGATGCCAATGGG 2064
QY 561 SerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArg 580
DB TCTCGCGGCTCATGTACTACCAACCACTCTACACCACTCC TCTGTGGGGCCCTCCGAGG 2124

QY	581	GLYAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCys	600
Db	2125	GGTGGGAGTCTGTACACAGCTTCTACCATGTGACTGCCACTTGAGCCAGTCCGTTGC	2184
QY	601	GlAlaAProProProAArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLys	620
Db	2185	CAGGCACCCCTCCAGATGCCCATCGGAGGCATCTGGTAGGACTGTGGGTAGTGGGAAG	2244
QY	621	ValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuVal	640
Db	2245	GTTGATCCCACTGTGCATACACAGCCCTCCACCAAGATACTGAAGATMAACCACTAGTG	2304
QY	641	GluValAlaProSerProGlyProProProThrLeuThrSerPheAsnIleProProGlyPro	660
Db	2305	GAGGTGCCCCCAGCCCTGGGGCCCCCACCCTCAACCACTTCAACATCCCACTGGGCC	2364
QY	661	PheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCys	680
Db	2365	TTCAGCTCCATGCACAGACTCCTGGAGACACAGAGTACGGGAGCCTGCCATAGCTCCTGC	2424
QY	681	LysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysPro	700
Db	2425	AAATATCTCAGCCCTTGTCTCCAAAGGCAGACAGATGGAGCCTGCGGGCCGGACAGTTGTCC	2484
QY	701	TyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSer	720
Db	2485	TACTGTCCCCGACAGAGACAGAGAGCCAGATGCCGTGACCATGTCAATGCTGTACTCA	2544
QY	721	AspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro	740
Db	2545	GACAGCGAGGCTGTGTATGAGTTCAACACAGACGCTCAGCACAGTACCTCCGGGATCCC	2604
QY	741	HisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAla	760
Db	2605	CACAGCCGGCGGCGACAGCCGAGCCCTGGGCCAGATGACAGACCTAGTTCTGTGCTGGCT	2664
QY	761	PheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArg	780
Db	2665	TTCTGGAGGCTGATCTGTACACATTCCGGAAGATCGTAGATAGCAATACTTTGGCCCGG	2724
QY	781	GlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGln	800
Db	2725	GGAATCATGATCGCCATCTGTGTCAATACACTCAGCATGGGCATCGAGTACCAGAGCAG	2784
QY	801	ProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAla	820
Db	2785	CCCGAGGAGCTCACCAACGCCCTGGAATCAGCAACATCGTCTTACCAGCCTCTTCGCC	2844
QY	821	LeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyr	840
Db	2845	TTGGAGATGCTGCTGAACCTGCTTGTCTACGGTCCCTTTGGCTACATTAGAATCCCTAC	2904
QY	841	AsnIlePheAspGlyValIleValValIleSerValTyrGluIleValGlyGlnGly	860
Db	2905	AAACATCTTGATGGTGCATTGTGTGCATCAGTGTGTGGAGATTGTGGCCAGAGGGA	2964
QY	861	GlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPhe	880
Db	2965	GGTGGCCTGTGCTGCTGCGGACCTTCCGCTGATGCGGTGCTGAAGCTGTGCGCTTC	3024
QY	881	LeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThr	900
Db	3025	CTGCCGGCCCTGCAGCGCCAGCTCGTGTGCTCATGAAGACCATGACAACGTGGCCACC	3084
QY	901	PheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPhe	920
Db	3085	TTCTGCATGCTCTCATGCTGTTCATCTTCAATCTTCAAGCATCTGGGCATGCATCTCTT	3144
QY	921	GlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAsp	940
Db	3145	GGTTGCAAGTTGCGATCTGAACGGGATGGGACACGTTGCCAGACCCGGAAGATTTCGAC	3204

QY	941	SerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLys	960
Db	3205	TCCCTGCTCTGGGCCATCGTCACTGCTTTCAAGATTGACTCAGAGAGACTGGAAATAAA	3264
QY	961	ValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeu	980
Db	3265	GTCTCTTACAAACGGCATGGCTTCCACATCGTCTTGGGCTGCTTTACTTCAATGCCCTC	3324
QY	981	MetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGlnGlyPhe	1000
Db	3325	ATGACTTTTGGCAACTATATGTCTTTAACCTGTGTGGCCATTCTTGTGGAAGATTTC	3384
QY	1001	GlnAlaGlnGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerVal	1020
Db	3385	CAGGACAGAGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTCTTTTCGCCAGTGTG	3444
QY	1021	AspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGlnHisAlaGln	1040
Db	3445	GATGTTGATGGGACAGAAAGACCGCTTGGCCCTGTGTGCTTGGAGAACACGGGAA	3504
QY	1041	LeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHis	1060
Db	3505	CTACGAAGACCTTTTGGCACCCCTCATCATCATACGGCTGCGACACCAATGTACAC	3564
QY	1061	ProLysSerSerSerThrGlyValGlyGlnAlaLeuGlySerGlySerArgArgThrSer	1080
Db	3565	CCCAAGAGCTCCAGCACAGAGTGTGGGGAAAGACATGGGCTTGACTTCGACGTACAGT	3624
QY	1081	SerSerGlySerAlaGluProGlyAlaAlaHisHisGlnMetLysCysProProSerAla	1100
Db	3625	AGCAGTGGGTCCGCTGAGCCTGAGCTGCGCCACCATGAGATGAATGTCCGCCAAGTCC	3684
QY	1101	ArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSer	1120
Db	3685	CGCAGCTCCCGCACAGTCCCTGAGTGGCGCAAGCAGCTGGAACACAGAGCGCTCCAGC	3744
QY	1121	ArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGlnArgArg	1140
Db	3745	AGGAACAGCCTGGGGCCGGGCCCCAGCCTTAAAGCGAGAGCCCGAGCGGGAGCGGAG	3804
QY	1141	SerLeuLeuSerGlyGlnGlnGlnLysSerGlnAspGlnGlnLysSerSerGlnGlnAsp	1160
Db	3805	TCCCTGCTGTCTGAGAGAGGGCCAGAGAGTCAAGATGAGAGAGAAATTCAAGAGAGAC	3864
QY	1161	ArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGlnArgGlnAlaLys	1180
Db	3865	CGGGCCAGCCCAAGCAGGCAAGTACCATCGCCACAGGGGTTCTTGGAACTGAGGCCAAG	3924
QY	1181	SerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGly	1200
Db	3925	AGTTCCTTTGACTGCTGACACCTCTGACAGTGCAGGCGGCTGCAACGCACAGCCAGCGGC	3984
QY	1201	ArgSerSerAlaSerGlnHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAla	1220
Db	3985	CGGAGCTCTGCTCTGAGACCAAGACTGTAATGGCAAGTCGGCTTCAAGGCGTTGGCC	4044
QY	1221	ArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGlnGlyAsn	1240
Db	4045	CGCAACCTGAGGACTGATGACCCCACTGATGGGATGGGATGATGACAATGATGAGGGAAT	4104
QY	1241	LeuSerLysGlyGlnArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArg	1260
Db	4105	CTGAGCAAGGGGAACGATACAAAGCCTGGGTGAGATCCCGGCTTCTGCTGTCGCCGA	4164
QY	1261	GluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuCys	1280
Db	4165	GAGCGAGATTCTGTGTGGCTATATCTTCTCTCCTCAGTCAAGGTTTGTCTCTGTGT	4224
QY	1281	HisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsn	1300
Db	4225	CACCGATCATCAACCAAGATGTTTGACCATGTGTGTCTCTCATCATCTTCTCTAAC	4284
QY	1301	CysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGlnArgIlePhe	1320

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Db 4285 TGTATCAACCATCGCTATGAGCGCCCCAAAATTGACCCCAAGCGGCTGAGCGCATCTTC 4344
Qy 1321 LeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysVal 1340
Db 4345 CTGACCCCTCTCCAACCTACATCTTCACGGCAGICTTTTCTAGCTGAATGACAGTGAAAGGTG 4404
Qy 1341 ValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeu 1360
Db 4405 GTGGCACTGGGCTGTGTCTTGGGGAGCAGGCGCTACCTGCGCAGCAGCTGGAATGTGCTG 4464
Qy 1361 AspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSer 1380
Db 4465 GACGGCTTGCTGGTGCATCTCCGTCATCGACATCCTGGTCTCCATGGTCTCCGACAGC 4524
Qy 1381 GlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeu 1400
Db 4525 GGCACCAAGATCCTTGGCATGCTGAGGGTGTGCGGCTGCTGCGGACCCCTGCGTCCACTC 4584
Qy 1401 ArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeu 1420
Db 4585 AGGGTCATCAGCCGGGCCAGGGAAGCTGAGCTGTGTAGAGACTCTGTATGTCATCCCTC 4644
Qy 1421 LysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeu 1440
Db 4645 AAACCCATGGCAACATGTGTGTCATTTGCTGTGTCAGGGTGAGAGACACAGAACTTC 4704
Qy 1441 GlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyLysAspThrArgAsnIle 1460
Db 4705 GGGGTGCAGCTCTTCAAGGGAAGTTCTTCTGTGTGCAGGGTGAGAGACACAGAACTTC 4764
Qy 1461 ThrAsnLysSerAspCysAlaGlnAlaIleSerTyrArgTrpValArgHisLysTyrAsnPhe 1480
Db 4765 ACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGATGGGTCCGCGACAAAGTACAACCTTT 4824
Qy 1481 AspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpVal 1500
Db 4825 GACAACTGGGCCAGGCTGTGATGTCCCTGTTTGTGCTGGCCTCCAAGATGTTGGGTT 4884
Qy 1501 AspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHis 1520
Db 4885 GACATCATGTATGATGGGTGGATGCTGTGGGTGGATCAGCAGCCCATCATGAACCAAC 4944
Qy 1521 AsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeu 1540
Db 4945 AACCCCTGGATGCTGTATACTTCATCTCTCTCTCTCATCGTGGCTTCTTGTCTCTG 5004
Qy 1541 AsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGlu 1560
Db 5005 AACATGTTTGTGGCGTGTGGTGAGAACTTCCATTAAGTGACAGACAGACCAGAGAGAG 5064
Qy 1561 GluGluAlaArgArgGluGluLysArgLeuArgLeuGluLysLysArgArgSer 1580
Db 5065 GAGAGGCGAGGGCGGTGAGAGAGAGCACTACGAGGCTGAGAAAGAGAGAGAGT 5124
Qy 1581 LysGluLysGlnMetAlaGlnAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1600
Db 5125 AAGGAGAAAGCAGATGGCCGGAAGCCCAAGTGCAAGCCCTACTACTGTGACTCTCGAGATTTC 5184
Qy 1601 ArgLeuLeuValHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1620
Db 5185 CGGCTCTTGTCCACCACTGTGTATCCAGCCACTACCTGGAACCTCTTCATCACTGGTGTTC 5244
Qy 1621 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1640
Db 5245 ATCGGCTGAACGTGTGTACTATGGCCATGGAACATTACAGCAGGCCCATCTCTGAGC 5304
Qy 1641 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPhe 1660
Db 5305 GAGGCTCTGAAGATCTGCATTACATCTTACCGTCATCTTGTCTTGAAGTCAAGTTTTC 5364
Qy 1661 LysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu 1680
|||||

Db 5365 AAACCTTGCGCTTTTGGCTTCGCGCTTCTTCTCCAGGACAGGTGGAAACCAAGCTGACCTG 5424
Qy 1681 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSer 1700
Db 5425 GCTATTGTGCTTGTCCATCATGAGGCAATCACACTGGAGAGATTGAGGTCAATCTGTTCG 5484
Qy 1701 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1720
Db 5485 CTGCCCATCAACCCCAACCATCATCCGTAATGAGGGTGTCCGCAATTGCTGAGTTCTG 5544
Qy 1721 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeu 1740
Db 5545 AAGCTGTGAAGATGCTGTGGCATGCGGGCACTGTGCACACGGTGATGCAGGCCCTG 5604
Qy 1741 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1760
Db 5605 CCCCAGGTGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTCATCTTGGCAGCTCTG 5664
Qy 1761 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1780
Db 5665 GCGGTGAGCTCTTTGAGAAGACCTGGAGTGTATGAGACACACCTTGTGAGGGCTTGGGT 5724
Qy 1781 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1800
Db 5725 CGGCATGCCACCTTAGAACTTTGGTATGGCCTTCTTGACCCCTCTCCAGTCTCCACT 5784
Qy 1801 GlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThr 1820
Db 5785 GGTGACAACTGGAATGATATTATGAAGACCCCTCCCGGAGCTGACCAAGAGTCCACC 5844
Qy 1821 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1840
Db 5845 TGCTACAAACACTGTCAATCTCCCTATCTACTTGTGTCTTGTGCTGACGGCCCAAGTTT 5904
Qy 1841 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1860
Db 5905 GTGCTGTCAACGTTGTCATAGCTGTGTGATGAAGCACCTGGAAGAAAGCAACAAGAG 5964
Qy 1861 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerPro 1880
Db 5965 GCCAAGAGAGAGCGGAGCTCGAGGCCAGCTGGAGTGAAGACGCTCAGCCCG 6024
Qy 1881 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSer 1900
Db 6025 CAGCCCACTCCCGCTGGCGAGCCCTTCTCTGCCCCGGGTGAGGGTGTCAACAGT 6084
Qy 1901 ThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGly 1920
Db 6085 ACTGACAGCCCTTAAGCCTGGGGCTCCACACACCACTGCCACATTGGAAGACGCTCGGGC 6144
Qy 1921 PheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGly 1940
Db 6145 TTCTCCCTTGAGCACCCCAAGATGTATCCCCCAAGAGGTGCCAGTCCCCCTAGGA 6204
Qy 1941 ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAsp 1960
Db 6205 CCAGACCTGCTGACTGTGAGGAAGTCTGTGTGTCAGCCGAGCGCACTCTGCCCCAATGAC 6264
Qy 1961 SerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGluHisArgGlyTrpGly 1980
Db 6265 AGCTACATGTGCCCAATGGGAGCACTGTGAGAGATCCCTAGACACAGGGGCTGGGG 6324
Qy 1981 LeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSer 2000
Db 6325 CTCCCAAGGCCCACTCAGGCTCCATCTTGTCCGTTCACTCCCAACAGACAGACACAGC 6384
Qy 2001 CysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThr 2020
Db 6385 TGCATCTTACAGCTTCCCAAGATGTGACTATCTGTCTCCAGCCTCATGGGGCTCCACC 6444
Qy 2021 TrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeu 2040
Db 6445 TGGGGCGCATCCCTAAACTACCCCACTGGCGGCTCCCTCTGTGCTCAGAGGCGCTCTC 6504
|||||

QY 2041 ArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlu 2060
|||
DB 6505 AGCGCCAGGAGCAATAGACTGACTCCCTGATGTGACAGGGCCTGGGTAGCCGGGAA 6564
QY 2061 AspleuleuSerGluValSerGlyProSerCysProleuThrArgSerSerPheTrp 2080
|||
DB 6565 GACCTGTGTTCAGAGGTGAGTGGGCCCTCTGCTGACCCGGTCTCATCTTCTGG 6624
QY 2081 GlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHis 2100
|||
DB 6625 GCGGGTCGAGCATCCAGGTGACAGCGCTTCCGGCATTCAGAGCAAAAGTCTCCAGACAC 6684
QY 2101 IleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProGlu 2120
|||
DB 6685 ATCCGCTGCCAGCCCTTGCCAGGCTTGAAACCCAGCTGGGCCAAGACCTCTCCAGAG 6744
QY 2121 ThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspleuleuPro 2140
|||
DB 6745 ACCAAGACAGCTTAGAGCTGACACGAGAGCTGAGCTGATTTCAAGAGACCTCTTCCC 6804
QY 2141 SerSerGlnGluGluProleuPheProArgAspleuleuLysCysTyrSerValGluThr 2160
|||
DB 6805 AGCAGCCAGGAAGAACCCCTGTCTCCACGGGACCTGAAGAAGTGCTACAGTGTAGAGACC 6864
QY 2161 GlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAla 2180
|||
DB 6865 CAGAGCTGACGGCGCAGGCTGGGTCTGGCTAGATGACAGCGAGACACTCATTTGCT 6924
QY 2181 ValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGly 2200
|||
DB 6925 GTCAAGTGTCTGACAGCGGCTCCCAACCCCGCTATGTCCAAAGCCCTCAAGCCTCGGG 6984
QY 2201 GlyGlnProleuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIle 2220
|||
DB 6985 GGCCAACTCTTGGGGGTCTGGGAGCCGGCCTAAGAAAAAATCAGCCCACTCATC 7044
QY 2221 SerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysLeu 2240
|||
DB 7045 TCTATAGACCCCCCGGAGAGCCAGGCTCTCGGCCCCCATGCACTCTGTGTCTGCCCTC 7104
QY 2241 ArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProleuAspSer 2260
|||
DB 7105 AGAGAGAGGGCGCGCCGCAAGTACTTAAGATCCCTCGGTCTCCAGCCCTTGACAGC 7164
QY 2261 ThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAsp 2280
|||
DB 7165 ACGGCTGCTCACTCCCTCCCAAGAAAGACACGCTGAGTCTCTGTGTTGTCTTGAC 7224
QY 2281 ProThrAspMetAspPro 2286
|||
DB 7225 CCAACAGACATGAGACCC 7242
RESULT 2
ADSI6295
ID ADSI6295 standard; DNA; 6942 BP.
XX
AC ADSI6295;
XX
DT 02-DEC-2004 (first entry)
XX
DE Rat voltage-dependent T type alpha 1G subunit calcium channel DNA.
XX
XX voltage-dependent ion channel; drug candidate;
XX aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
XX anticonvulsant; antiarrhythmic; rat; alpha 1G subunit; ds.
OS Rattus norvegicus.
XX
XX US2004175761-A1.
XX
XX 09-SEP-2004.
XX

PF 01-MAR-2003; 2003US-00377139.
XX
XX 01-MAR-2003; 2003US-00377139.
PR
XX
XX (MACK/) MACKINNON R.
PA (MACK/) MACKINNON A L.
PA (JIAN/) JIANG Y.
PA (RUTA/) RUTA V.
XX
PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
XX
XX MPI; 2004-642122/62.
DR REFSEQ; NM_031601.
XX
XX Screening drug candidates that target voltage dependent ion channel
PT protein, involves contacting screening protein with chemical compound,
PT which is drug candidate and determining whether chemical compound binds
PT to screening protein.
XX
PS Disclosure; SEQ ID NO 7; 61pp; English.
XX
XX The invention relates to the composition of matter suitable for use in
CC identifying chemical compounds that bind to voltage-dependent ion channel
CC proteins. The composition comprises a screening protein that consists of
CC an ion channel voltage sensor domain of the ion channel protein
CC immobilised on a solid support. The invention is useful for identifying
CC chemical compounds (drug candidate) that bind to voltage-dependent ion
CC channel proteins. The drug candidate of the invention is utilised for
CC treating a condition mediated by aberrant electrical activity that
CC initiates uptake or release of neurotransmitters and contraction of
CC muscles. The drug candidate of the invention is also utilised for
CC treating epilepsy and arrhythmia. The present sequence is a voltage-
CC dependent calcium channel DNA.
XX
SQ Sequence 6942 BP; 1383 A; 2126 C; 1961 G; 1472 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 6942
Score: 11980.00 Matches: 2283
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 3
Query Match: 99.60% Indels: 2
DB: 13 Gaps: 0
US-09-611-257A-24 (1-2287) x ADSI6295 (1-6942)
QY 1 MetLeuProHisArgValProArgCysValArgThrProProleuArgGlySerAlaArg 20
|||
DB 16 ATGCTCCCCCACCAGGTCCCGCTGGCGTAGAGACACTCTGAGGGGCTCCGCTCGC 75
QY 21 ProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGlu 40
|||
DB 76 CCCTCTTCGACACCCCGGGGCCCCGGCTGGCCAGAGATGACGAGAGAGGATGAG 135
QY 41 ArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGly 60
|||
DB 136 CCGGCGCGGAGAGTCCGGACAGCCCGTAGCTTACGCAAGCTCAACGACTGTCCGGGG 195
QY 61 ProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGlu 80
|||
DB 196 CCGGGGCGGAGAGGCGCGGGGTGACGGAAGAACCCGGGACAGCGCGGACTCCGAGG 255
QY 80 IaGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAsp 100
|||
DB 256 CGAGGGGCTGCCGTACCCGGGCTTAGCCCGGTGTTTCTTACTTGAGCCAGAGACA 315
QY 100 eArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSer 120
|||
DB 316 GCGGCGCGGAGAGCTGTGTCTCCGACGCTGTAAACCGTGTTCGAGGAGTCAAGTA 375
QY 120 etLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIle 140
|||
DB 376 TGCTGTATTTCTTCTCAACTGTGTGACTGTGGGTATGTTCAGGCCGTGTAGGACATTG 435

QY		140	IaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspSphenllePheAlaPheP	160
Db		436	CCTGTGACTCCAGCGCTGCCGGATCCTGCAGAGCCTTGATGACTTTCATCTTGCCCTCT	495
QY		160	heAlaValGlumetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrL	180
Db		496	TTCCTGTGAATGTGTGTGAAGATGTTGGCCCTTGCGCATCTTTGGAGAATAATTACC	555
QY		180	eugLYasPTHTTrPaSnARgLeuAspPhePheIleValIleAlaGlymetLeuGluTyrS	200
Db		556	TGGAGACACTTGGAACCGGCTTGACTTTTCATTGTTCATTGCAGGGATGCTGGAGTAAT	615
QY		200	erLeuAspLeuGlnAsnValserPheseraAlaValArgThrValArgValLeuArgProL	220
Db		616	CGCTGACCTGCAGAACTCACTTCTCCGAGTCAGACAGTCCGTGTGCTGCCGCC	675
QY		220	eUArgAlaIleasnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrL	240
Db		676	TCAGGGCCATTAAACGGGTGCCAGCATGCGCATTCCTGTCACATTACTGCTGACACCT	735
QY		240	eUPrometLeuGlyAsnValleuleuleucysPhePheValPhePheIlePheGlyIleV	260
Db		736	TGCCTATGCTGGGCAACGCTCTGCTGCTGTGTTCTTCTGCTTTTTCATCTTTGGCATCG	795
QY		260	aIGlyValGlnLeuTPraIagIyleuleuArgAsnArgCysPheLeuProGluAsnPheS	280
Db		796	TGGCGCTCCAGCTGTGGGCAAGACTGCTTCGCAACCGGTGCTTCTCCCGAACAATTCA	855
QY		280	erLeuProLeuSerValaspLeuGluProTyrTyrGlnThrGluAsnGluaspGluSerP	300
Db		856	GCCTCCCCCTGAGCGTGAGACTGAGCCTTATTACCAAGACAGAGATGAGACGAGAGCC	915
QY		300	roPheIleCysSerGlnProArgGluasnGlymetArgSerCysArgSerValProThrl	320
Db		916	CCTTCATCTGCTCTCAAGCTTCGGAGAATGCATGAGATCTCTGCAGAGTGTGCCACAC	975
QY		320	eUArgGlyGlyGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerS	340
Db		976	TGCGTGGGGAAGCGGTGTGGCCACCTGCAGTCTGAGACTATGAGACCTATAACAGTT	1035
QY		340	erSerAsnThrThrCysValAsnTPrasnGlnTyrTyrThrAsnCysSerAlaGlyGluH	360
Db		1036	CCAGCAACACCACCTGTGTCAACTGGAAACAGTACTATACCAACTGCTCTGCGGCGCAGC	1095
QY		360	isAsnProPheLysGlyAlaIleasnPheAspAsnIleglyTyrAlaTripleAlaIleP	380
Db		1096	ACAAACCCCTTCAAAGGCGCCATCAACTTGCACAACATTGGCTATGCTGATGCCATCT	1155
QY		380	heGlnValIleThrLeuGluGlyTyrPvalAspIleMetTyrPheValMetAspAlaHisS	400
Db		1156	TCCAGGTCACTCACACTGGAGGGCTGGGTGCACATCATGTACTTCGTAATGAGCGCTCACT	1215
QY		400	erPheTyrAsnPhelIeTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleA	420
Db		1216	CCTTCTACAACCTTCATCTCACTTCTTCTCATCATCGTGGGCTCCTTCTTCATGATCA	1275
QY		420	snLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnL	440
Db		1276	ACCTGTGCTGTGTGTGATTGCCACGCAGTTCCTCCGAGACCAACAAGCGGAGAGTCAAC	1335
QY		440	eumetArgGluGlnArgValArgPheLeuSerAsnAlaserThrLeuAlaserPheserg	460
Db		1336	TGATGCGGAGCAGCGTGTACGATTCTCTGTCCAATGTACGACCCTGGCAAGCTTCTCTG	1395
QY		460	IuProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaA	480
Db		1396	AGCCAGGCACTGCTATGAGAGACTACTCAAGTACCTGTGTACATCCTCCGAAAAGCAG	1455
QY		480	IaARGArgLeuAlaGlnValaserArgAlaIleGlyValArgAlaGlyLeuLeuSerSerP	500
Db		1456	CCCGAAGGCTGGCCAGGCTCTTAGGGCTATAGCGTGTGGGGCTGGGCTGCTCAGCAGCC	1515

QY	500	roValAlaIaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgA	520
Db	1516	CAGTGGCCCGTAGTGGGACAGAGCCCCAGCCAGTGGCAGCTGCATCGCTCACACCGTC	1575
QY	520	rgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisLeuG	540
Db	1576	GTCTGTCTGTCCACCACCTGGTCCACCACCATCACCACTACCACTACCACTGG	1635
QY	540	lYAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG	560
Db	1636	GTAATGGAGAGCTCAGAGTTCCTCCGGGGCCAGCCAGAGATCCAGACAGGAGATCCAAATG	1695
QY	560	lYSerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProA	580
Db	1696	GGTCTCGCGGCTCATGTCTACCAACCACTCTACACCACTCCCTCTGGGGGCCCTCCGA	1755
QY	580	rgGlyAlaGluSerValHisSerPheThrHisAlaAspCysHisHisLeuGluProValArgC	600
Db	1756	GGGTGCGGAGTCTGTACACAGCTTTCACCATGTGACTGCCACTTGGAGCCAGCTCCGTT	1815
QY	600	YSGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL	620
Db	1816	GCCAGGACCCCCCTCCAGATGCCCATCGAGGAGCATGTGTAGGACTGTGGGTAGTGGGA	1875
QY	620	YsValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuV	640
Db	1876	AGGTGTACCCCACTGTGCATACCAAGCCCTCCACCAGAGATACTGAAGGATAAAGCACTAG	1935
QY	640	aIGluValAlaProSerProGlyProProThrLeuThrHisSerPheAsnIleProProGlyP	660
Db	1936	TGGAGTGGCCCCAGCCCTGGGCCCCCACCCTCACAGCTTCAACATCCCACTTGGGC	1995
QY	660	roPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerC	680
Db	1996	CCTTCAGCTCCATGCACAAGCTCTGGAGACACAGAGTACGGAGCCTGCCATAGCTCCT	2055
QY	680	YsLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysP	700
Db	2056	GCAAAATCTCCAGCCCTGTCTCCAAAGGACAGACAGTGGAGCTGGGGCCGAGACTGTGC	2115
QY	700	roTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspS	720
Db	2116	CCTACTGTGCCCCGACAGAGAGAGAGCCAGAGTCCGCTGACCATGTCTACTGCTGACT	2175
QY	720	eRAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspP	740
Db	2176	CAGACAGCAGAGCTGTGTATGAGTTCAACAGAGAGCTCAGACAGTGAACCTCCGGGATC	2235
QY	740	roHisSerArgArgGlnArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuA	760
Db	2236	CCCACAGCGCGGCGGACAGACGGGAGCTGGGCCAGATGCAGAGCCTAGTTCTGTGCTGG	2295
QY	760	lApheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyA	780
Db	2296	CTTTCGTGAGGCTGATCTGTGACACATTCGGAAGATGTAGATAGCAATACTTGGCC	2355
QY	780	rgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluG	800
Db	2356	GGGGAATCATGATCGCCATCTGTGTCATATACACTCAGCATGGGCATCGAGTACCAAGACC	2415
QY	800	lInProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheA	820
Db	2416	AGCCCGAGAGCTCACCAAGCCCTGGAATCAGCAACATCGTCTTACACAGCCCTCTTCG	2475
QY	820	lAlaGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProT	840
Db	2476	CCTTGGAGATGTGCTGAACGTCTGTCTACGGTCCCTTGGCTACATTAAGATCCCT	2535
QY	840	YrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnGlnG	860
Db	2536	ACAACATCTTTGATGTGTGTATGTGTATCATCAGTGTGTGGGAAGATTGTGGGCCAGCAGG	2595
QY	860	lYgIlyGlyLeuSerValLeuArgThrPheArgLeuMetCArgValLeuLysLeuValArgP	880

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Db 2596 GAGGTGCGCTGCTGGTGCTGGGACCTTCCGCTGATGGGGTGCTGAAGCTGGTGGCT 2655
QY 880 heLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaIat 900
Db 2656 TCCTGCCGGCCCTGCAGCGCCAGCTCGTGCTCATGAGACCATTGGACACACGTGGCCA 2715
QY 900 hrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuP 920
Db 2716 CCTTCGATGCTCTCTCATGCTGTTCATTCTTCATCTTCAGCATCTGGGCATGCACTCT 2775
QY 920 heGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPhea 940
Db 2776 TTGGTTGCAGTTCCGATCTGAACGGGATGGGACACAGTTGCCAGACCGGAAGATTTCG 2835
QY 940 spSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnL 960
Db 2836 ACTCCCTGCTCTGGGCCATCGTCACTGCTTTAGATTCTGACTCAGGAAGACTGGAATA 2895
QY 960 ysValLeuTyrrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrrPheIleAla 980
Db 2896 AAGTCCCTTAACAACGGCATGGCTCCACATCGTCTGGGCTGCTCTTACTTCATCGCCC 2955
QY 980 eumetThrPheGlyAsnTyrrValLeuPheAsnLeuValAlaIleLeuValGlnGlyP 1000
Db 2956 TCATGACTTTTGGCAACTAATGCTCTTTAACTGCTGTGGCCATTCTTGTGAAGGAT 3015
QY 1000 heGlnAlaGlnGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerV 1020
Db 3016 TCCAGGCAGAGGAGATGCCACCAAGTGTAGTCAGAGCCTGATTTCTTTCCGCCAGTG 3075
QY 1020 aLAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGlnHisAlaG 1040
Db 3076 TGGATGGTGAATGGGGAACAGAAAGAGGCTTGCCCTGGTGCTTTGGAGAACACGCGG 3135
QY 1040 luleuArgLysSerLeuLeuProProleuIleIleHisThrAlaAlaThrProMetSerH 1060
Db 3136 AACTACGAAGAGCCTTTTGCCACCCCTCATCATCCATACGGCTGCGACACCAATGTAC 3195
QY 1060 isProLysSerSerSerThrGlyValGlyAlaLeuGlySerGlySerArgArgThrs 1080
Db 3196 ACCCCAAGAGCTTCCAGCACAGGTGTGGGGGAAGCACTGGGCTCTGCTCGACGTACA 3255
QY 1080 erSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSera 1100
Db 3256 GTAGCAGTGGGTCCGCTGAGCCTGAGCTGCCACCATGAGATGAATAATGCCGCCAAGTG 3315
QY 1100 laArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgSers 1120
Db 3316 CCGCGAGCTCCCGCACAGTCCCTGAGTGGCGCAAGCAGCTGACACGAGCGCTCCA 3375
QY 1120 erArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyLysArgA 1140
Db 3376 GCAGGAACAGCCTGGGCCCCGGCCAGCTTAAAGCGAGAGGCCGAGCGGAGCGGA 3435
QY 1140 rgSerLeuLeuSerGlyGlyGlyGlnGlnLysSerGlnAspGlyGlnLysSerSerGlyLys 1160
Db 3436 GGTCCCTGCTGTCTGAGAGGGCCAGGAGAGTCAAGATGAGGAGGAAAGTTCAGAAAGG 3495
QY 1160 spArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGlyLysArgGlyAla 1180
Db 3496 ACCGGGCGAGCCACAGGAGTGAATGCCACAGGGGTTCTTGGAAACGTGAGGCCA 3555
QY 1180 ysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerG 1200
Db 3556 AGAGTTCCTTTGACTGCTGACACTGTGACAGGTGCCGGGGCTGCACCGCACAGCCAGCG 3615
QY 1200 lYArgSerSerAlaSerGlnHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA 1220
Db 3616 GCCGGAAGCTCTGCTCTGAGACCAAGACTGTAAATGGCAAGTCGGCTTCAGGGCGTTTG 3675
QY 1220 laArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGlyLys 1240
|||||

Db 3676 CCGGCACCTGAGAGCTGATGACCCCAACTGGATGGGATGATGACATGATGAGGAA 3735
QY 1240 snLeuSerLysGlyGlyLysArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysA 1260
Db 3736 ATCTGAGCAAAAGGGGAACGATACAAAGCCTGGGTCAGATCCCGGCTTCTGCTGTGCC 3795
QY 1260 rgGluArgAspSerTrpSerAlaTyrrIlePheProProGlnSerArgPheArgLeuLeu 1280
Db 3796 GAGAGCGAGATTCTGTGGGCTTATATCTTCTCTCCTCAGTCAAGGTTTCGTCCTGT 3855
QY 1280 ySHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuA 1300
Db 3856 GTACCGGATCATCACCCCAAGATGTTGACCAATGTGCTCGTCAATCATCTTCTCA 3915
QY 1300 snCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIleP 1320
Db 3916 ACTGATCAACCATCGCTATGAGCGCCCAAAATGACCCCAAGCGCTGAGCGCATCT 3975
QY 1320 heLeuThrLeuSerAsnTyrrIlePheThrAlaValPheLeuAlaGluMetThrValLysV 1340
Db 3976 TCCTGACCTCTTCCAACTACATCTTCACGCGCAGTCTTCTAGCTGAATGACAGTGAAG 4035
QY 1340 alValAlaLeuGlyTyrrCysPheGlyGlyGlnAlaTyrrLeuArgSerSerTrpAsnVal 1360
Db 4036 TGGTGCACTGGGCTGTGCTTTGGGGAGCAGGCTTAACCTCGCAGCAGCTGGAATGTGC 4095
QY 1360 euAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspS 1380
Db 4096 TGGACGGCTTCTGCTGCTCAATCTCCGTATCGACATCTGCTCTCCATGCTCTCCGACA 4155
QY 1380 erGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProL 1400
Db 4156 GCGGCACCAAGATCCTTGGCATGTGAGGGTGTGCGGCTGCTGCGACCTGCTGCAC 4215
QY 1400 euArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerL 1420
Db 4216 TCAGGGTATCAGCCGGGCCAGGGAAGTCTGCTGTGTCAAGGTGAGAGACTGTGATGCC 4275
QY 1420 euLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleL 1440
Db 4276 TCAAAACCATTTGGCAACATTTGTGTCATTTGCTGCTTCTTCATCATTTTGGAAATTC 4335
QY 1440 euGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnI 1460
Db 4336 TCGGGTGACCTCTTCAAGGGAAGTCTTCTGTGTCAAGGTGAGGACACCAAGTACAAC 4395
QY 1460 leThrAsnLysSerAspCysAlaGluAlaSerTyrrArgTrpValArgHisLysTyrrAsn 1480
Db 4396 TCACTAACAAATCCGACTCGGTGAGGCCAGCTACCGATGGGTCCGGCACAACTACAAC 4455
QY 1480 heAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpV 1500
Db 4456 TTGACAACTGGGCCAGGCTGTGATGCCCTGTTGTGCTGGCTCCAAAGATGGTTGGG 4515
QY 1500 alaSpIleMetTyrrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnH 1520
Db 4516 TTGACATCATGTATGATGGGCTGGAATGCTGTGGTGTGATCAGACCCCATCATGAACC 4575
QY 1520 isAsnProTrpMetLeuLeuTyrrPheIleSerPheLeuLeuIleValAlaPhePheVal 1540
Db 4576 ACAACCCCTGATGTGCTATATCTTCTCTTCTCTCATCGTGCCCTTCTTTGTCC 4635
QY 1540 euAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGlnG 1560
Db 4636 TGAACATGTTGTGGCGGTGTGTGAGAACTTCCATTAAGTGCAGACACACGAGAGG 4695
QY 1560 lGlyGlnAlaArgArgArgGlyGlnLysArgLeuArgLeuGlyLysLysArgArgS 1580
Db 4696 AGGAGAGGCGAGCGCGGTGAGGAGAAAGCACTACGAGGCTTGAGAAAAAGAAAGGA 4755
QY 1580 erLysGlyLysGlnMetAlaGlnAlaGlnCysLysProTyrrTyrrSerAspTyrrSerArgP 1600
Db 4756 GTAAAGAGAAAGAGATGGCCGAAGCCAGTGCAGACCCCTACTACTCTGACTACTGAGAT 4815
|||||

QY	1600	hEaRgLeuLeuValHIShISLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyY	1620
Db	4816	TCCGGCTCCTGTGCCACCACTGTGTACCAGCCACTACCTGGACCTTTCATCACTGGTG	4875
QY	1620	allIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuA	1640
Db	4876	TCATCGGGCTGAACGTGTCACTATGGCCATGGAACTTACCAGACAGCCCGAGATCCTGG	4935
QY	1640	spGIuAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValP	1660
Db	4936	ACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTTGTCTTGAGTCAGTTT	4995
QY	1660	hElySLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAspL	1680
Db	4996	TCAAACTGTGGCCTTTGGCTCCGCCGTTTCTTCCAGACAGGTGAACCACTGTGACC	5055
QY	1680	eUAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuS	1700
Db	5056	TGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGAGAGAGATTGAGGTCAATCTGT	5115
QY	1700	eRLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValL	1720
Db	5116	CGCTGCCCATCAACCCCACTCATCCGTATCATGAGGGTGCTCCGCAATTGCTCGAGTTC	5175
QY	1720	eULysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaL	1740
Db	5176	TGAAGCTGTGAAGATGGCTGTGGCATGCGGGCACTGTGCACACGGTGATGCAGGCC	5235
QY	1740	eUProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaL	1760
Db	5236	TGCCCCAGGTGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTCATCTTGGACGCTC	5295
QY	1760	eUGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuG	1780
Db	5296	TGGCGCTGAGCTCTTGGAGACCTGGAGTGTATGAGACACACCCTTGTGAGGGCTTGG	5355
QY	1780	LYaRgHISAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerT	1800
Db	5356	GTCGGCATGCACTTATGGAACCTTGGTATGGCCTTCTGACCCCTCTCCGAGTCTCCA	5415
QY	1800	hRGLyAspAsnTyrAsnGlyIleMetLysAspProSerArgAspCysAspGlnGlnSerT	1820
Db	5416	CTGGTGACAACCTGGAATGTAATTATGAAGGACACCCCTCCGGGACTGTGACCAGGAGTCCA	5475
QY	1820	hRCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnP	1840
Db	5476	CCTGCTACAACAACCTGTCACTCTCCCTATCTACTTGTGTCTTCTGCTGACGGCCAGT	5535
QY	1840	heValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysG	1860
Db	5536	TTGTGCTGTGTCACGCTGTCTATAGCTGTGTCTGATGAAGCACTTGAAGAAAGCAACAAG	5595
QY	1860	IuAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerP	1880
Db	5596	AGGCCAAGAGAGAGCCGAGCTCGAGCCGAGCTGAGCTGGAGATGAAGACGCTCAGCC	5655
QY	1880	roGlnProHisSerProLeuGlySerProPheLeuTyrProGlyValGluGlyValAsnS	1900
Db	5656	CGCAGCCCCCACTCCCGCTGGGCGAGCCCTTCTCTGCGCCGGGGGTGAGGGGTGTCAACA	5715
QY	1900	eRThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerG	1920
Db	5716	GTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCCTCGG	5775
QY	1920	LYPheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuG	1940
Db	5776	GCTTCTCCCTTGAGCACCCACGATGTTACCCCAACCCGAGAGGTGCAGTCCCCCTAG	5835
QY	1940	LYProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnA	1960
Db	5836	GACCAGACCTGCTGACTGTGAGGAAGTCTGTGTCAAGCCGAGACGCACTCTCGCCCAATG	5895

Accession	Gene	Species	Position	Sequence	Length
QY	spSerlyrmetCysArgasnGlySerThrAlaGlnArgSerLeuGlyHisArgGlyTrpG	1960	1980		
Db	ACAGCTACATGTGCCGCAATGGAGCACTGCTGAGAGATCCCTAGGACACAGGGGCTGGG	5896	5955		
QY	lYleuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrS	1980	2000		
Db	GGCTCCCAAGGCCAGTCAAGCTCCATCTTGTCCGTTCACTCCCAACGACAGACACCA	5956	6015		
QY	erCysIleLeuGlnLeuProLysAspValHisTrpLeuLeuGlnProHisGlyAlaProT	2000	2020		
Db	GCTGCATCTTACAGCTTCCCAAGATGTGCATATCTGCTCCAGCCTCATGGGGCTCCA	6016	6075		
QY	hrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProL	2020	2040		
Db	CCTGGGGGGCCATCCCTAAACTAACCCACCTGGCGGCTCCCTCTGACTCAGAGGCTTC	6076	6135		
QY	euArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArg	2040	2060		
Db	TCAGGCGCCAGGCGCAATAGGACTGACTCCCTGGATGTGCAGGGGCTGGGTACCCGG	6136	6195		
QY	luAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerPheT	2060	2080		
Db	AAGACTGTGTTCAGAGGTGAGTGGGCCCTCTGCTTCAACCCGGTCTCATCTTCT	6196	6255		
QY	rpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysH	2080	2100		
Db	GGGGCGGGTCAGCATCCAGGTGACAGCGCTTCCGGCATCCAGACMAAGTCTCCAAGC	6256	6315		
QY	isIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProPro	2100	2120		
Db	ACATCCGCTGCCAGCCCTTGGCCAGGCTGGAACCACTGGGCCAAGAGACCTCCAG	6316	6375		
QY	luThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuP	2120	2140		
Db	AGACCAAGACGACTTAGAGCTGACACGAGAGCTGAGCTGATTCAGGAGACTCCTTC	6376	6435		
QY	roSerSerGlnGluProLeuPheProArgAspLeuLysCysTrpSerValGluT	2140	2160		
Db	CCAGCAGCCAGGAAGAACCCCTGTTCACACGGGACTTGAAGAAGTGCTACAGTGAAGA	6436	6495		
QY	hrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleA	2160	2180		
Db	CCAGAGCTGCAGGCGCAGGCTGGGTCTGCTAGATGAACAGCGAGACACTTCCATTG	6496	6555		
QY	laValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuG	2180	2200		
Db	CTGTCACTGTCTGGACAGCGGCTCCCAACCCGCTATGTCCAAAGCCCTCAAGCCTCG	6556	6615		
QY	lyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProSerI	2200	2220		
Db	GGGCGCAACTCTTGGGGGTCTGGGAGCCGCGCTAAGAAAAAACTCAGCCCACTCACTA	6616	6675		
QY	leSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysL	2220	2240		
Db	TCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCCATGCACTCTGTTCTGCGC	6676	6735		
QY	euArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspS	2240	2260		
Db	TCAGGAGAGGGGCGCGGCACTGACTTAAGGATCCTCGGTCTCCAGCCCTTGACA	6736	6795		
QY	erThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerA	2260	2280		
Db	GCACGGCTGCTCACCCTCCCAAGAAAGACACGCTGAGTCTCTGTGTTGTCTTCTG	6796	6855		
QY	spProThrAspMetAspPro	2280	2286		
Db	ACCCAACAGACATGAGCCCC	6856	6875		

XX 18-JUL-2000 (first entry)
DT Rat pancreatic T-type calcium channel cDNA.
XX
DE Rat; pancreatic T-type calcium channel alpha subunit; insulin;
XX pancreatic beta cell; alphaIG; low voltage activated Ca2+ channel family;
KW antidiabetic; calcium influx; L type calcium channel; NIDDM;
KW type II diabetes; non-insulin dependent diabetes mellitus; ss.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT misc_feature 1..157
FT /tag= b
FT /note= "Region upstream to the coding region of
FT pancreatic T-type calcium channel protein"
FT 2..7285
FT /tag= a
FT /product= "Pancreatic T-type calcium channel alpha
FT subunit"
FT /transl_except= (pos:11..13, aa:Xaa)
FT /transl_except= (pos:7022..7024, aa:Xaa)
FT /transl_except= (pos:7112..7114, aa:Xaa)
FT /note= "Xaa corresponds to in-frame stop codon. This
FT region includes sequence upstream to the coding region of
FT pancreatic T-type calcium channel protein. Does not
FT include stop codon"
FT /partial
FT 158..7285
FT /tag= c
FT /product= "Pancreatic T-type calcium channel alpha
FT subunit"
FT /note= "This region is claimed as SEQ ID NO: 1"
XX
PN WO200015845-A1.
XX
PD 23-MAR-2000.
XX
PF 26-AUG-1999; 99WO-US019675.
XX
PR 26-AUG-1998; 98US-0098004P.
PR 27-JAN-1999; 99US-0117399P.
XX
PA (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
XX
PI Li M;
XX
XX WPI; 2000-271475/23.
DR P-PSDB; AAY70720.
XX
PT Novel nucleic acids encoding pancreatic T-type calcium channels used for
PT regulation of T-type calcium channels and treatment of type II diabetes.
PS Example 1; Page 114-119; 124pp; English.
XX
XX The present cDNA encodes a protein that includes pancreatic T-type
CC calcium channel alpha subunit derived from rat insulin secreting beta
CC cell line, INS-1. The protein shows 96.3 % identity to the neuronal T-
CC type calcium channel alpha subunit (alphaIG). The T-type Ca2+ channel
CC from INS-1 (alphaIG-INS) and neuronal alphaIG are alternative splice
CC isoforms of the same gene. The INS-1 isoform is also expressed in brain,
CC neonatal heart and kidney besides pancreatic beta cells. T-type Ca2+
CC channel belongs to the family of low voltage activated Ca2+ channels. The
CC present sequence is used for treating diseases associated with abnormal
CC expression or function of T-type calcium channels. They are especially
CC used for treating type II diabetes. Modulators of pancreatic T-type Ca2+
CC channel e.g. antisense oligonucleotides, ribozymes and inhibitors are
CC used in methods for modifying insulin secretion by pancreatic beta cells,
CC basal calcium levels, potential L type calcium channel activity,
CC pancreatic cell death, pancreatic beta cell proliferation and calcium
CC influx through L type calcium channels in cells
XX

SQ Sequence 7286 BP; 1467 A; 2224 C; 2064 G; 1531 T; 0 U; 0 Other;
Alignment Scores: 0 Length: 7286
Pred. No.: 11829.00 Matches: 2270
Score: 97.72% Conservative: 1
Percent Similarity: 97.68% Mismatches: 15
Best Local Similarity: 98.35% Indels: 38
Query Match: 3 Gaps: 2
DB: 3
US-09-611-257A-24 (1-2287) x AAZ52309 (1-7286)
QY 1 MetLeuProHisArg-ValProArg-CysValArgThrProProLeuAArgGlySerAla 20
DB 58 ATGCTCCCCCACCAGGGGTCCCGGTTGCTGAGACACCTCTTGAGGGGCTCCGCTC 117
QY 20 rgProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetG 40
DB 118 GCCCTCTTCGACCCCGGGGGCCCGGCTGGCCAGAGATGAGACGAGAGATGG 177
QY 40 lAArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProg 60
DB 178 AGCGGGCCCGAGAGAGTCGGGACAGCCCGTACTTCACGACGCTCAACGACTGTCCGG 237
QY 60 lYProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerG 79
DB 238 GGGCGGGGGCGGAGGGGGCGGGGTTCAGCGGAAAAAGAACCCGGGCGAGCGGACTCCGA 297
QY 79 uAlaGluGlyLeuProTyProAlaLeuAlaProValValPhePheTyLeuSerGlnAs 99
DB 298 GCGGAGGGGCTGCCGTACCCGCGCTAGCCCGGTGTTTCTTCTTACTTGAGCCAGGA 357
QY 99 pSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSe 119
DB 358 CAGCCGCCCGGAGAGCTGTGTCTCCGACAGGTCTGTAAACCGTGTGAGCGAGTCA 417
QY 119 rMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspI 139
DB 418 TATGCTGTGTCATTCTTCTCAACTGTGTGACTCTGGGTATGTTACAGGCCGTGAGACAT 477
QY 139 eAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPh 159
DB 478 TGCTGTGACTCCACGCGCTGCCGATCTTCGACGCCCTTCGATGACTTCTTGCCCTT 537
QY 159 ePheAlaValAlaGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTy 179
DB 538 CTTTGCTGTGAAATGTGTGAAGATGTGTGGCCATCTTTGGGAAGAAATGTTA 597
QY 179 rLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTy 199
DB 598 CTTGGAGACACTTGGAACGGGCTTGACTTTTTCATTGTGATTGCAGGATGCTGAGTA 657
QY 199 rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgPr 219
DB 658 TTGCTGGAACCTGCAAGACGTCAAGCTTCTCCGACGTCAAGACAGTCCGTGTGCGACC 717
QY 219 oLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspTh 239
DB 718 GCTCAGGGCCATTAAACCGGTGCCCAAGCATGCCATTCTGTCACATTACTGCTGACAC 777
QY 239 rLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyI 259
DB 778 CTTGCTATGCTGGCAACGCTCTGCTGTCTGTCTTCTTCTTCTTCTTCTTCTTGGCAT 837
QY 259 eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPh 279
DB 838 CGTGGGGTTCAGCTGTGGGAGAGACTGTTCGCAACGATGCTTCCCGAAGAACTT 897
QY 279 eSerLeuProLeuSerValAspLeuGluProTyTrpGlnThrGluAsnGluAspGluSe 299
DB 898 CAGCCTCCCCCTGAGCGTGAAGCTGAGCCTTATTACACAGACAGAGAATGAGACGAGAG 957
QY 299 rProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProTh 319

Db 958 CCCCTTCATCTGCTCTCAGCCCTCGGAGATGCGATCGCTGCAAGAGTGTGCCAC 1017
QY 319 rLeuArgGlyGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSe 339
Db 1018 ACTGCGTGGGAGGCGGTGTGGCCCACTTGACAGTCTGGACTATGAGACCTATTAACAG 1077
QY 339 rSerSerAsnThrThrCysValAsnTrpAsnGluTyrTyrThrAsnCysSerAlaGlyG1 359
Db 1078 TTCAGCAACACCACACTGTGTCAACTGGAACAGTACTATACCACACTGTGCGGGCGA 1137
QY 359 uHisAsnProPheLysGlyAlaAlaLeAsnPheAspAsnIleGlyTyrAlaTrpIleAlaI 379
Db 1138 GCACAACCCCTTCAAGGCGCCATCAACTTGACAACATTGGCTATGCTGGATCGCAT 1197
QY 379 ePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaH1 399
Db 1198 CTTCCAGGTCATCACTGAGGGCTGGGTGACATCATGTACTTCGTAATGACGCTCA 1257
QY 399 sSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetI1 419
Db 1258 CTCCTTCTACAACCTTCATCTACTTCATTCTTCATCATCGTGGCTCTCTTCATGAT 1317
QY 419 eAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerG1 439
Db 1318 CAACCTGTGCTGTGGTGAATTGCCACGCACTTCTCCGAGACCAACAGCGGAGAGTCA 1377
QY 439 nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe 459
Db 1378 GCTGATGCGGAGCAGCGTGTACGATTCTGTCCAATGTAGCACCTTGCAAGCTTCTC 1437
QY 459 rGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAl 479
Db 1438 TGAGCCAGGCAAGCTGCTATGAGAGAGTACTCAAGTACCTGTGTACATCTCCGAAAGC 1497
QY 479 aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe 499
Db 1498 AGCCCGAAGGCTGGCCAGGTCCTTAGGGCTATAGGCGTGGGGCTGGCTCAGCAG 1557
QY 499 rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr 519
Db 1558 CCCAGTGGCCCGTAGTGGGCAAGAGCCCCCAAGCCCAAGTGCGCACTGCTCACACCG 1617
QY 519 gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisHisHisIle 539
Db 1618 TCGTCTGTCTGTCCACCACTGTGTCCACCACCATCACACCACCAATCACACTACCACT 1677
QY 539 uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs 559
Db 1678 GGGTAATGGACGCTCAGATTCCCCGGGGCAGCCAGAGATCCAGGACAGGATGCCAA 1737
QY 559 nGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPr 579
Db 1738 TGGGTCTCGCCGGCTCATGTACCACCACTCTTACACCACTCCCTCTGGGGGCCCTCC 1797
QY 579 oArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValAr 599
Db 1798 GAGGGGTGCGAGTCTGTACACAGCTTCTACCATGTGACTGCCACTTGGAGCCAGTCCG 1857
QY 599 gCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerG1 619
Db 1858 TTGCCAGGCACCCCCTCCAGATGCCCATCGGAGGCATCTGGTAGGACTGTGGTAGTGG 1917
QY 619 yLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe 639
Db 1918 GAAGGTATCCCACTGTGCATACCAAGCCCTTCCACAGAGATACTGAAGATAAAGCACT 1977
QY 639 uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProG1 659
Db 1978 AGTGAGGTGGCCCCCAGCCCTGGGGCCCCCACTCACCAGCTTCAACATCCACACTGG 2037
QY 659 yProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSe 679

Db 2038 GCCCTTACGTCCTCATGCACAAGCTCTGGAGACACAGAGTACGGGAGCCTGCCATAGCTC 2097
QY 679 rCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCy 699
Db 2098 CTGCAAAATCTCCAGCCCTTGCTCCAAAGCAGACAGTGGAGCCTGCGGGCCGAGAGTTG 2157
QY 699 sProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAs 719
Db 2158 TCCCTACTGTGCCCCGAGACAGAGAGAGAGAGCCAGAGTCCGCTGACCATGTATGCTGA 2217
QY 719 pSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAs 739
Db 2218 CTCAGACAGCGAGCTGTGTATGATTCAACAGAGACGCTCAGCACAGTGAACCTCCGGA 2277
QY 739 pProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLe 759
Db 2278 TCCCACAGCCGCGCGGACAGCGGAGCCTGGGCCAGATGCAAGCCTAGTTCTGTGCT 2337
QY 759 uAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheG1 779
Db 2338 GGCTTCTTGAGAGCTGATCTGTGACACATTCGGAAAGATCGTAGATAGCAAAATACTTGG 2397
QY 779 yArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisG1 799
Db 2398 CCGGGAATCATGATCGCCATCTGTGCAATACACTCAGCATGGGCATCGAGTACCAGCA 2457
QY 799 uGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPh 819
Db 2458 GCAGCCCGAGAGCTCACCAACGCCCTGGAATCAGCAACATCGTCTTACCAGCCTCTT 2517
QY 819 eAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnPr 839
Db 2518 CGCCTTGAGATGCTGCTGAACCTGTTCTTACGSGTCCCTTTGGCTACATTAAAGATCC 2577
QY 839 oTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnG1 859
Db 2578 CTACAACATCTTTGATGTGTGTCATTGTGTGTCATCAGTGTGTGGAGATTGTGGGCCACA 2637
QY 859 nGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAr 879
Db 2638 GGGAGGTGGCTGTGCGGTGCTGCGGACCTTCCGCTGATGCGGGTCTGAAGCTGTGCG 2697
QY 879 gPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAl 899
Db 2698 CTTCTCGCCGCGCCTGCAGCGCCAGCTCGTGTGTCATGAAGAACCATGACAAACGTGGC 2757
QY 899 aThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLe 919
Db 2758 CACCTTCTGCATGCTCTCTCATGTCTTCACTTCATCTTCACGATCCTGGGCATGCTCT 2817
QY 919 uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPh 939
Db 2818 CTTTGGTTGCAAGTTCCGATCTGACGGGATGGGACACGTTGCCAGACCAGAAATTT 2877
QY 939 eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAs 959
Db 2878 CGACTCCCTGCTCTGGGCCCATCGTCACTGCTTTCAGATTCTGACTCAGGAAGACTGGA 2937
QY 959 nLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAl 979
Db 2938 TAAAGTCTCTAACAAACGCGCATGCGCTCCACATCGTCTGGGCTGCTCTTACTTCATTCGC 2997
QY 979 aLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluG1 999
Db 2998 CCTCATGACTTTGGCAACTATGTCTTTAACTGCTGTGGTGGCCATTCTGTGGAAGG 3057
QY 999 yPheGlnAlaGlu-----GlyAspAlaThrLysSerGluSerGluProAspPhePh 1003
Db 3058 ATTCCAGGCAGAGAAATCGGCAACGGGAAGATGCGAGTGCACAGTTAAGCTGTATTCA 3117
QY 1004 -----GlyAspAlaThrLysSerGluSerGluProAspPhePh 1016
Db 3118 GCTGCTGTCAACTCTCAGGGGGGAGATGCCACCAAGTGTGAGTCAAGACCTGATTTCTT 3177

Qy	1016	eSerProSerValaBpGlyAspGlyAspArgLysValSerGluAlaLeuValAlaLeuG	1036
Db	3178	TTGGCCCAAGTGTGATGCTGATGGGACAGAAAGACGCTTGCCCTGGCTTGGG	3237
Qy	1036	YGLuHiSaLaGluLeuAArgLysSerLeuLeuProProLeuIleIleHisThrAlaLaTh	1056
Db	3238	AGAACACGCGGAACTAAGAAAGACCTTTTGGCACCCCTCATCATCATGAGCTGCGAC	3297
Qy	1056	rPrometSerHisProLysSerSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySe	1076
Db	3298	ACCAATGTCACTACCCACAGACTCCAGACACAGGTGTGGGGGAAGCACTGGGCTCTGGCTC	3357
Qy	1076	rArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCy	1096
Db	3358	TCGACGTACCAAGTAGCAGTGGGTCCGCTGAGCCTGAGCTGCCACCATGAGATGAATC	3417
Qy	1096	sProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe	1116
Db	3418	TCCGCCAAGTGCCTGCACTCCCGCACAGTCCCTGAGTGCAGCAAGCAGCTGACCAAG	3477
Qy	1116	rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe	1136
Db	3478	CAGCGGCTCCAGCAGGAACACCTGGGGCCGGCCCCCAGCCTAAAGCGGAGAGCCGAG	3537
Qy	1136	rGlyGluArgArgSerLeuLeuSerGlyGlyGluGlyGlnGluSerGlnAspGluGluSe	1156
Db	3538	CGGGGACGGAGTCCCTGCTGTCTGAGAGGGGCCAGAGAGTCAAGATGAGGAGGAAG	3597
Qy	1156	rSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuG	1176
Db	3598	TTCAAGAAGAGACCGGGCCAGCCACAGCAGCAGTGCATCGCCACAGGGGTTCTTGA	3657
Qy	1176	uArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisAr	1196
Db	3658	ACGTGAGGCCAAGAGTTCCTTGAACCTGACCTGACACACTGACAGTGCCTGGGCTGACCG	3717
Qy	1196	gThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSe	1216
Db	3718	CACAGCCAGCGGCGGAGCTTGCTCTGAGCACCAAGACTGTAATGGCAAGTCCGGCTTC	3777
Qy	1216	rGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAs	1236
Db	3778	AGGGCGTTTGGCCCGCACCTGAGACTGATGACCCCACTGATGGGATGATGACAA	3837
Qy	1236	naSpGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuPr	1256
Db	3838	TGATGAGGGAATCTGAGCAAGGGGAACGATACAAAGCTGGGTCCAGATCCCGGCTTCC	3897
Qy	1256	oAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPh	1276
Db	3898	TGCCTGTTGCCGAGCGAGATTCTGTGTCGGCTATATCTTCTCCTCAGTCAAGGTT	3957
Qy	1276	eArgLeuLeuCySHisArgIleIleThrHisLysMetPheAspHisValValLeuValIl	1296
Db	3958	TCGTCTCTGTGTCAACCGATCATCACCAAGATGTTTGACCATGTGTCTCTGTCAT	4017
Qy	1296	eIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAl	1316
Db	4018	CATCTTCTCAACTGTATACCACTCGCTATGAGCGGCCCAAAATTGACCCCCACAGCGC	4077
Qy	1316	agLuarGlyIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluWe	1336
Db	4078	TGAGGCATCTTCTGACCCCTCCAACTACATCTTCAAGCAGTCTTCTAGCTGAAT	4137
Qy	1336	rThrValLysValValAlaLeuGlyTrpCysPheGlyGlnGlnAlaTyrLeuArgSerSe	1356
Db	4138	GACAGTGAAGGTGTGGCACTGGGCTGTGCTTTGGGGAGCAGGCCCTACCTGCGCAGCAG	4197
Qy	1356	rTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMe	1376
Db	4198	CTGGAATGTGCTGACGCGCTTGTGTGCTCATCTCCGTATGACATCTGTGTTCCAT	4257

QY	1376	tValSerAspSerGlyThrIysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgTh	1396
Db	4258	GGTCTCCGACACGGCGCACCAAGATCTTGGCATGTGAGGGTGCTGCGGCTGCGGAC	4317
QY	1396	rLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLe	1416
Db	4318	CCTGCGTCCACTCAGGGTCATCAGCCGGGCCAGGAGCTGAAGCTGTGTGAGAGACTCT	4377
QY	1416	uMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleI	1436
Db	4378	GATGTCATCCCTCAACCCATTGGCAACATTGTGTTCATTGTGCTGTGCTTCATCAT	4437
QY	1436	ePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyLys	1456
Db	4438	TTTTGAATCTCGGGTGACGCTCTCAAGGGAAGTTCTTCGTGTGTCAAGGCTGAGGA	4497
QY	1456	pThrArgAsnIleThrAsnLysSerAspCysAlaGlnIleAserTyrArgTrpValArgHi	1476
Db	4498	CACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGATGGGTCCGCA	4557
QY	1476	sLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLy	1496
Db	4558	CAAGTACAACCTTTGACCAACCTGGGCCAGGCTCTGATGTCCCTGTTGTGCTGGCTCCAA	4617
QY	1496	sAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnPr	1516
Db	4618	GGATGTTGGGTTGACATCATGTATGATGGGCTGATGTGTGGTGATCAGCAGCC	4677
QY	1516	oIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAl	1536
Db	4678	CATCATGAACCAACACCCTGGATGCTGCTATACTTCATCTCCTTCCTCATCTGCGC	4737
QY	1536	aPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGl	1556
Db	4738	CTTCTTGTCTGAACATGTTTGTGGCGCTGTGTGTGAGAACTTCCATATGTGACAGAA	4797
QY	1556	nHisGlnGluGluGluValAlaArgArgGluGluLysArgLeuArgArgLeuGluLy	1576
Db	4798	GCACCAGAGAGAGAGAGCGGCGGTGAGAGAAAGCACTACGAGGCTGAGAA	4857
QY	1576	sLysArgArg-----SerLysGluLysGlnMe	1585
Db	4858	AAAGAGAGGAATCTAATGTTGAGCATGTAAATTGCTTCGGCAGCTCAGCCAGCGCTGC	4917
QY	1585	tAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHi	1605
Db	4918	GTCAGAAAGCCAGTGCAGAGCCCTACTACTGTGACTACTCGAGATTCCGGCTCCTGTCCA	4977
QY	1605	sHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnVa	1625
Db	4978	CCACCTGTGTACAGCCACTACCTGGAACCTTCATCACTGTGTGCATCGGGCTGAACGT	5037
QY	1625	lValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIl	1645
Db	5038	GGTCACTATGGCCATGGAACATTACAGCAGCCCAAGATCTTGAGAGCTTGGAAGAT	5097
QY	1645	eCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLysLeuValAlaPh	1665
Db	5098	CTGCAATTACATCTTTAACCGTCATCTTTGTCTTTGAGTCAGTTTCAAACTGTGGCTT	5157
QY	1665	eAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLe	1685
Db	5158	TGGCTTCCGCGTTTCTTCCAGAGACAGGTGGAACCACTGGAACCTGGCTATTGTCTTCT	5217
QY	1685	uSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnPr	1705
Db	5218	GTCATCATGGGCATCACACTGAGAGGATTGAGGTCAATGCTTCGCTGCCCATCAACC	5277
QY	1705	oThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMe	1725
Db	5278	CACCATCATCCGTATCATGAGGGTGCTCCGCATTGCTCGAGTTCTGAAGCTGTGAAGAT	5337
QY	1725	tAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAs	1745

Db 5338 GGCTGTGGCATGCGGGCACTGCTGGACACGGTGATGCAGGCCCTGCCAGGTGGGAA 5397
QY 1745 nLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaIaLeuGlyValGluLeuPh 1765
Db 5398 CCTGGGAACTTCTCTTCATGTTATTGTTTTCATCTTTGCAGCTCTGGGCGGTGAGCTCTT 5457
QY 1765 eGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPh 1785
Db 5458 TGGAGACCTGGAGTGTATGAGACACACCTTGTGAGGGCTTGGGTGGCATGCCACCTT 5517
QY 1785 eArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAs 1805
Db 5518 TAGGAAC TTGTGTATGGCTTTCTGACCCCTCTCCGAGTCTCCACTGGTGACAACTGAA 5577
QY 1805 nGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrVa 1825
Db 5578 TGGTATTATGAAGACACCCCTCCGGGACTGTGACAGAGTCCACCTGCTACACACTGT 5637
QY 1825 ILleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnVa 1845
Db 5638 CATCTCCCTATCTACTTTGTGTCTCTTCGTGCTGACGGCCCAAGTTGTGCTGTCAACGT 5697
QY 1845 lValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAl 1865
Db 5698 GGTCTATAGCTGTGTGATGAAGCACCTGGAGAAAGCAACAAAGAGGCCAAAGAGAGAGC 5757
QY 1865 aGluLeuGluValaGluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerPr 1885
Db 5758 CGAGCTCGAGGCCGAGCTGGAAGCTGAGATGAAGACGCTCAGCCCGCCGACCCCACTCCC 5817
QY 1885 oLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLy 1905
Db 5818 GCTGGGCAGCCCTCTCTGCGCCGCGGGTGAAGGTGTCAACAGTCTTGACAGCCCTAA 5877
QY 1905 sProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluH 1925
Db 5878 GCCTGGGGCTCCACACACCACTGCCACATGGAGCAGCCTCGGGCTCTCCCTTGAGCA 5937
QY 1925 sProThrmMetValProHisProGluGluValProValProLeuGlyProAspLeuLeuTh 1945
Db 5938 CCCCACGATGGTACCCCAACCCCGAGGAGGTGCCAGTCCCCCTAGGACCAAGACCTGTGAC 5997
QY 1945 rValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysAr 1965
Db 5998 TGTGAGGAAGTCTGGTGTCAGCCGAGCGCACTCTCTGCCAATGACAGCTACATGTGCCG 6057
QY 1965 gAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGl 1985
Db 6058 CAATGGGAGCACTGTGAGAGATCCCTAGGACACAGGGGCTGGGGCTCCCCAAAGCCCA 6117
QY 1985 nSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLe 2005
Db 6118 GTCAGGCTCCATCTTGTCCGTTCACTCCCAACAGACAGACACAGCTGCATCCTACAGCT 6177
QY 2005 uProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIlePr 2025
Db 6178 TCCCAAGATGTGCATATCTGCTCCAGCCTCATGGGGCCCCCACTGGGGGGCCCATCCC 6237
QY 2025 oLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaI 2045
Db 6238 TAAACTACCCCACTGGCCGCTCCCTCTGGCTCAGAGGCCCTCTCAGGGCGCCAGGCAGC 6297
QY 2045 aIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGl 2065
Db 6298 AATTAAGACTGACTCCCTGGATGTGAGGGCCTGGGTAGCCGGGAAGACCTGTTGTCAGA 6357
QY 2065 uValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIl 2085
Db 6358 GGTGAGTGGGCCCTCTGCTGCTGACCCGGTCTCATCTTCTGGGGCGGGTGCAGCAT 6417
QY 2085 eGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAl 2105

Db 6418 CCAGGTGACAGCGCTTCCGGCATCCAGACGAACAAAGTCTCCAAGCACATCCGCTGCCAGC 6477
QY 2105 aProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerIe 2125
Db 6478 CCCTTGCCAGGCGCTGGAACCCAGCTGGGCCAAAGAACCTTCCAGAGACCAAGAGAGCTT 6537
QY 2125 uGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGl 2145
Db 6538 AGAGCTGACACGGAAGCTGAGCTGATTTCAAGAGACCTCTCCAGAGACCGAGAAGA 6597
QY 2145 uProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrGlnSerCysArgAr 2165
Db 6598 ACCCTGTCCCAACGGGACCTGAAGAACTGTACAGTGTAGAGAACCAAGAGCTGCAGGCG 6657
QY 2165 gArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAs 2185
Db 6658 CAGGCTGGGTCTGCTAGATGAACAGCGGAGACACTTCATTGCTGTCAAGCTGTCTGGA 6717
QY 2185 pSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuGl 2205
Db 6718 CAGCGGCTCCCAACCCCGCTATGTCCAAGCCCTCAAGCCTCGGGGCCAAACCTTTGG 6777
QY 2205 YGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProPr 2225
Db 6778 GGGTCTGGGAGCGCGCTAAGAAATAAATCAGCCCAACCATATCTATAGACCCCC 6837
QY 2225 oGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlaPr 2245
Db 6838 GGAGAGCCAGGCTCTCGGCCCAATGCAGTCTGTGTCTGCTCAGAGAGGAGCGCC 6897
QY 2245 oAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaIaSerPr 2265
Db 6898 GGCCAGTGACTTAAGATCCCTCGGTCTCCAGCCCCCTTGACAGCAGCGCTGCTCAC 6957
QY 2265 oSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetAs 2285
Db 6958 CTCCCAAGAAAGACACGCTGAGTCTCTGTGTTGTCTTGACCCCAACAGACATGGA 7017
QY 2285 pPro 2286
Db 7018 CCCC 7021
RESULT 4
AAx83485
ID AAx83485 standard; cDNA; 6762 BP.
XX
AC AAx83485;
XX
DT 07-DEC-1999 (first entry)
XX
DE Rat T-type voltage-gated Ca channel alpha-1-g (rcav11a) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
OS Rattus sp.
XX
PN W09929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
XX
DR P-PSDB; AAY14590.
PT New T-type voltage-gated calcium channels.

XX Disclosure; Page 67-76; 138pp; English.

CC This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-g designated rCaV1.1a. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAX83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods are also disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
XX
SQ Sequence 6762 BP; 1362 A; 2044 C; 1917 G; 1439 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6762
Score: 11798.00 Matches: 2250
Percent Similarity: 99.78% Conservative: 0
Best Local Similarity: 99.78% Mismatches: 2
Query Match: 98.09% Indels: 3
DB: 2 Gaps: 0

US-09-611-257A-24 (1-2287) x AAX83485 (1-6762)

QY 34 TrpThrArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
DB 2 TGGACGAGGAGGAGATGAGCGGGCGCCGAGAGTCCGGACAGCCCGTAGCTTCACGC 61
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
DB 62 AGCTCAACGACCTGTCCGGGGCCGGGGCCGGCAGGGGGCGGTGACGAGAAAGAAC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValAlP 93
DB 122 CGGGCAGCGCGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCGGTGTT 181
QY 93 hePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 113
DB 182 TCTTCTACTTGAGCCAGACAGCCGCCCGGAGCTGGTGTCTCCGACGGTCTGTAAAC 241
QY 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
DB 242 CGTGGTTCGAGGAGTACATATGCTGTCTTCTCACTGTGTGACTCTGGGTATGT 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhea 153
DB 302 TCAGGCCGTGTGAGACATTGCTGTGACTCCAGCGCTGCCGATCCTGCAGGCCCTCG 361
QY 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
DB 362 ATGACTTCATCTTTGCCCTTCTTGTGTGAGAAATGGTGTGAAGATGGTGCCCTTGGCA 421
QY 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
DB 422 TCTTTGGGAAGAAATGTACCTGGGAGACATTGGAACCGGCTTGACTTTTCATTGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
DB 482 TTGCAGGAGATGTGAGTATTGCTGTGACCTGCAGAACGTACAGCTTCTCCGACGTCA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
DB 542 CAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCACGACATGCGATTCTCG 601

QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValIleuLeuLeuCysPhePhe 253
DB 602 TCACATTACTGTGACACCTTGCCCTATGCTGGCAACGTCCTGCTGCTTCTTCG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
DB 662 TCTTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGGACGAGACTGCTTCGCAACGGT 721
QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
DB 722 GCTTCCTCCCGAAGACTTCAGCTCCCTCCCTGACCGTGGACCTGAGCTTATTACAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
DB 782 CAGAGAAATGAGACGAGAGCCCTTCATCTGCTCTCAGCTCGGAGAAATGGCATAGAT 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333
DB 842 CCTGCAGAGATGTGCCACACTGCGTGGGAGCGGTGTGGCCACCTGCAAGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
DB 902 ACTATGACACCTATTAACAGTTCCAGCAACACCACTGTGTCACTGGAACCACTACTATA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
DB 962 CCAACTGCTCTGCGGGCGAGACAACCCCTTCAAGGCGCCATCACTTGACAACATTG 1021
QY 373 lYTyraIaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetC 393
DB 1022 GCTATGCTGTGATCGCCATCTTCAGGTTCATCATCTGAGGGCTGGGTGACATCATGT 1081
QY 393 YrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
DB 1082 ACTTCGTAATGAGACGCTCACTCCTTCTACAACCTTCATCTTCTTCATCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
DB 1142 TGGGCTCTTCTTCATGATCACTGTGCTGTGTGTGATTGCCACGCACTTCCGAGA 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
DB 1202 CCAAAACGCGGAGAGTCACTGATGCGGAGCAGCGTGAAGATTCTGTCATTAAGTACTG 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
DB 1262 GCACCTCGCAAGCTTCTGTAGCCAGGACAGCTGTATGAGAGTACTCAAGTAACTGG 1321
QY 473 alTyrIleLeuArgLysAlaIlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
DB 1322 TGTACATCTCCGAAAGACGCCGAAGCTGGCCAGGCTCTTAGGGTATAGGCGTGC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
DB 1382 GGGCTGGGCTGCTCAGCAGCCAGTGCGCCGTAGTGGGCAAGAGCCCAAGTGGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisIleSH 533
DB 1442 GGTGACTCGCTCACACCGTGTGTCTGTCCACCACTGGTCCACCACTACCAACC 1501
QY 533 lSHIshIshIshTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
DB 1502 ACCATCACCACTACCACTGGGTATGGAGCTCAGAGTTCCCGGGCCAGCCAGAGA 1561
QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
DB 1562 TCCAGGACAGGATGCCAATGGGTCTGCCGCTCATGTCAACACCACTTACACCCA 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
DB 1622 CTCCCTCTGGGGGCCCTCCGAGGGGTGCGAGTCTGTACACAGCTTCAACATGCTGACT 1681
QY 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613

Db 1682 GCCACTTGAGCCAGTCCGTGGCCAGGACCCCTCCAGATGCCCATCGGAGGATCTG 1741
Qy 613 lYargThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 633
Db 1742 GTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAAGCCCTCCACAGAGA 1801
Qy 633 lEleuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653
Db 1802 TACTGAAGATAAAGCACTAGTGAGGTGGCCCCAGCCCTGGGCCCCCACTCACCA 1861
Qy 653 eapheaSnileProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSert 673
Db 1862 GCTTCAACATCCCACTGGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGTA 1921
Qy 673 hrcGlyAlaCySHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAGGCGACAGTGAAG 1981
Qy 693 lAcYsgLysProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera 713
Db 1982 CCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGACGAGGACGAGAGTCCG 2041
Qy 713 lAspPhiSValMetProAspSerSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CTGACCATGTGCTGCTGACTCAGACAGCGAGGCTGTATGAGTTCAACAGAGCGCTC 2101
Qy 733 lnhISerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGAGCCTGGGCCAGATG 2161
Qy 753 lAgIuProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2162 CAGAGCCTTAGTTCTGTGTGGCTTTCTTGAGAGGTGATCTGTGACACACTCCGGAAGATCG 2221
Qy 773 aLaspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2222 TAGATAGCAAAATACTTGGCCCGGGGAATCATGATCGCCATCCTGGTGACATACTAGCA 2281
Qy 793 etcGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2282 TGGGCATCGAGTACCAGCAGCAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAACA 2341
Qy 813 lValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProp 833
Db 2342 TCGTCTTCACCAGCCTTTCGCTTGAGAGTGTGCTGAAAAGTGTCTTACGGTCCCT 2401
Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
Db 2402 TTGGCTACATTAAAGATCCCTTACAACATCTTGATGTGTGTCATTGTGTCATCAGTGTGT 2461
Qy 853 rpgIuIleValGlyGlnGlnGlyGlyLysLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2462 GGGAGATTGTGGCCAGCAGGAGGTGCGCTGCGGTGTCGGGACCTCCGCTGATGC 2521
Qy 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2522 GGGTGTCTGAAGCTGTGGCTTCTCTGCCGCGCTGCAGCGCAGCTGTGGTGTCTCATGA 2581
Qy 893 ySThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
Db 2582 AGACCATGGACAACGTGGCCACCTTCTGCATGTCTCTCATGTCTTTCATCTTTCATCTTCA 2641
Qy 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
Db 2642 GCATCCTGGGCATGCACTCTTTGGTTGCAAGTTCCGATCTGAACGGGATGGGACACAGT 2701
Qy 933 euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953
Db 2702 TGCACAGACCGGAAGATTTCGACTCCCTGTGCTGGGCCATCGTCACTGTCTTTCAGATTTC 2761
Qy 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA 973

Db 2762 TGACTCAGGAAGACTGGAATAAAGTCTCTCTACAAACGGCAGTGGCTCCACATCGTCTTGGG 2821
Qy 973 lAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
Db 2822 CTGCTCTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTAAACCTGTGG 2881
Qy 993 aLAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP 1013
Db 2882 TGGCCATTCTTGGAAGGATTCAGGAGAGGAGATGCCAACCAAGTGTGAGTCAGACC 2941
Qy 1013 roAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuV 1033
Db 2942 CTGATTTCTTTTCGCCAGTGTGATGGTGTGATGGGACAGAAAGAGCGCTTGCGCTGG 3001
Qy 1033 aLAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProLeuIleIleHisT 1053
Db 3002 TGGCTTTGGGAACAACGGGAACCTACGAAAGAGCCTTTTGGCACTTCATCATTCATA 3061
Qy 1053 hrcAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuG 1073
Db 3062 CGGCTGCAGACCAATGTACACACCCCAAGAGCTCCAGACAGGTGTGGGGGAAGCACTGG 3121
Qy 1073 lYserGlySerArgArgThrSerSerSerGlySeraAlaGluProGlyAlaAlaHisHisG 1093
Db 3122 GCTCTGCTCTGCAGTACCAAGTAGAGTGGGTCCGCTGAGCTTGAGCTGCCACCATG 3181
Qy 1093 lMetLysCysProProSerAlaArgSerSerProHisSerProTrpSeraAlaAsers 1113
Db 3182 AGATGAATGTCCGCCAAGTAGTCCCGCAGCTCCCGCACAGTCCCTGAGTGGCGGACGA 3241
Qy 1113 erTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA 1133
Db 3242 GCTGGACCAAGCAGCGCTCCAGCAGGAACAGCCTGGGCGGCCCCCAGCCTAAAGCGGA 3301
Qy 1133 rgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnLysGlnAspG 1153
Db 3302 GGAAGCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGAGAGGGCCAGGAGTCAAGATG 3361
Qy 1153 lGluGluSerSerGluGluLysAspArgAlaSerProAlaGlySeraSpHisArgHisArg 1173
Db 3362 AGGAGAAAGTTCAAGAAAGAGACCGGGCAGCCAGCAGGCAGTGACCATCGCCACAGGG 3421
Qy 1173 lYserLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG 1193
Db 3422 GTTCCTTGAACGTGAGGCCAAGAGTTCTTTGACCTGCTGACACTTGACAGTGGCGG 3481
Qy 1193 lYleuHisArgThrAlaSerGlyArgSerSeraLaserGluHisGlnAspCysAsnGlyL 1213
Db 3482 GGCTGACCCGCACAGCCAGCGCGGAGCTCTGCCTGTAGCAACCAAGACTGTATGGCA 3541
Qy 1213 ySSeraLaserGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA 1233
Db 3542 AGTCGGCTTCAGGGCGTTTGGCCCGCACCTTGAGGACTGTATGACCCCAACTGGATGGG 3601
Qy 1233 sPAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS 1253
Db 3602 ATGATGACAAATGATGAGGAAATCTGAGCAAAAGGGAACGCAITAAGCCTGGGTGAGAT 3661
Qy 1253 erArgLeuProAlaCysCysArgGluArgAspSerTrpSeraAlaTyrIlePheProProG 1273
Db 3662 CCCGGCTTCCTGCTGTTGGCCGAGCGAGATTCCTGTGCGGCTATATCTTCCCTCTC 3721
Qy 1273 lnsErArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV 1293
Db 3722 AGTCAAGGTTTCGTCTCCTGTGTACCGGATCATCACCCACAGAATGTTTGACCATGTGG 3781
Qy 1293 alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP 1313
Db 3782 TCCTCGTCATCATCTTCTCAACTGTATCAACCATCGCTATGAGCGGCCCAAAATTGACC 3841
Qy 1313 roHisSeraLagluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL 1333
Db 3842 CCCACAGCGCTGAGCGCATCTTCTGACCTCTCCAACTACATCTTCAAGGACAGTCTTTC 3901

Db 6062 TGCAAGGCGCTGGTAGCCGGGAAGACCTGTTGTACAGAGTGAGTGGGCCCTCCTGCCCTC 6121

Qy 2073 eutHrArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyI 2093

Db 6122 TGACCCGGTCTCATCTCTTGGGGCGGGTGCAGCATCCAGGTGCAGACGCGTTCCGGCA 6181

Qy 2093 leGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS 2113

Db 6182 TCCAGAGCAAAGTCTCCAAGCACATCCGCTGCAGCCCTTGCCAGGCTTGAACCCA 6241

Qy 2113 exTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT 2133

Db 6242 GCTGGGCCAAGACCCCTCCAGAGACCAGAACAGACTTAGAGCTGACACGAGCTGAGCT 6301

Qy 2133 rplLeSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuL 2153

Db 6302 GGATTTCAGGAGACCTCCTCCAGCAGCAGCAGGAAGAACCCCTGTTCCACGGGACCTGA 6361

Qy 2153 yslYsCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspG 2173

Db 6362 AGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGGCAAGCCTGGGTCTGGCTAGATG 6421

Qy 2173 lglGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuC 2193

Db 6422 AACAGCGGAGACACTCCATTGCTGTACGTGTCTGACAGCGGCTCCCAACCCCGCTTAT 6481

Qy 2193 ysProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysL 2213

Db 6482 GTCCAAGCCCCCTCAAGCCTCGGGGGCCAAACCTCTTGGGGGTCTCGGAGCGGCTAAGA 6541

Qy 2213 yslYsLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgProp 2233

Db 6542 AAAAAGCTCAGCCACCCAGATATCTCTATAGACCCCGGAGAGCAGGGGCTCTCGGCCCC 6601

Qy 2233 roCysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProS 2253

Db 6602 CATGACAGCTCTGTTGCTGTCTCCTCAGAGAGAGGGCGCGCCAGTGACTTAAGATCCCT 6661

Qy 2253 erValSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeus 2273

Db 6662 CGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCTCCCAAAGAAAGACACGCTGA 6721

Qy 2273 exLeuSerGlyLeuSerSerAspProThrAspMetCaspPro 2286

Db 6722 GTCTCTGTGTTGTCTTGAACCAACAGACATGACCCC 6762

RESULT 5

AAK83487 standard; cDNA; 6816 BP.

ID AAK83487

AC AAK83487;

XX 07-DEC-1999 (first entry)

DT

XX Rat T-type voltage-gated Ca channel alpha-1-G (rCav1.1c) cDNA.

DE

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;

KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

OS Rattus sp.

XX

PN WO9929847-A1.

XX 17-JUN-1999.

PD

XX 30-OCT-1998; 98WO-US023161.

PF

XX 05-DEC-1997; 97US-00985809.

PR

XX (LOYO) UNIV LOYOLA CHICAGO.

PA

XX Perez-Reyes E, Cribbs LL;

P1

XX WPI; 1999-394972/33.

DR P-PSDB; AAY14592.

XX New T-type voltage-gated calcium channels.

PT

XX Disclosure; Page 85-94; 138pp; English.

PS

XX This sequence represents the coding region for a rat T-type voltage-gated

CC calcium (Ca) channel alpha-1-G designated rCav1.1c. Voltage gated channels

CC are membrane bound glycosylated proteins formed of several subunits. The

CC large alpha subunits form a pore in the membrane that is selective for a

CC given ionic species. Each alpha subunit contains 4 domains (I, II, III

CC and IV) and each domain contains 6 putative transmembrane helical

CC segments (S1-S6). T-type Ca channels are activated at a lower voltage

CC than L- or N-type channels. Characteristics of T-type channels include

CC short current time, slow activation kinetics near threshold, fast

CC inactivation kinetics and slow tail current. The sequences AAX83481-

CC X83492 represent novel T-type voltage-gated Ca channel genes from humans

CC and rats. Each of the novel Ca-channels contains a putative IVS4 region

CC comprising the amino acid sequence AAY14598. Cells expressing the T-type

CC voltage-gated calcium channel proteins can be used to screen for drugs

CC which affect calcium channels. Methods are also disclosed for treating a

CC disease or disorder associated with a deficiency in a native T-type

CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

XX

SQ Sequence 6816 BP; 1373 A; 2058 C; 1932 G; 1453 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 6816

Score: 11767.00 Matches: 2248

Percent Similarity: 98.90% Conservative: 0

Best Local Similarity: 98.90% Mismatches: 5

Query Match: 97.83% Indels: 20

DB: 2 Gaps: 1

US-09-611-257A-24 (1-2287) x AAX83487 (1-6816)

Qy 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53

Db 2 TGCACGAGAGAGAGATGAGCGGGCGCGGAGAGTCCGGACAGCCCGTAGCTTCACGC 61

Qy 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspP 73

Db 62 AGCTCAACGACCTGTCCGGGCGGGGCGGCGGAGGCGGGGTGACGGAAGAGACC 121

Qy 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValAlP 93

Db 122 CCGGCGAGCGCGACTCCGAGCGGAGGGGTGCCGTACCCGGCGCTAGCCCCGGTGT 181

Qy 93 hepHeTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113

Db 182 TCTTCTACTTGAGCCAGACAGACCGCCCGGAGCTGTGTCTCCGACGGTCTGTACC 241

Qy 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133

Db 242 CGTGGTTGAGCGAGTCAGTATGTGTGATCTTCTCAACTGTGTGACTGTGGTATGT 301

Qy 133 hepArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153

Db 302 TCAGGCCGTGTGAGCATTTGCCTGTGACTCCAGCGCTGCCGATCCTCAGAGCCTTCG 361

Qy 153 spAspPheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGlyI 173

Db 362 ATGACTTCATCTTGCCCTTCTTGTGCTGTGGAATGTGTGATGTGTGGCTTGGGCA 421

Qy 173 lepHeGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193

Db 422 TCTTTGGGAAGAAATGTTAAGCTGGGAGACATTGGAACCGGCTTTTTCATTGTCA 481

Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213

Db 482 TTGCAGGAGATGCTGAGTATTCGTGACTGCAGAACGTACGCTTCTCCGACGTACAGGA 541

QY	213	hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV	233
Db	542	CAGTCCGTGTGTCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATTTCTCG	601
QY	233	alThrLeuLeuLeuAspThrLeuPrometLeuGlyAsnValLeuLeuLeuCysPhePheV	253
Db	602	TCACATTACTGCTGACACCTTGCCCTATGCTGGGCAACGTCCTGCTCTGTCTTCTCG	661
QY	253	alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC	273
Db	662	TCTTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGGCAGGACTGCTTCGCAACCGGT	721
QY	273	ysPheLeuProGluAsnDheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT	293
Db	722	GCTTCCTCCCCGAGACTTCAGCCTCCCCCTGAGCTGGAACCTGAGCCTTATTACAGA	781
QY	293	hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS	313
Db	782	CAGAGAATGAGACGAGAGCCCTTCATCTGCTCTCAGCCTCGGAGAATGGCATGAGAT	841
QY	313	erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA	333
Db	842	CCTGCAGAGTGTGCCACACTGCTGGGGAAGCCGCTGTGGCCCACTGCAGTCTGG	901
QY	333	sPTyrgluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrT	353
Db	902	ACTATGAGACCTATTACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCACTACTATA	961
QY	353	hrAsnCysSerAlaGlyGlnHisAsnProPheGlyAlaIleAsnPheAspAsnIleG	373
Db	962	CCAACCTGCTGCGGGCGAGACAACCCCTTCAAAAGGCCCATCACTTGACAACATTG	1021
QY	373	lyTyralaTrpIleAlaIlePheGlnValIleThrLeuGlnGlyTrpValAspIleMetT	393
Db	1022	GCTATGCCCTGGATCGCCCATCTTCCAGTCAACACTGAGGGGCTGGTGCACTCATGT	1081
QY	393	yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV	413
Db	1082	ACTTCGTAATGAGCGCTCACTCTTCTTACAACCTTCACTTCACTTCTTCTCATCATCG	1141
QY	413	alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT	433
Db	1142	TGGGCTCCTTCTTCATGATCAACTGTGCTGTGTGATGTCACGCAAGTTCTCCGAGA	1201
QY	433	hrLySglnArgGluSerGlnLeuMetArgGlnArgValArgPheLeuSerAsnAlaS	453
Db	1202	CCAAACAGCGGAGAGTCACTGATGCGGAGCAGCGTATGCAATTCTGTCCAATGCTA	1261
QY	453	erThrLeuAlaSerPheSerGluProGlySerCysTyrGlnGlnLeuLeuLysTyrIleuV	473
Db	1262	GTAACCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGAGCTACTCAAGTACCTGG	1321
QY	473	alTyrIleLeuArgLySAlaIleArgArgLeuAlaGlnValSerArgAlaIleGlyValA	493
Db	1322	TGTACATCTCTCGAAAAGCAGCCCGAAGGCTGGCCCAAGTCTTAGGGCTATAGGCGTGC	1381
QY	493	rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS	513
Db	1382	GGGCTGGGGCTGCTCAGCAGCCCACTGGCCCGTAGTGGCAGGAGCCCAAGCCAGTGCA	1441
QY	513	erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH	533
Db	1442	GCTGCACTCGCTCACACCGCTGCTGTCTGTCCACCACTGTGTCCACCACTACACACC	1501
QY	533	lshHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI	553
Db	1502	ACCATCACCACTACCACTGGGTATGGGACGCTCAGAGTTCCCGGGGCCAGCCCAAGAGA	1561
QY	553	legLAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProt	573
Db	1562	TCCAGGACAGGGATGCAATGGGTCTTCCCGGCTCATGCTACCAACCACTTACACCCA	1621

QY	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheThrHisAlaAspC	593
Db	1622	CTCCCTCTGGGGGCCCTCCGAGGGGTGGAGTCTGTACACAGCTTCTTACATGCTGACT	1681
QY	593	ySHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG	613
Db	1682	GCCACTTGAGGCCAGTCCGTTGTCACAGCACCCCTCCAGATGCCCATCGGAGCATCTG	1741
QY	613	lyArgThrValGlySerGlyLysValTyProThrValHisThrSerProProGluI	633
Db	1742	GTAGGACTGTGGTAGTGGGAAGGTGTACCCCACTGTGCATACAGCCCTCCACACAGA	1801
QY	633	leleuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs	653
Db	1802	TACTGAAGATAAAGCACTAGTGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACCA	1861
QY	653	erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT	673
Db	1862	GCTTCAACATCCCACTGGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACAGAGTA	1921
QY	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
Db	1922	CGGAGCCTGCCATAGCTCTGCAAAATCTCCAGCCCTTGCTCCAAAGCAGACAGTGAG	1981
QY	693	laCysGlyProAspSerCysProTyrcysAlaArgThrGlyAlaGlyGluProGluSera	713
Db	1982	CCTGCGGGCCGAGACAGTGTCTCTACTGTGCCCCGACAGAGACAGAGCCAGAGTCCG	2041
QY	713	laAspHisValMetProAspSerAspSerGluAlaValTyrcyluPheThrGlnAspAlaG	733
Db	2042	CTGACCATGTCTATGCTCTGACTCAGACAGCAGGCTGTATAGATTACACACAGAGCTC	2101
QY	733	lnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA	753
Db	2102	AGCACAGTAGCCTCCGGATCCCAACAGCCGCGGACAGCGGAGCCTGGGCCCAAGATG	2161
QY	753	laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV	773
Db	2162	CAGAGCCTAGTCTGTGCTGGCTTCTTGAGGCTGATCTGTACACATTCGGAAGATCG	2221
QY	773	alaSerLysTyrrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM	793
Db	2222	TAGATAGCAATACTTTGGCCGGGAATCATGATCGCATCTGTCATATACATCAGCA	2281
QY	793	etGlyIleGluTyrrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
Db	2282	TGGGCATCGAGTACCAGCAGCAGCCCGAGGAGCTCACCAACGCCCTGGAATCAGCACA	2341
QY	813	leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrcylProP	833
Db	2342	TGCTCTTCACCAGCCTCTTCGCTTGAGATGCTGTGAACCTGCTGTACGGTCCCT	2401
QY	833	heGlyTyrrIleLysAsnProTyrrAsnIlePheAspGlyValIleValIleSerValT	853
Db	2402	TTGGCTACATTAGAATCCCTACAACATCTTTGATGGTGTTCATTTGGTCATCAGTGTG	2461
QY	853	rrGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA	873
Db	2462	GGGAGATTGTGGCCAGCAGGGAAGGTGGCTGTCTGGTCTCGGACCTTCGGCTGATGC	2521
QY	873	rgValleuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893
Db	2522	GGGTGCTGAAGCTGTGTGGCTTCTGCGGCCCTGCAGCCGACGCTCGTGTCTCATGA	2581
QY	893	yrThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
Db	2582	AGACCATGGAACAAGTGGCACTTCTGCATGCTCCTCATGTCTTTCATCTTCATCTTCA	2641
QY	913	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL	933
Db	2642	GCATCTCGGGCATGCATCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGACAGCT	2701
QY	933	eudProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953

Db 2702 TGCCAGACCGGAAGATTTCGACTCCCTGCTGTGGGCATCGTCACTGTCTTTCAGATTTC 2761
Qy 953 euThrgIngluAspTrpAsnLysValLeuTyraSnglyMetAlaSerThrSerSerTrpa 973
Db 2762 TGACTCAGGAAGACTGGAAATAAAGTCCCTCTACACGGCATGGCTCCACATCGTCTTGGG 2821
Qy 973 laAlaLeuTyrrPheIlleAlaLeuMetThrPheGlyAsnTyrrValLeuPheAsnLeuLeuV 993
Db 2822 CTGCTCTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTTTAACTGTCTGG 2881
Qy 993 aAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP 1013
Db 2882 TGGCCATTCTTGTGAAGATTCCAGGACAGGAGATGCCACCAAGTCTGAGTCAGAGC 2941
Qy 1013 roAspPhePheSerProSerValAspGlyAspGlyAspArgLysblybArgLeuAlaLeuV 1033
Db 2942 CTGATTTCTTTTCCGCCAGTGTGATGTGATGGGACAGAAAGAGCCCTTGGCCCTGG 3001
Qy 1033 aAlaAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisT 1053
Db 3002 TGGCTTTGGAGAACACGGGAACTACGAAGAAGCCTTTTGGCACCCCTCATTCATATA 3061
Qy 1053 hAlaAlaThrProMetSerHisProLysSerSerThrGlyValGlyGluAlaLeuG 1073
Db 3062 CGGCTGCAGACCAATGTCAACCCCAAGAGCTCCAGACAGTGTGGGGAAACACTGG 3121
Qy 1073 LysSerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisG 1093
Db 3122 GCTCTGGCTCTCGACGTACAGTAGCAGTGGGTCCGCTGAGCCTGAGCTGCCACCATG 3181
Qy 1093 LuMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS 1113
Db 3182 AGATGAATGTCCGCCAAGTCCCGCAGCTCCCGCACAGTCCCTGAGTGGCGGCAAGCA 3241
Qy 1113 eTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA 1133
Db 3242 GCTGGACCAAGAGCGCGCTCCAGACAGAAACAGCTTGGGCCGGGCCCTTAAAGCGGA 3301
Qy 1133 rGSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspG 1153
Db 3302 GGAAGCCGAGCGGGAGCGGAGGTCCCTGTGTGTGAGAGGGCCAGAGAGTCAAGATG 3361
Qy 1153 LuGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG 1173
Db 3362 AGGAGAAAGTTCAGAAAGAGAACCGGGCCAGCCACAGGACAGTGAACATCGCCACAGGG 3421
Qy 1173 LysSerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG 1193
Db 3422 GTTCCTTGGAACGTGAGGCCAAGATTCTTGTGACTTGCTGACACTGTGCAGAGTGCCGG 3481
Qy 1193 LysLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213
Db 3482 GGTGCACCCGACACAGCCGAGCGCCGAGCTCTGCTCTGAGCACCAAGACTGTATGGCA 3541
Qy 1213 ySerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA 1233
Db 3542 AGTCGGCTTCAGGGCGTTTGGCCCCGACCCCTGAGGACTGATGACCCCAACTGGATGGGG 3601
Qy 1233 sPAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS 1253
Db 3602 ATGATGACAATGATGAGGGAAATCTGAGCAAAAGGGAAACGACAGACAAGCCTGGGTCA 3661
Qy 1253 exArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrrIlePheProProG 1273
Db 3662 CCGGCTTCCTGCTGTGCGAGAGCGAGATTCTGTGTCGGCTATATCTTCCCTCCTC 3721
Qy 1273 LnsErArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV 1293
Db 3722 AGTCAAGGTTTCGTCTCTGTGTACCCGATCATCAACCAAGATGTTTGACCATGTGG 3781
Qy 1293 alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP 1313

Db 3782 TCCTCGTCATCATCTTCCTCAACTGTATCAACCATCGCTATGAGCGCCCAAAATTGACC 3841
Qy 1313 roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrrIlePheThrAlaValPheL 1333
Db 3842 CCCACAGCGCTGAGGGCATCTTCTGACCCCTCTCCAACACTACATCTTCAACGGCAGTCTTC 3901
Qy 1333 euAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrrL 1353
Db 3902 TAGCTGAATGACACTGAAGGTGTGGCACTGGGCTGTGTGTTGGGGAGCAGGCCCTACC 3961
Qy 1353 euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL 1373
Db 3962 TGGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGTCTCATCTCCGTCAATCGACATCC 4021
Qy 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393
Db 4022 TGGTCTCATGTGTCTCCAGACGGCACCAAGATCCTTGGCATGTGAGGGTGTGGCGC 4081
Qy 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413
Db 4082 TGCTGCGAGACCTGCGTCCACTCAGGGTCAATCAGCCGGGCCAGGAAGCTGAAGCTGTGG 4141
Qy 1413 aGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaP 1433
Db 4142 TAGAGACTGTGATGTATCCCTCAAAACCATTTGGCAACATTTGTGTCTGTGCTG 4201
Qy 1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453
Db 4202 TCTTCATCATTTTGAATTTCTCGGGGTGCAAGCTTTCAAAGGGAAGTCTTCGTGTGTC 4261
Qy 1453 LngLysLysAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrrArgT 1473
Db 4262 AGGGTGAGGACACCAAGAAATCACTAACAAATCCGACTGCCCTGAGGCCACTACCGAT 4321
Qy 1473 rpValArgHisLysTyrrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493
Db 4322 GGGTCCGGCACAAATTAACAATTGACAACCTGGGCCAGGCTGTGATGTCCCTGTTGTGC 4381
Qy 1493 euAlaSerLysAspGlyTrpValAspIleMetTyrrAspGlyLeuAspAlaValGlyValA 1513
Db 4382 TGGCTCCAAAGGATGTTGGGTGACATCATGTATGATGGGCTGTGATGCTGTGGGTGG 4441
Qy 1513 spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrrPheIleSerPheLeuL 1533
Db 4442 ATCAGACGCCCATGATGAACCAACACCCTGGATGCTGTATATCTCATCTCTCTCC 4501
Qy 1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL 1553
Db 4502 TCATCGTGGCTTCTTGTCTCTGAACATGTTGTGGCGGTGGTGGAGAATTCCATTA 4561
Qy 1553 ySAspArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeuArgA 1573
Db 4562 AGTCAGACAGACCAAGAGAGAGAGAGGGCGGCGGTGAGGAGAAAGCACTACCGGA 4621
Qy 1573 rGLeuGluLysLysArgArgSerLysGluLysGlnMetAla----- 1586
Db 4622 GCGTGGAGAAAAGAGAAAGAGTAAGGAGAAAGCAGATGGCCGATCTAATGTTGACGATG 4681
Qy 1587 -----GluAlaGlnCysLysProTyrrTyrs 1595
Db 4682 TAATTGCTTCGGGAGCTCAGCCAGCGCTGCTCAGAAAGCCCAAGCCCTACTACT 4741
Qy 1595 eAspTyrrSerArgPheArgLeuLeuValHisHisLysCysThrSerHisTyrrLeuAspL 1615
Db 4742 CTGACTACTCGAGATTCGGGCTCCTTGTCCACCACTGTGTACAGCCACTACCTGAGCC 4801
Qy 1615 euPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrrGlnG 1635
Db 4802 TCTTCATCACTGGTGTATCGGGCTGAACGTGTCACTATGGCCATGGAACATTACCAAGC 4861
Qy 1635 LnPProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrrIlePheThrValIlePheV 1655
Db 4862 AGCCCCAGATCCTGAGCAGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTGG 4921

PD 17-JUN-1999.
XX
XX 30-OCT-1998; 98WO-US023161.
XX
XX 05-DEC-1997; 97US-00985809.
XX
XX (LOYO) UNIV LOYOLA CHICAGO.
XX
XX PI Perez-Reyes E, Cribbs LL;
XX
XX
XX WPI; 1999-394972/33.
XX
XX P-PSDB; AAY14591.
XX
XX
XX New T-type voltage-gated calcium channels.
XX
XX
XX Disclosure; Page 76-85; 138pp; English.
XX
XX
XX This sequence represents the coding region for a rat T-type voltage-gated
XX calcium (Ca) channel alpha-1-G designated rCavT1b. Voltage gated channels
XX are membrane bound glycosylated proteins formed of several subunits. The
XX large alpha subunits form a pore in the membrane that is selective for a
XX given ionic species. Each alpha subunit contains 4 domains (I, II, III
XX and IV) and each domain contains 6 putative transmembrane helical
XX segments (S1-S6). T-type Ca channels are activated at a lower voltage
XX than L- or N-type channels. Characteristics of T-type channels include
XX short current time, slow activation kinetics near threshold, fast
XX inactivation kinetics and slow tail current. The sequences AAX83481-
XX X83492 represent novel T-type voltage-gated Ca channel genes from humans
XX and rats. Each of the novel Ca-channels contains a putative IVS4 region
XX comprising the amino acid sequence AAY14598. Cells expressing the T-type
XX voltage-gated calcium channel proteins can be used to screen for drugs
XX which affect calcium channels. Methods are also disclosed for treating a
XX disease or disorder associated with a deficiency in a native T-type
XX calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
XX
XX Sequence 6795 BP; 1366 A; 2055 C; 1923 G; 1451 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6795
Score: 11751.50 Matches: 2244
Percent Similarity: 99.07% Conservative: 1
Best Local Similarity: 99.03% Mismatches: 8
Query Match: 97.70% Indels: 13
DB: 2 Gaps: 1

US-09-611-257A-24 (1-2287) x AAX83486 (1-6795)

QY 34 TrpThrArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACGAGGAGGAGATGGAGCGGGCGCGAGAGTGGGACAGCCCGGTAGCTTCACGC 61
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
Db 62 AGCTCAACGACCTGTCCGGGGCCGGGGCGCGGCGGGGTCCGACGAAAGGACC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACC GGCGCTAGCCCCGGTGT 181
QY 93 hepheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 113
Db 182 TCTTCTACTTGAGCCAGGACAGCCGCCGCGAGCTGTGTCTCCGACGGTCTGTAAAC 241
QY 113 roTrrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CGTGGTTCGAGCGAGTCAGTATGTGTCATCTTCTCAACTGTGTGACTCTGGGTATGT 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGluAlaPheA 153
Db 302 TCAGGCCGTGTGAGACATGTGCTGTGACTCCAGCGCTGCCGATCCGACAGCCTTCG 361
QY 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173

Db 362 ATGACTTCATCTTTCCTTCTTTCCTGTGGAATGTGTGAGATGTGTGCCCTTGGCA 421
QY 173 lePheGlyLysIysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
Db 422 TCTTTGGGAAGAAATGTATACCTGGAGACACTTGGAACCGGCTTGACTTTTCATTGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TTGCAGGGATGCTGAGATATTCCGTGACCTGCAGAACGTCAAGCTTCTCCGAGTCAGGA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTCTGCGACCGCTCAGGGCCATTAAACGGGTGCCCATGCGCATTTCTCG 601
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACATTACTGTGGACACCTTGCTGATGCTGGCAACGTCCTGCTGCTGTTCTTCG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGAGACTGCTTCGCAACCGGT 721
QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspIleGluProTyrTyrGlnT 293
Db 722 GCTTCTCCCGAGAACTTCAGCCTCCCGCTGAGCGTGACCTGGAGCCTTATTACCA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGATGAGGACGAGAGACCCCTTCACTGTCTCTCAGCCTCGGAGAGATGGCATGAGAT 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGGAGTGTGCCCACTGCTGGGGGAAGGCGGTGTGGCCCACTGCAGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGACCTATTAAGTTCCAGCAACCACTGTGTCAACTGGAAACAGTACTATTA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCTGGCGGCGAGCACCAACCCCTTCAAAGCGCCATCACTTGACCAACATTG 1021
QY 373 lYTyrrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
Db 1022 GCTATGCTGTGATGCCATCTTCCAGGTCAACACTGGAGGCTGGGTGCACATCATGT 1081
QY 393 yrrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACTTCGTATGAGCGCTCACTCCTTCTTCAACTTCATCTACTTCTTCTCATCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTCTTATGATCAACCTGTGCTGTGTGATTGCCAGATTCTCCGAGA 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAAACAGCGGAGAGTCACTGATGCGGAGCAGCGTGTACGATTCTCTGCCAATGCTA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCCCTGGCAAGCTTCTCTGAGCCAGGCACTGCTATGAGGAGCTACTCAAGTACCTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCTCCGAAAGAAGACGCCCGAAGCTGGCCCAAGTCTTAGGGCTATAGCGCTGC 1381
QY 493 rGAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGCTGGGCTGCTCAGACAGCCCAAGTGGCCCTGTAAGTGGCAGGAGCCCAAGCAGTGGA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisSH 533
Db 1442 GCTGCACTGGCTCACACCGTGTGTGTCTGTCCACCACCTGTGTCCACCACATCACACC 1501

QY	533	ISHISHIHIEYTHISLEUGLYASNGLYTHIRLEUARGVALPROARGALASERPROGLUI	553
Db	1502	ACCATCACCACCTACCACTGGGTAATGGAGCGCTCAGAGTTCCCGGGCCAGCCAGAGA	1561
QY	553	LEGASPARGASPARAASNGLYSERARGARGLEUWETLEUPROPROPROSERTHRPROT	573
Db	1562	TCCAGGACAGGATGCCAATGGGTCTCGCCGGCTCATGTACCACCACTCTACACCCA	1621
QY	573	HRPROSERGLYIPROPROARGGLYALAGLUSERVALHISERPHETHISALASPC	593
Db	1622	CTCCCTTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGTGACT	1681
QY	593	YSHISLEUGLUPROVALARGCYSGLNALAPROPROPROARGCYSPROSERGLUALASERG	613
Db	1682	GCCACTTGAGCCAGTCCGTTGTCAGGACACCCCTCCAGATGCCATCGAGGCACTGTG	1741
QY	613	LYARGTHRVALGLYSERGLYLYSVALTYRPROTHRVALHISTHRSERPROPROGLUI	633
Db	1742	GTAGAGCTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACAGAGA	1801
QY	633	LELEULYASPLYSALEUVALGLUVALALAPROSERPROGLYPROPROTHRLEUTHRS	653
Db	1802	TACTGAAGGATAAAGCACTAGTGGAAGGTGCCCCCAGCCCTGGGGCCCCCACCCTCACCA	1861
QY	653	ERPHEASNIIEPROPROGLYPROPHESERSERMETHISLYSLEULEUGLUTHRGINSERT	673
Db	1862	GCTTCAACATCCCACTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGTA	1921
QY	673	HRGLYALACYSHISSESECYSLYSILESESERPROCYSERLYSALASPSERGLYA	693
Db	1922	CGGAGCCTGCCATAGTCTCTGCAAAATCTCAGCCCTTGCTCCAAGCAGACAGCTGGAG	1981
QY	693	IACYGLYPROASPSERCYSPROTYRCYSALARGTHRGLYALAGLYLUPROGLUSERA	713
Db	1982	CCTGGGGCGCGACAGTGTTCCTACTGTGCCCGAGACGAGACAGAGCCAGAGTCCG	2041
QY	713	IASPHISVALMETPROASPSERASPSERGLUALAVALTYRGLUPHETHRGINASPDLAG	733
Db	2042	CTGACCATGTCTATGCTCTGACTCAGACAGCGAGCTGTGTATGAGTTCACACAGACGCTC	2101
QY	733	INHISERASPLEUARGASPPROHISERARGARGGLNARGSERLEUGLYPROASPA	753
Db	2102	AGCACAGTAGCTCCGGGATCCCAACAGCCGGCGGACAGCGGAGCCTGGGGCCGAGTG	2161
QY	753	IAGLUPROSERSEVALLEUALAPHETRPARGLEUIECYASBPTHRPHARGLYILEV	773
Db	2162	CAGAGCCTAGTCTGTGTGGCTTCTTGAGGCTGATCTGTGACACATTCCGGAAGATCG	2221
QY	773	ALASPSERLYSTRPHEGLYARGGLYILEMETILEALILEUVALASNTHRLEUSERM	793
Db	2222	TAGATAGCAATACTTTGGCCGGGAATCATGATCGCCATCCTGTCATATACACTGACA	2281
QY	793	ETGLYILEGLUTYRHIEGLUCINPROGLUGLULEUTHRASNALALEUGLUILESERASNI	813
Db	2282	TGGGCATCGAGTACCACGAGCAGCCGAGGAGCTCACCAACGCCCTGGAAATCAGCACACA	2341
QY	813	LEVALPHETHRSERLEUPHEALALEUGLUMETLEULEULYSLEULEUVALTYRGLYPROP	833
Db	2342	TGCTCTTACCACGCTTTCGCTTGAGAGATGCTGTGAACCTGCTGTCTACGGTCTCT	2401
QY	833	HEGLYTYRIIELYASNPCTRYASNIIEPHEASPGLYVALIIEVALIIESESERVALT	853
Db	2402	TTGGCTACATTAGAATCCCTACAACATCTTTGATGGTGTCAATTGTGTCATCAGTGTGT	2461
QY	853	RPGLUIIEVALGLYGLINGLYGLYGLYLEUSERVALLEUARGTHRPHARGLEUMETA	873
Db	2462	GGGAGATTGTGGCCACGAGGAGGTGGCCTGTCCGTGTGCGGACCTCCCGCTGATGC	2521
QY	873	RGVALLEULYSLEUVALARGPHELEUPROALALEUGLNARGGLNLEUVALIIEUWETL	893
Db	2522	GGGTGCTGNAAGCTGTGTGCGCTTCTGCCCCGCTGCAGCGCCAGACTCGTGTGCTCATGA	2581

QY	893	YSTHrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
Db	2582	AGACCATGACACACGTGGCCACCCTTCTGCATGCTCTCATGCTGTTCATCTTCATCTTCA	2641
QY	913	erIleLeuGIyMeChIseuPheGIyCysIyPheAlaSerGIyArgAspGIyAspThrL	933
Db	2642	GCATCCTGGGCATGCATCTCTTGGTTGCAGTTCCGATCTGAACGGATGGGACACGT	2701
QY	933	eUPrAspArgIyAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953
Db	2702	TGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATTTC	2761
QY	953	eUTHrGlnGIyAspTrpAsnIySvalLeuTyraSngIyMetAlaSerThrSerSerTrpA	973
Db	2762	TGACTCAGGAAGACTGGAATTAAGTCTCTTACAACGGCATGGCTCCACATCGTCTTGGG	2821
QY	973	laAlaLeuTyrrPheIleAlaLeuMetThrPheGIyAsnTyrrValLeuPheAsnLeuY	993
Db	2822	CTGCTCTTACTTCACTCGCCCTCATGACTTTTGGCACTATGTGCTCTTAACCTGCTGG	2881
QY	993	aAlaIleLeuValGIyGIyPheGlnAlaGIyAspAlaThrIySerSerGIySerGIyup	1013
Db	2882	TGGCCATTCTTGTGGAAGATTCCAGGCAGAGGAGATGCCACCAAGTCTGAGTCAGACC	2941
QY	1013	roAspPhePheSerProSerValAspGIyAspGIyAspArgIySylsArgLeuAlaLeuV	1033
Db	2942	CTGATTCTTTTCGCCAGTGTGATGTGATGGGACAGAAAGAGCGCTTGGCCCTGG	3001
QY	1033	aAlaLeuGIyGIyIleAlaGIyLeuArgIySerLeuLeuProProLeuIleIleHisT	1053
Db	3002	TGGCTTTGGAGAACACGCGGAAGTACGAAGAAGCTTTTGGCCACCCCTCATCTTCATA	3061
QY	1053	hrrAlaAlaThrProMetSerHisProIySerSerSerThrGlyValGIyGIyAlaLeuG	1073
Db	3062	CGGCTCGACACCAATGTTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTGG	3121
QY	1073	IySerGIySerArgArgThrSerSerSerGIySerAlaGIyProGIyAlaIleHisIG	1093
Db	3122	GCTTGCTCTTCGACGTACCAAGTAGAGTGGGTCCCTGAGCTTGAGCTGCCACCATG	3181
QY	1093	IuMetIySCySProProSerAlaArgSerSerProHisSerProTrpSerAlaIleSers	1113
Db	3182	AGATGAATATGTCGCGCAAGTGCCCGAGCTCCCGCACAGTCCCTGAGTGGCGCAAGCA	3241
QY	1113	erTrpThrSerArgArgSerSerArgAsnSerLeuGIyArgAlaProSerLeuIySArgA	1133
Db	3242	GCTGACCACGAGCGCGCTCCAGCAGAACAGCCTGGCGCCGCCCAAGCTTAAGCGGA	3301
QY	1133	rgSerProSerGIyGIyArgArgSerLeuLeuSerGIyGIyGlnGIyGlnIySerGIyAspG	1153
Db	3302	GGAGCCCCGAGCGGGGAGCGGAGGTCCCTGCTGTGTGAGAGGGCCAGAGAGTCAAGATG	3361
QY	1153	IuGIyGlnIySerSerGIyGIyAspArgAlaSerProAlaGIySerAspHisArgHisArgG	1173
Db	3362	AGGAGGAAGTTCAGAGAGAGGACCGGGCCAGCCCAAGCAGTGAACCATCGCCACAGGG	3421
QY	1173	IySerLeuGIyArgGIyAlaIlySerSerPheAspLeuProAspThrLeuGlnValProG	1193
Db	3422	GTTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCTGACACTCTGCAGAGTCCGG	3481
QY	1193	IyLeuHisArgThrAlaSerGIyArgSerSerAlaSerGIyIleGlnAspCySAsnGIyL	1213
Db	3482	GGCTGCACCGCACAGCCAGCGCGCGGAGCTGTGCTTGAGACCAAGAAGTGAATGGCA	3541
QY	1213	IySerAlaSerGIyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGIyA	1233
Db	3542	AGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGGACTGATGACCCCAACTGGATGGGG	3601
QY	1233	spAspAspAsnAspGIyGIyAsnLeuSerIyGIyGIyArgIleGlnAlaTrpValArgS	1253
Db	3602	ATGATGACAAATGATGAGGGAATCTGAGCMAAGGGGAACGATACAAGCCTGGGTCAAGT	3661
QY	1253	erArgLeuProAlaCySArgGIyArgGIyArgAspSerTrpSerAlaTyrrIlePheProProG	1273

Db 3662 CCCGGCTTCCTGCTGTGGCCGAGAGCGAGATTCCTGGTCCGCTATACTTTCCTCCTC 3721
QY 1273 InSerArgPheArgLeuLeuCySHisArgIleIleThrHisLysMetPheAspHisVal 1293
Db 3722 AGTCAAGGTTTCGTCTCTGTGTACCCGGATCATCACCCACAAGATGTTGACCATGTGG 3781
QY 1293 alleuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAsp 1313
Db 3782 TCCTCGTCATCATCTTCTCAACTGTATCACCATCGCTATGAGCGCCCAAAATTGACC 3841
QY 1313 roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPhe 1333
Db 3842 CCCACAGCGCTGAGCGCATCTCTGACCCTCTCCAACATACTACATCTTCACGGCAGTCTTC 3901
QY 1333 euAlaGluMetThrValLysValAlaIleuGlyTrpCysPheGlyGluGlnAlaTyr 1353
Db 3902 TAGCTGAATGACAGTGAAGGTGGTGGCACTGGGCTGGTCTTGGGGAGACAGCCCTACC 3961
QY 1353 euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIle 1373
Db 3962 TGGCGACGACGTGGAATGTGCTGGAACGGCTTGCTGCTCATCTCCGTCATCGACATCC 4021
QY 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArg 1393
Db 4022 TGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGTGAGGGGTGCTGGCG 4081
QY 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuVal 1413
Db 4082 TGGTCGCGACCCCTGCGTCCACTCAGGGTCATCAGCCGGCCAGGGAATGAAGCTGTGG 4141
QY 1413 alGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCysAlaP 1433
Db 4142 TAGAGACTGTGATGTCATCCCTCAAAACCATGGCAACATTGTGTCATTGTGCTGCTC 4201
QY 1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCys 1453
Db 4202 TCTTCATCATTTTGGAAATCTCGGGGTGCAGCTTCAAGGGAAGTTCTTCGTGTGC 4261
QY 1453 InGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArg 1473
Db 4262 AGGGTGAGGACACCAAGAAATCATCACTAACAAATCCGACTGCGCTGAGGCCACGTA 4321
QY 1473 rpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheVal 1493
Db 4322 GGGTCCGGCACAGTAACAATTGACAACCTGGGCCAGGCTTGATGTCCCTGTTGTGC 4381
QY 1493 euAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyVal 1513
Db 4382 TGGCTCCCAAGGATGTTGGGTTGACATCATGTATGATGGCTGGAATGCTGTGGGTGG 4441
QY 1513 spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeu 1533
Db 4442 ATCAGCAGCCCATCATGAACCAACACCCCTGATGCTGCTATACTCATCTCCTCTCC 4501
QY 1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHis 1553
Db 4502 TCATCGTGGCTTCTTGTCTCTGAACATGTTGTGGCGGTGGTGGAGAACTTCATA 4561
QY 1553 ySCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArg 1573
Db 4562 AGTGCAGACAGCACCGAGGAGGAGGAGGCGGCGGTGAGAGAAAGCACTACGGA 4621
QY 1573 rgLeuGluLysLysArgArg-----SerLysG 1582
Db 4622 GGCTGGAGAAAAAGAGGAATCTAATGTTGACGATGTAATGCTTCCGGCAGCTCAG 4681
QY 1582 LuLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArg 1602
Db 4682 CCAGCGGTGCGTCAGAAAGCCCAAGTCAAGCCCTACTACTCTGACTACTCGAATTCGGC 4741
QY 1602 euLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleG 1622

Db 4742 TCCTTGTCACCAACCTGTGTACCAGCCACTACCTGAGCCTCTTCATCACTGGTGCATCG 4801
QY 1622 lYLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGlu 1642
Db 4802 GGCTGAACGTGTCACTATGAGCCATGGAACATTACCAGCAGCCCATGATCCTGAGCAGG 4861
QY 1642 laLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLys 1662
Db 4862 CTCTGAAGATCTGCAATTACATCTTAACGTCATCTTGTCTTGAAGTCAAGTTTCAAC 4921
QY 1662 euValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAla 1682
Db 4922 TTGTGGCCTTGGCTTCGCCGCTTCTTCCAGGACAGGTGGAACCAAGTGGACCTGGCTA 4981
QY 1682 leValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSerLeu 1702
Db 4982 TTGTGCTTGTTCATCATGAGGCATCACACTGAGAGAGATTGAGGTCAATCTGTCCGTGC 5041
QY 1702 roIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLys 1722
Db 5042 CCATCAACCCCAACATCATCCGATCATAGAGGGTGTCCGCATGTCTCGAGTTCTGAAGC 5101
QY 1722 euLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuPro 1742
Db 5102 TGTGAAGATGCTGTGGCATGGCGCACTGCTGCACACGGTGATGCAGGCCCTGCC 5161
QY 1742 InValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGly 1762
Db 5162 AGTGGGGAACCTGGGACTTCTCTTCATGTATTGTTTCATCTTGCAGCTCTGGGCG 5221
QY 1762 alGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArg 1782
Db 5222 TGGAGCTCTTTGAGACACCTGGAAGTGTATGAGACACACCTTGTGAGGGCTTGGGTCCG 5281
QY 1782 isAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGly 1802
Db 5282 ATGCCACCTTTAGGAACCTTGGATGGCCTTTCGACCCTCTCCGAGTCTCCACTGGTG 5341
QY 1802 spAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerThrCys 1822
Db 5342 ACAACTGAATGATATTATGAAGACACCTCCGGACTGTGACCAGAGTCCACTGTCT 5401
QY 1822 yrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheVal 1842
Db 5402 ACAACACTGTCACTCCCTATCTACTTGTGTCTTCGCTGACGGCCCAAGTTGTGC 5461
QY 1842 euValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAla 1862
Db 5462 TGGTCAACGTGTATAGCTGTGTGATGAAGCACCTGGAAGAAAGCAACAAGAGGCCA 5521
QY 1862 ySGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerProGln 1882
Db 5522 AGGAGGAGGCCAGCTCGAGGCCGAGCTGGAAGTGAAGACGCTCAGCCCGCAGC 5581
QY 1882 roHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThr 1902
Db 5582 CCCACTCCCCGCTGGGCAGCCCTTCTCTGGCCCCGGGGTGAAGGGGTGCAACAGTACTG 5641
QY 1902 spSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaIleAspGlyPhe 1922
Db 5642 ACAGCCCTAAGCTGGGGCTCCACACCACTGCCCACTTGAAGCAGCCTCGGGCTTCT 5701
QY 1922 erLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyPro 1942
Db 5702 CCCTTGAGCAACCCACAGATGTACCCACCCGAGAGGTGCCAGTCCCCCTAGACACAG 5761
QY 1942 spLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSer 1962
Db 5762 ACCTGCTGACTGTGAGGAAGTGTGTGTACGCCGACGCACCTCTGCCCCAATGACACT 5821
QY 1962 yrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLeu 1982
Db 5822 ACATGTGCCGAATGGAGCACTGTGAGAGATCCCTAGGACACAGGGGCTGGGGCTCC 5881

OY 1982 rolyenlaglnSerGlySerileuSerValHisSerGlnProAlaAspThrSerCysI 2002
DB 5882 CCAAGCCAGTCAAGGCTCCATCTGTCCGTCACTCCCAACGACAGACACCACTGCA 5941
OY 2002 leleuGlnleuProlyAspValHisTyrleuGlnProHisGlyAlaProThrTrpG 2022
DB 5942 TCCTACAGCTTCCCAAGATGTGCACTATCTGCTCCAGCCTCATGGGGCTCCACCTGGG 6001
OY 2022 lyaAlaileProlySleuProProGlyArgSerProleuAlaGlnArgProleuArg 2042
DB 6002 GCGCATCCCTAACTACCCCACTGCGCTCCCTCTGGCTCAGAGGCTCTCAGGC 6061
OY 2042 rgglnAlaAlaileArgThrAspSerleuAspValGlnGlyleuGlySerArgGluAspL 2062
DB 6062 GCCAGGCAATAGAGACTGACTCCCTGATGTGACGGCCTGGGTAGCCGGAAGACC 6121
OY 2062 euleuSerGluValSerGlyProSerCysProleuThrArgSerSerPheTrpGlyG 2082
DB 6122 TGTTGTCAAGGTGAGTGGCCCTCTGCTGACCCGGTCTCATCTTCTGGGGCG 6181
OY 2082 lySerSerileGlnValGlnArgSerGlyIleGlnSerlyValSerlyHisIleA 2102
DB 6182 GGTCCAGCATCCAGGTGACAGCAGCTTCGGCATCCAGACAAAGTCTCCAAGCACATCC 6241
OY 2102 rgleuProAlaProCysProGlyleuGluProSerTrpAlaLysAspProProGluThra 2122
DB 6242 GCCTGCCAGCCCTTGCCCAAGGCTTGGAACCCAGCTGGGCCAAGACCTTCCAGAGACCA 6301
OY 2122 rgsSerSerleuGluAspThrGlnleuSerTrpIleSerGlyAspLeuLeuProSers 2142
DB 6302 GAAGCAGCTTAGAGCTGACACAGGAGCTGAGTGAATTGACAGAGACCTCTTCCAGCA 6361
OY 2142 erglnGlnGluProleuPheProArgAspLeuLysCysTyrSerValGlnThrGlnS 2162
DB 6362 GCCAGAGAAAGACCCCTGTCCACGGGACCTGAAGAAGTGCTACAGTGTAGAGACCCAGA 6421
OY 2162 erCysArgArgArgProGlyPheTrpLeuAspGlnArgArgHisSerileAlaValS 2182
DB 6422 GCTGCAGGCGCAGGCTGGGTTCTGGCTAGATGAACAGCGAGACACTCCATTGCTGTC 6481
OY 2182 erCysleuAspSerGlySerGlnProArgleuCysProSerProSerSerleuGlyG 2202
DB 6482 GCTGTCTGACAGCGGCTCCCAACCCGCTATGTCCAAGCCCTCAAGCCTCGGGGGCC 6541
OY 2202 lnProleuGlyGlyProGlySerArgProlySlySleuSerProProSerIleSeri 2222
DB 6542 AACCTTGGGGGTCTCTGGAGCCGGCTTAAGAAAACTCAGCCACCCAGTATCTTA 6601
OY 2222 leAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysleuArg 2242
DB 6602 TAGACCCCCCGAGAGACGAGGCTCTGGGCCCCCATGACGTCTGTGTCTGCTCAGGA 6661
OY 2242 rgaArgAlaProAlaSerAspSerlyAspProSerValSerSerProleuAspSerThra 2262
DB 6662 GGAGGGCGCGCCCACTGACTTAAGATCCCTCGGTCTCCAGCCCCCTTGACAGCAGCG 6721
OY 2262 laAlaSerProSerProlySlyAspThrleuSerleuSerGlyleuSerSerAspProT 2282
DB 6722 CTGCCTCACCTTCCCAAGAAAGACAGCTGAGTCTCTGTGTTTGTCTTGTGACCCAA 6781
OY 2282 hrAspMetAspPro 2286
DB 6782 CAGACATGACCCC 6795
RESULT 7
AAx83488 standard; cDNA; 6741 BP.
XX AAx83488;
XX
DT 07-DEC-1999 (first entry)
XX

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav1d) cDNA.
XX
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; db.
XX
OS Rattus sp.
XX
PN W09929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
DR P-PSDB; AAY14593.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 94-103; 138pp; English.
XX
CC This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-G designated rCav1d. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAx83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods are also disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6741 BP; 1355 A; 2041 C; 1908 G; 1437 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 6741
Score: 11747.50 Matches: 2242
Percent Similarity: 99.47% Conservative: 1
Best Local Similarity: 99.42% Mismatches: 3
Query Match: 97.67% Indels: 9
DB: 2 Gaps: 1
US-09-611-257A-24 (1-2287) x AAx83488 (1-6741)
OY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
DB 2 TGAGCAGAGAGAGATGAGCGGGCGCGGAGAGATCGGGACAGCCCCGTAGCTTCAAGC 61
OY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
DB 62 AGCTCAAGACCTGTCCGGGGCGGGGCGCGGAGGGGCGGGTGCAGCGAAAGAAC 121
OY 73 roGlySerAlaAspSerGluAlaGlnGlyLeuProTyrProAlaLeuAlaProValValP 93
DB 122 CGGCGAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGTAGCCCGGTGTT 181
OY 93 hePheTyrleuSerGlnAspSerArgProArgSerTrpCysleuArgThrValCysAsp 113
DB 182 TCTTCTACTTAGACCAAGACAGACCGCGCGGAGCTGTCTCCGACGGTCTGTAACC 241
OY 113 roTrpPheGluArgValSerMetLeuValIleleuLeuAsnCysValThrleuGlyMetP 133

|||||
Db 242 CGTGTTCGAGCGAGTCACTATGCTGTGTCATCTTCTCAACTGTGTGACTCTGGGTATGT 301
Qy 133 hearqProCysgluAspIleAlaCysaspSerGlnargCysArgIleleuGlnAlaphea 153
Db 302 TCAGGCCGTGTGAGGACATTGCTGTGACTCCAGCGCTGCCGGATCTGCAGAGCCCTTCG 361
Qy 153 spAspPheIlePheAlaphePheAlaValGluMetValValLysMetValAlaleuGlyI 173
Db 362 ATGACTTCATCTTGTCCCTCTTTGCTGTGTGAATGGTGTGAAGATGTGGCCTTGGGA 421
Qy 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
Db 422 TCTTTGGGAAGAAATGTTAAGTTCGGAGACACTTGGAACCGGCTTGACTTTTCATTGTCA 481
Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAAGCTTCCGCAAGTCAAGA 541
Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTGCCAGCCGCTCAGGGCCATTAAACGGGTGCCCAAGCATGCGCATTCCTCG 601
Qy 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACATTAAGTCTGACACCTTGCCCTATGCTGGCAAAGTCCGTGCTGCTGTGTTCTTCG 661
Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGGCAGAGACTGTTCGCAACCGGT 721
Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCCTCCCGAGAACTTCAGCCTCCCGCTGAGCGTGGACCTGAGCCTTATTACCAAGA 781
Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGATGAGGACGAGAGCCCCCTTCATCTGCTCTCAGCCTCGGAGAGATGCATGAGAT 841
Qy 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGGAGTGTGCCCACTGCGCTGGGGAGGCGGTGTGGCCCACTGCAAGTCTGG 901
Qy 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGACCTATAACTTCCAGCAACACCACTGTGTCAACTGTGAACCAAGTACTATA 961
Qy 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAGCGCCATCAACTTGACAACATTG 1021
Qy 373 lYTyAlaIATrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetT 393
Db 1022 GCTATGCCCTGATCGCCATCTTCCAGGTCACTCACTGGAGGGCTGGGCGACATCATGT 1081
Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACTTCGTAATGAGACGCTCACTCTTCTACAACCTTCATCTACTTCATTCCTCATCATCG 1141
Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGTGGTGTGATTGCCACCGAGTTCTCCGAGA 1201
Qy 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAAACAGCGGAGAGTCACTGATGCGGAGACGCTGTACGATTCTGTCCAATGCTA 1261
Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGlyGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCCCTGGCAAGCTTCTCTGAGCCAGGACAGCTGTATGAGGAGCTACTCAAGTACCTGG 1321
Qy 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
|||||

Db 1322 TGTAATCTCCGAAAAGCAGCCCCGAAGCTGGCCCAAGTCTCTAGGGCTATAGCGGTGC 1381
Qy 493 rGAlaGlyLeuLeuSerSerProValAlaIaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGCTGGGTCTTCAGACAGCCAGTGGCCCGTAGTGGGAGAGAGCCCAAGCCAGTGGCA 1441
Qy 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisSH 533
Db 1442 GCTGACACTCGCTCACACCGTGTGTCTGTCCACCACTGGTCCACCACTATCACCACC 1501
Qy 533 iSHHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ACCATCACCACTAACCACTGGGTAAATGGAGCGCTCAGAGTTCCCCGGGCGACCCGAGA 1561
Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProT 573
Db 1562 TCCAGGACAGGAGTGCCAATGGTCTCCCGGCTCATGTCTAACCAACCACTTACACCCA 1621
Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CTCCTCTGGGGCCCTCCAGAGGGTGGAGTGTGTACACAGCTTCTTACCATGTGACT 1681
Qy 593 ySHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTGAGCGCAAGTCCGTTGCCAGGACCCCTCCAGATGCCCATCGAGGCACTCG 1741
Qy 613 lYArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
Db 1742 GTAGACTGTGGGTAGTGGGAGGTGTAACCCCACTGTGCATACCAAGCCCTCCACCAAGA 1801
Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrS 653
Db 1802 TACTGAAGATAAAGCACTAGTGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCACCA 1861
Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSert 673
Db 1862 GCTTCAACATCCCACTGGGCCCTTCAAGCTTCATGCACAAGCTCCTTGAGACACAGATA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CGGAGCCTGCATAGCTCCTGCAAAATCTCCAGCCCTTGTCTCAAGGCAGACAGTGGAG 1981
Qy 693 lAcysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyLupProGluSera 713
Db 1982 CCTGCGGCGCGGACAGTTGTCCCTACTGTGCCCGACAGAGCAGAGCCAGAGTCCG 2041
Qy 713 lAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CTGACCATGTGATGCTGCTGACTCAGACAGCGAGGCTGTGTATGAGTTCAACAGAGCGCTC 2101
Qy 733 lnhIsSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGTACTCCGGGATCCCAACAGCCGGCGGACAGCGGAGCCCTGGGCCCATG 2161
Qy 753 lAgLuProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2162 CAGAGCCTAGTTCTGTGCTGCTGTGAGGCTGATCTGTGACACATTCCGGAAGATCG 2221
Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2222 TAGATAGCAAAATACTTTGGCCGGGGAATCATGATCGCCATCTGTGTCAATACACTGACA 2281
Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2282 TGGGCATCGAGTACACAGAGCAGCCGAGGAGAGCTCACCAAGCCCTGGAAATCAGACA 2341
Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
Db 2342 TCGTCTTCAACAGCCTCTTCGCTTGAAGATGCTGCTGAAGCTGCTGTCTACGGTCCCT 2401
Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
Db 2402 TTGGCTACATTAAAGATCCCTACACACTCTTTGATGGTGTCAATTGTGTATCATCAGTGT 2461
|||||

Db 4622 GGCTGGAGAAAAAGAGAGG-----AAAGCCAGTGCAGCCCT 4660
QY 1593 yTYrSerAspTYrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTYrL 1613
Db 4661 ACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCACCACTGTGTACCAAGCCACTACC 4720
QY 1613 euAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisT 1633
Db 4721 TGGACCTCTTCATCAGTGGTGTCTCATCGGGCTGAACTGTCTACTATGGCCATGGAACAT 4780
QY 1633 yTGInGInProGInIleLeuAspGluAlaLeuYsIleCysAsnTYrIlePheThrValI 1653
Db 4781 ACCAGCAGCCCCAGATCCTGGAAGAGCTTGAGATCTGCAATTACATCTTTACCGTCA 4840
QY 1653 lePheValPheGluSerValPheYsLeuValAlaPheAlaPheArgArgPheGlnA 1673
Db 4841 TCTTTGTCTTGAGTCAGTTTCAAACTGTGGCTTTGGCTTCGGCGTTTCTTCAGG 4900
QY 1673 sPARGTpAsnGlnLeuAspLeuAlaIleValIleuLeuSerIleMetGlyIleThrLeuG 1693
Db 4901 ACAGGTGAACCAAGCTGGAAGCTGCTATGTGTCTGTCCATCATGGGCATCACACTGG 4960
QY 1693 luGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgV 1713
Db 4961 AGGAGATTGAGGTCAATCTGTCTGCTGCCCATCAACCCCAATCATCTGATGAGGG 5020
QY 1713 alLeuArgIleAlaArgValLeuYsLeuLeuYsMetAlaValGlyMetArgAlaLeuL 1733
Db 5021 TGTCCCGCATTGCTCGAGTTCTGAAGCTGTGAAGATGGCTGTGGCAATGCGGCACACTGC 5080
QY 1733 euHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuL 1753
Db 5081 TGCAACAGGTGATGACAGCCCTGCCCAAGGTGGGAACTGGGACTTCTCTTCATGTTAT 5140
QY 1753 euphePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluL 1773
Db 5141 TGTTTTTCATCTTTGCAGCTCTGGGCGTGAGCTCTTTGAGAGACCTGAGGTGATGAGA 5200
QY 1773 hchISProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheL 1793
Db 5201 CACACCTTGTGAGGGGCTGGGTCGGCATGCCACTTTAGGAACTTTGGATGGCCCTTTC 5260
QY 1793 eutThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetYsAspProSerA 1813
Db 5261 TGAACCTCTTCCGAGTCTCCACTGCTGTGACAACTGGAATGTATATGAAGACACCCCTCC 5320
QY 1813 rGAspCysAspGlnGluSerThrCysTYrAsnThrValIleSerProIleTYrPheValS 1833
Db 5321 GGGACTGTGACCAGGAGTCCACTGTCTACAACACTGTCTATCTCCCTATCTACTTTGTGT 5380
QY 1833 erPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetYsH 1853
Db 5381 CCTTCGTGCTGACCGCCAGATTGTGTCTGTCAACGTGTCTATAGCTGTGCTGATGAAGC 5440
QY 1853 leLeuGluGluSerAsnYsGluAlaYsGluGluAlaGluLeuGluAlaGluLeuGluL 1873
Db 5441 ACCTGGAAGAAAGCAACAAGAGAGGCCAAGAGAGGCCGAGCTCGAGGCCGAGCTGAGAC 5500
QY 1873 euGluMetYsThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrp 1893
Db 5501 TGGAGATGAAGACGCTCAGCCCCGACGCCCTCTCCCGCTGGGCAGCCCTTCTCTGGC 5560
QY 1893 roGlyValGluGlyValAsnSerThrAspSerProYsProGlyAlaProHisThrThra 1913
Db 5561 CCGGGGTGAGGGGTGTCAACAGTACTGACAGCCCTTAAGCCTGGGGCTTCACACACCACTG 5620
QY 1913 laHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProG 1933
Db 5621 CCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCACGATGATACCCACCCCG 5680
QY 1933 luGluValProValProLeuGlyProAspLeuLeuThrValArgYsSerGlyValSerA 1953

Db 5681 AGGAGTGCACGTCCCCCTAGGACCAAGCTGCTGACTGTGAGGAAGTCTGTGTCAACC 5740
QY 1953 rgThrHisSerLeuProAsnAspSerTYrMetCysArgAsnGlySerThrAlaGluArgS 1973
Db 5741 GGACGCACTCTTGCCCAATGACAGTACATGTGCCGCAATGGGAAGCACTGTGAGAGAT 5800
QY 1973 erLeuGlyHisArgGlyTYrPGLyLeuProLYsAlaGlnSerGlySerIleLeuSerValH 1993
Db 5801 CCTTAGGACACAGGGGCTGGGGCTCCCAAGCCAGTCAAGGCTCCATCTGTGCCGTTTC 5860
QY 1993 isSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLYsAspValHisTYrLeuL 2013
Db 5861 ACTCCCAACCAAGACAGACACAGCTGCATCTACAGCTTCCCAAGATGTGACACTATCTGC 5920
QY 2013 euGlnProHisGlyAlaProThrTYrPGLyAlaIleProLYsLeuProProProGlyArgS 2033
Db 5921 TCCAGCCTCATGGGGCTCCCACTGGGGCGCCATCCCTAAACTAACCCCACTGGCGGCT 5980
QY 2033 erProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspV 2053
Db 5981 CCCCTCTGGCTCAGAGGCTCTCAGGGCCAGGACGAATGAAGACTGACTCCCTGATG 6040
QY 2053 alGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProL 2073
Db 6041 TGCAGGGCTGGGTAGCCGGGAAGACTGTTGTACAGAGTGAAGTGGCCCTCTGCCCTTC 6100
QY 2073 euThrArgSerSerPheTrpGlyClySerSerIleGlnValGlnGlnArgSerGlyYr 2093
Db 6101 TGACCCGGTCCCTCATCTCTTCTGGGGGGGTGAGCATCCAGGTGCAAGACGTTCCGGCA 6160
QY 2093 leGlnSerLYsValSerLYsHisIleArgLeuProAlaProCysProGlyLeuGlnProS 2113
Db 6161 TCCAGAGCAAGTCTCCAAAGACATCCGCTTGCCAGCCCTTGCCCAAGGCTGGAACCCA 6220
QY 2113 erTrpAlaLYsAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT 2133
Db 6221 GCTGGGCCAAGACCTTCCAGAGACCAAGACAGCTTAGAGCTGGAACAGGAGCTGAGCT 6280
QY 2133 rpIleSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuL 2153
Db 6281 GGATTTCAGGAGACTCTCTCCAGACGCCAGAAAGAACCTGTTCACAGGGAGCTGA 6340
QY 2153 ySLYsCysTYrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspG 2173
Db 6341 AGAAGTGTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGCCTGGGTTCTGGCTAGATG 6400
QY 2173 luGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuL 2193
Db 6401 AACAGCGAGACACTCCATTGTCTGAGCTGTGTGACAGCGGCTCCCAACCCCGCTAT 6460
QY 2193 ySProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLYsL 2213
Db 6461 GTCCAAGCCCTCAAGCCTCGGGGGCCAACCTTTGGGGGTCTTGGAAGCCGGCTTAAGA 6520
QY 2213 ySLYsLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgProP 2233
Db 6521 AAAAAGTCAAGCCCAAGTATCTTATAGACCCCGGAGAGCCAGGGCTCTCGGCCCTC 6580
QY 2233 roCysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLYsAspProS 2253
Db 6581 CATGCACTCTGTGTCTGCTCAGAGAGAGGGCGCGCCAGTGAAGTAAAGATCCCT 6640
QY 2253 erValSerSerProLeuAspSerThrAlaAlaSerProSerProLYsLYsAspThrLeuS 2273
Db 6641 CGGTCTCCAGCCCTTGACAGCAGCGGCTGCCTCACCCCTCCCAAGAAAGACACGCTGA 6700
QY 2273 erLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286
Db 6701 GTCTCTGTGTTTGTCTTGACCAACAAGACATGAGACCC 6741
RESULT 8
AAD04756
ID AAD04756 standard; cDNA; 7741 BP.

XX AAD04756;
AC
XX 17-JUL-2001 (first entry)
DT
XX Human T-type low voltage activated calcium channel alphaI-g-c cDNA.
DE
XX Human T-type low voltage activated calcium channel alphaI-g-c; stress;
KW epilepsy; schizophrenia; depression; sleep disorder; Cushing's disease;
KW endocrine disorder; respiratory disorder; peripheral muscle disorder;
KW muscle excitability; fertilisation; contraception; hypertension;
KW neuronal firing regulation; cardiovascular disorder; gene therapy;
KW forensic analysis; epidemiological study; neuroleptic; ss.
XX
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT 1..522
FT 5'UTR /tag= a
FT 523..7344
FT CDS /tag= b
FT /product= "Human T-type low voltage activated calcium
FT channel alphaI-g-c protein"
FT /transl_except= (pos:3934..3936, aa:Gln)
FT /transl_except= (pos:3946..3948, aa:Gln)
FT /transl_except= (pos:5560..5562, aa:Pro)
FT /transl_except= (pos:5569..5571, aa:Gln)
FT /note= "The CDS is specifically claimed in claim 2 as SEQ
FT ID NO:3"
FT 7345..7741
FT 3'UTR /tag= c
FT
XX
XX WO200130844-A1.
XX
XX 03-MAY-2001.
XX
XX 06-OCT-2000; 2000WO-US027761.
XX
XX 26-OCT-1999; 99US-00426998.
XX
XX (ORTH) ORTHO-MCNEIL PHARM INC.
XX
XX PA Dubin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;
XX PI
XX
XX WPI; 2001-300486/31.
XX
XX P-PSDB; AAE01019.
XX
XX
XX New nucleic acid encoding human calcium channel protein, useful for
PT identifying specific modulators and potential pharmaceuticals for
PT treating e.g. epilepsy.
PT
XX
XX Claim 2; Page 76-81; 115pp; English.
XX
XX The invention relates to isoform of human T-type low voltage activated
XX calcium channel (alphaI-g-c) cDNA and protein. Cells transformed with
XX calcium channel DNA to express calcium alphaI-g-c channel protein are used
XX to identify specific modulators (antagonists or agonists). These
XX modulators are useful as therapeutic agents and are used for treating
XX wide range of calcium alphaI-g-c channel-mediated disorders, e.g. stress
XX epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,
XX endocrine disorders, respiratory disorder, peripheral muscle disorder,
XX muscle excitability, fertilisation, contraception, disorders involving
XX hypertension, neuronal firing regulation, potentiation of synaptic
XX signals and cardiovascular disorders (e.g. atherosclerosis, cardiac
XX hypertrophy, angina pectoris). Calcium alphaI-g-c channel DNA is useful
XX for isolating and identifying related molecule mutations. It is also
XX optionally used as antisense sequences, in gene therapy. Calcium channel
XX alphaI-g-c DNA, protein and antibodies are useful for forensic analysis,
XX diagnosis and epidemiological studies, by standard hybridisation or
XX immunological assays. The present sequence is T-type low voltage
XX activated calcium channel alphaI-g-c cDNA. This sequence is isolated from
XX human thalamus cDNA library

Sequence 7741 BP; 1469 A; 2496 C; 2287 G; 1489 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 0 Length: 7741
Score: 11066.50 Matches: 2134
Percent Similarity: 93.81% Conservative: 33
Best Local Similarity: 92.38% Mismatches: 112
Query Match: 92.01% Indels: 31
DB: 4 Gaps: 5
US-09-611-257A-24 (1-2287) x AAD04756 (1-7741)
QY 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
DB 431 CCGCCGGGGCCCCCGGGTTGCGTGAGACACCTCCTGAGGGGCGCGCTTGCCCTCT 490
QY 23 SerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAla 42
DB 491 CCGATCGCCCGGGCGCCCGGCTGGCCAGAGATGACGAGAGAGATGACGGCG 550
QY 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62
DB 551 CCGAGAGTCGGGACAGCCCGGAGCTTCATGCGGCTCAACGACCTGCGGGGGCGG 610
QY 63 Ala-AlaGlyAla-GlySerThrGlyLysAspProGlySerAlaAspSerGluAlaGlu 82
DB 611 GCCGGCCGGGGCGGGGTCAGCAAGAAAGACCCGGGCAAGCGGACTCCGAGCGGAG 670
QY 82 1LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgp 102
DB 671 GGCTGCCGTACCCGCGCGTGGCCCGGTTGTTCTTCTTACTTGAGCCAGACAGCGCC 730
QY 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV 122
DB 731 CGCGAGCTGTGTCTCCGACAGGTCTGTAAACCCGTGTTGAGCGCATCAGCATGTTG 790
QY 122 al1leuLeuAsnCysValThrleuGlyMetPheArgProCysGluAsp1leAlaCysA 142
DB 791 TCATCTTCTCAACTGCGTGAACCTTGCGCATGTCGGCCATGCGAGCATCGCCTGTG 850
QY 142 spSerGlnArgCysArg1leuGlnAlaPheAspAspPhe1lePheAlaPhePheAlav 162
DB 851 ACTCCAGCGCTGCCGATCTGACGCCCTTGATGATCATCTTGCTTTGCGCG 910
QY 162 alGluMetValValLysMetValAlaLeuGly1lePheGlyLysCysTyrleuGlyA 182
DB 911 TGAGATGTGTGTGAAGATGTGCCCTTGCGCATCTTGGAAGAAAGTGAACCTGGAG 970
QY 182 spThrTrpAsnArgLeuAspPhePhe1leVal1leAlaGlyMetLeuGluTyrSerLeuA 202
DB 971 ACACCTGGAACCGGCTTGACTTTTCATGTCATGCAAGGATGCTGAGTACTCGCTGG 1030
QY 202 sPLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgA 222
DB 1031 ACCTGCAGAACGTCAAGCTTCTCAGCTGTCAAGACAGTCCGTGTGCGACCGCTCAGGG 1090
QY 222 la1leAsnArgValProSerMetArg1leLeuValThrleuLeuAspThrleuProm 242
DB 1091 CCATTAACCGGGTGCCAGCATGCGCATCTTGTCAGTTGCTGCTGATACGCTGCCA 1150
QY 242 etLeuGlyAsnValLeuLeuLeuCysPhePheValPhePhe1lePheGly1leValGlyV 262
DB 1151 TGCTGGGCAACGTCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTGCG 1210
QY 262 alGluLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuP 282
DB 1211 TCCAGCTGTGGGCGAGGCTGCTTCGAAACGATGCTTCTTACCTGAGAAATTTCAGCCTCC 1270
QY 282 roLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheI 302
DB 1271 CCCTGAGCGTGAGACCTGAGCGGCTATTACAGACAGAGAAAGAGATGAGAGCCCTTCA 1330
QY 302 leCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgG 322

Db 1331 TCTGCTCCCGACCGCCAGAACGGCATGCGGTCTGCAGAGCGGTGCCCCACGCTGCGCG 1390
Qy 332 YGUGUGLYGLYGLYProProCysSerLeuAspTyrGluThrTyrAsnSerSerSera 342
Db 1391 GGGACGGGGCGGTGGCCCCACTTGCGGTCTGGACTATGAGGCCCTACAAACAGCTCCAGCA 1450
Qy 342 snThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsn 362
Db 1451 ACACCACTGTGTCAACTGGAAACAGTACTACCAACTGTCTCAGCGGGGAGCACAAACC 1510
Qy 362 roPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnV 382
Db 1511 CCTTCAAGGGCGCCATCACTTGACAACATTGGCTATGCCTGGATCGCATCTTCCAGG 1570
Qy 382 aIIleThrLeuGluGlyTTrpValAspIleMetTyrPheValMetAspAlaHisSerPhe 402
Db 1571 TCATCAGCTGGAGGGCTGGGTCCAGATCATGTACTTGATGGATGCTCATTCCTTCT 1630
Qy 402 yrasnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeu 422
Db 1631 ACAATTTCACTACTTCACTCTCTCATCATCGTGGCTCTTCTTCAATGATCAACTGT 1690
Qy 422 yslLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuMet 442
Db 1691 GCCTGGTGTGATTGCCACGAGTTCTCAGAGACCAAGCAGCGGGAAGCCAGCTGATGC 1750
Qy 442 rglGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluPro 462
Db 1751 GGGACAGCGTGTGCGGTTCCTGTCCAACGCCAGCACTTGCTAGCTTCTCTGAGCCCG 1810
Qy 462 lYserCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArg 482
Db 1811 GCACTGTCTATGAGAGCTGTCTCAAGTACCTGGTGTACATCCTTGTAAAGCAGCCCGCA 1870
Qy 482 rglLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProVal 502
Db 1871 GGGTGGCTCAGGTCTCTGGGGCAGCAGGTGTGGGGTTGGGCTGCTGCAGACCCACAGC 1930
Qy 502 laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeu 522
Db 1931 CCCTCGGGGGCCAGGAGAACCCAGCCAGCAGCAGCTGCTCTCGCTCCACCGCCCTAT 1990
Qy 522 erValHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHis 542
Db 1991 CCGTCCACCACCTGTGTGACCAACCAACCACTACCACTACCACTGGGCAATG 2050
Qy 542 lYThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySer 562
Db 2051 GGAAGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGACAGGAGTCCATGGGTCCC 2110
Qy 562 rgaArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGly 582
Db 2111 GCAAGCTCATGTGTGCCACCACTTCGACGCTGTGCCCTCTCCGGGGCCCCCTGTGCG 2170
Qy 582 laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGln 602
Db 2171 CAGAGTCTGTGCACAGCTTCTACCATGCGACTGCCACTTAGAGCCAGTCCGCTGCAGG 2230
Qy 602 laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysVal 622
Db 2231 CGCCCCCTCCAGGTCCCATCTGAGGCATCCGGCAGGACTGTGGGCACGGGAAGTGT 2290
Qy 622 yTrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGlu 642
Db 2291 ATCCCAACGTGCACACAGCCCTCCACCGAGAGCTGAAAGAGAAAGCACTAGTAGAGG 2350
Qy 642 alaAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPhe 662
Db 2351 TGGCTGCCAGCTCTGGGCCCCAACCTCACCAGCTCAACATCCCAACCGGGCCCTACA 2410
Qy 662 erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI 682

Db 2411 GCTCCATGCACAAGCTGTGAGACACAGAGTACAGGTGCTGCTGCCAAAGCTCTTGCAAGA 2470
Qy 682 leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC 702
Db 2471 TCTCAGCCCTTGTGTAAGCAGACAGTGGAGCCTGTGTGTCCAGACAGCTGCCCTACT 2530
Qy 702 ysaAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsp 722
Db 2531 GTGCCCGGGCGGGGAGGGAGGTGGAGCTCGCCGACCGTGAATGCTGACTCAGACA 2590
Qy 722 erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHis 742
Db 2591 GCGAGGCACTTATGAGTTCAACAGAGATGCCAGACAGCACTCCGGGACCCCAACA 2650
Qy 742 erArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT 762
Db 2651 GC--CGGCGGCAACGAGCCTGGGCCCAATGCAGAGGCCCACTGTGTGCGGCTTCT 2707
Qy 762 rpaArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI 782
Db 2708 GGAAGCTAATCTGTGACACCTTCGAAAGATTGTGAGACAGCAAGTACTTGGCCGGGAA 2767
Qy 782 leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnPro 802
Db 2768 TCATGATCGCCATCTGTGTCAACACATCAGCATGGGCATGCAATACACAGCAGCCCG 2827
Qy 802 lGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeu 822
Db 2828 AGGAGCTTACCAACGCCCTAGAAATCAGCAACATCGTCTTCAACAGCCTTTGCGCTGG 2887
Qy 822 luMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI 842
Db 2888 AGATGCTGTGAAGCTGCTGTGTATAGTCCCTTGCTACATCAAGAATCCCTACACA 2947
Qy 842 lePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnGlnGlyG 862
Db 2948 TCTTCGATGTGTCAATTGTGTCAATCAGCGTGTGGAGATCGTGGGCCAGCAGGGGGCG 3007
Qy 862 lYLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeu 882
Db 3008 GCCTGTGGTGTGCGGACCTTCGCTGATGCGTGTGCTGAAGCTGTGTGCGCTTCTGC 3067
Qy 882 roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC 902
Db 3068 CGGCGCTGCAGCGGACGCTGTGTGTCTATGAAGACCATGGAACAAGTGCACCTTCT 3127
Qy 902 ysmetLeuLeuMetLeuPheIlePheSerIleLeuGlyMetHisLeuPheGlyC 922
Db 3128 GCATGCTGTATGCTCTTCACTTCACTTCAAGCATCCGCGCATGCATCTTCGGCT 3187
Qy 922 yslYsPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSer 942
Db 3188 GCAAGTTTGCCTCTGAGCGGGATGGGACACCTCGCAGACCGGAAGATTGTGACTCT 3247
Qy 942 eulLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysVal 962
Db 3248 TGCTCTGGGCCATGTCACTGTCTTTCAGATCTGAACCCAGAGGAACTGGAACAAGTCC 3307
Qy 962 eutYrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMet 982
Db 3308 TCTACAATGGTATGGCTCCACGTCGTCTGGCGGCCCTTATTTCAATTGCTCCATGA 3367
Qy 982 hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGln 1002
Db 3368 CCTTCGCAACTAGTGTCTTCAATTGTCTGTGCGCAATTGTGTGAGGGCTTCCAGG 3427
Qy 1002 laGlu----- 1003
Db 3428 CGAGGAATACGAACGGGAAGATGCGAGTGACAGTTAACTGTATTACAGTGCCTG 3487
Qy 1004 -----GlyAspAlaThrLysSerGluSerGluProAspPhePheSerPros 1019
Db 3488 TCGACTCCCGAGGGGAGATGCCAACAAAGTCCGAATCAGAGCCCGATTCTTCTCACCCA 3547

Qy	1019	erValAspGlyAspGlyAspArgLysLysArgGluAlaLeuValAlaLeuGlyGluHisA	1039
	:::		
Db	3548	GCCTGATGATGGGACAGAGAAGTGTGGCTTGTGCTCCGGAGAGCACC	3607
Qy	1039	laGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrPromets	1059
Db	3608	CGGAGCTCGGAGAGCCTGTGCTGCCCTTCATCATCCACACGCGCCACACCATGT	3667
Qy	1059	erHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgT	1079
Db	3668	CGCTGCCAAGACGACACGAGCGGCTGGGCGGAGCGCTGGCCCTCGCTCGCGCCGA	3727
Qy	1079	hrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProS	1099
Db	3728	CCAGACGACGCGGTGCGGACAGCCTGGGCGGCC---CACGATGAAGTCACGCCCA	3784
Qy	1099	erAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS	1119
Db	3785	GGCCCCGACGCTCTCCGACAGCCCCCTGGAGCGCTGACAGCAGTGCAGCAGCGCT	3844
Qy	1119	erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA	1139
Db	3845	CCAGCCGGACAGCCTCGGCCCTGCACCCAGCCTGAAGCGGAGAGCCCAAGTGAAGAC	3904
Qy	1139	rgArgSerLeuLeuSerGlyGlyGlyGlyGlnGluSerGlnAspGluGluGluSerSerGluG	1159
Db	3905	GGCGGTCCTGTTGTGCGGAGAGGCCAGAGAGCCAGATGAAGAGAGAGCTCAGAAAG	3964
Qy	1159	luAspArgAlaSerProLagLysSerAspHisArgHisArgGlySerLeuGluArgGluA	1179
Db	3965	AGGAGCGGGCCAGCCCTGCGGCACTGACCATCGCCACAGGGGGTCCCTGAGCGGAGG	4024
Qy	1179	laLysSerSerPheAspIleuProAspThrLeuGlnValProGlyLeuHisArgThrAlaS	1199
Db	4025	CCAAGAGTTCCTTGACCTGCACAGACACACTGCAGGTGCCAGGGCTGCATCGCACTGCCA	4084
Qy	1199	erGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL	1219
Db	4085	GTCGCGCAGAGGCTCTGCTTCTGAGCACAGGACTGCATGCGCAAGTCGGCTTCAGGCGCC	4144
Qy	1219	euAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluG	1239
Db	4145	TGGCCCGGGCCCTGCGGCTGATGACCCCCACACTGATGGGATGACGCCGATGACGAGG	4204
Qy	1239	lyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysC	1259
Db	4205	GCAACTGAGCAAGGGAAGGAGCGGTCGGCGGTGATCCGAGCCGACTCCCTGCTGCT	4264
Qy	1259	ysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuL	1279
Db	4265	GCCTCGAGCGAGACTCTGTGTACGCTTACATCTTCCTCTCAGTCCAGGTTCCGCTCC	4324
Qy	1279	euCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheL	1299
Db	4325	TGTGTACACCGGATCATCACCCACAAGATGTCGACCACGTGTCTTGTTCATCATCTTCC	4384
Qy	1299	euAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgI	1319
Db	4385	TTAAGTCATCACCATCGCCATGAGCGCCCCCAAAATTGACCCCAAGCGGTGAACGA	4444
Qy	1319	lePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValL	1339
Db	4445	TCTTCTGACCCCTCTCCAATTACATCTTCACCGCAGTCTTTCGGCTGAATGACAGTGA	4504
Qy	1339	ysValValAlaLeuGlyTrpCysPheGlyGlyGlnAlaTyrLeuArgSerSerTrpAsnV	1359
Db	4505	AGGTGTGAGCACTGGGCTGTGTCTTCGGGAGACAGCGGTACTTCGGGAGCAGTTGGAACG	4564
Qy	1359	alLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerA	1379
Db	4565	TGCTGACGGGCTGTGTGTCTCATCTCCGTCATGACATTCGTGTCTCATGTCTCTG	4624

Qy	1379	spSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgP	1399
Db	4625	ACAGCGGCAACCAAGATCCTGGGCATGCTGAGGGTGCTGCGGCTGCTGCGGACCTGCGCC	4684
Qy	1399	roLeuArgValIleSerArgIaGlnGlyLeuLysLeuValValGluThrLeuMetSerS	1419
Db	4685	CGCTCAGGTCGATCAGCCGGGCGCAGGGGCTGAAGCTGGTGTGAGACGCTGATGTCT	4744
Qy	1419	erLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGlyI	1439
Db	4745	CACtGAACCCATCGGCAACATTTGATCATCTGCTGTGCTTCTTCATCATTTTCGGCA	4804
Qy	1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1459
Db	4805	TCTTGGGGTGCAAGCTCTTCAAGGGAAGTTTTCGTGTGCCAGGCGAGGATACCAAGA	4864
Qy	1459	snIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrA	1479
Db	4865	ACATCACCAATAATCGGACTGTGCCGAGGCCAGTTACCGGTGGTCCGGCAACAAGTACA	4924
Qy	1479	snPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyT	1499
Db	4925	ACTTTGACAACTTGCCAGGCCCTGATGTCCCTGTTCGTTTGGCCTCCAAGATGGTT	4984
Qy	1499	rpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetA	1519
Db	4985	GGGTGACATCATGTACGATGGGCTGGATGCTGTGGGGGTGSAACGACGACCATCATGA	5044
Qy	1519	snHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheV	1539
Db	5045	ACCACACCCCTGGATGCTGCTGACTTCATCTGTTCTGCTCATTTGTGGCCTTCTTGG	5104
Qy	1539	alLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGlnG	1559
Db	5105	TCCTGAACATGTTTGTGGTGTGTGTGAGAACTTCACAAGTGTCCGACGACCAAG	5164
Qy	1559	IuGluGluGluAlaArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgA	1579
Db	5165	AGGAAGAGAGGCCCGCGCGGAGAGAAAGCGCTTACGAAGACTGGAAGAAAAGAA	5224
Qy	1579	rgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA	1599
Db	5225	GGAGTAAGAGAGACAGATGGCTGAAGCCAGTGCAAACTTACTCCGACTACTCCC	5284
Qy	1599	rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrG	1619
Db	5285	GCTTCGGGCTCTGCTCCACCACCTTGTCACACGACCACTACTGACCTTTCATCACAG	5344
Qy	1619	IyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL	1639
Db	5345	GTGTCATCGGGCTGAACGTGTACCATGGCCATGAGCACTTACAGACGCCCAAGATTCC	5404
Qy	1639	euaSpGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV	1659
Db	5405	TGGATGAGGCTTGAAGATCTGCAACTACATCTTCACTGTCACTTTGTCTTGGAGTCAG	5464
Qy	1659	alPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuA	1679
Db	5465	TTTTCAAACTTGTGGCCTTTGTTTCCGTTCCGTTCTTCCAGACAGGTGGAACCAAGCTGG	5524
Qy	1679	spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL	1699
Db	5525	ACCTGGCCATGTGTGCTGTCCATCATGGGCATCACGCTGAGGAGAAATCGAGGTCAAG	5584
Qy	1699	eusErLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV	1719
Db	5585	CCTCGCTGCCCATCAACCCACCATCATTCGTCATCATGAGGCTGTGCGCATTGGCCGAG	5644
Qy	1719	alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA	1739
Db	5645	TGCTGAAGCTGCTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGGAACACGTCATGACG	5704
Qy	1739	IaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA	1759

Db 5705 CCCTGCCCCAGGTGGGGAACCTGGGACTTCTTCATGTTGTTTTCATCTTGACAG 5764
Qy 1759 lAlEuglYValGlUleuPheGlYAspLeuGlUcYsAspGlUThrHisProCysGlUglYL 1779
Db 5765 CTCTGGGGCGGTGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCC 5824
Qy 1779 eUGlYARghIsAlaThrPheaRgAsnPheGlYMeCAlaPheLeuThrleuPheaRgValS 1799
Db 5825 TGGGCGTCATGCAACCTTTCGGAACCTTGGCATGGCCTTCTTAACCTCTTCCGAGTCT 5884
Qy 1799 eRThrGlYAspAsnTrpAsnGlYlLeMeTlYsAsPProSerARgAsPCysAspGlnglUs 1819
Db 5885 CCAcAGGTGACAATGGAA TGGCATTATGAAGGACACCTCCGGACTGTGACAGAGT 5944
Qy 1819 eRThrCysTYrAsnThrValIlEsSerProIlEtyrPheValSerPheValleuThraLaG 1839
Db 5945 CCAcCTGCTACACACGCGTCACTCGCCTATCTACTTGTGTCTTCCGTGACGGCCC 6004
Qy 1839 lInPheValleuValAsnValValIlEAlaValleuMeTlYshIsLeuGlUSeRAsnL 1859
Db 6005 AGTTCGTGCTAGTCAACGTGTGATCGCCGTCTGATGAAGCACTTGAGAGAGCAACA 6064
Qy 1859 YSGlUAlaLYSGlUglUAlaGlUleuGlUAlaGlUleuGlUleuGlUleuMeTlYsThrLeuS 1879
Db 6065 AGGAGGCCAAGAGAGAGGCGGAGCTAGAGGCTGAGCTGAGATGAAGACCCCTCA 6124
Qy 1879 eRProGlNProHisSerProleuGlYSerProPheLeuTrpProGlYValGlUglYValA 1899
Db 6125 GCCCCAGCCCCCACTCGCCACTGGGCGAGCCCTTCCTCTGGCCTGGGGTCGAGGGCCCCCG 6184
Qy 1899 snSerThrAspSerProLYsProGlYAlaProHisThrThraLanHisIlEglYAlaAlas 1919
Db 6185 ACAGCCCCGACAGCCCCAGCCTGGGGCTGTGCAcCCAGCGGCCAGCGAGATCAGACCT 6244
Qy 1919 eRglYPheserLeuGlUhiSProThrMeTValProHisProGlUglUValProValProl 1939
Db 6245 CCCACTTTTCCCTGGAGCAcCCCAcGATGcAGcCCCAcCCCAcGAGcTGCCA----- 6297
Qy 1939 euGlYProAspLeuLeuThrValARglYsSerGlYValSerARgThrHisSerLeuProA 1959
Db 6298 --GGACCAGACTTACTGACTGTGCGGAAGTCTGGGGTCAcCCGAACGCACTCTGCCCCA 6355
Qy 1959 snAspSerTYrMeTcYsArgAsnGlYSerThrAlaGlUArgSerLeuGlYhiSARgGlYT 1979
Db 6356 ATGACAGCTACATGTGTGCGCATGGGAGCACTGCCGAGGGGCCCTGGGACACAGGGGCT 6415
Qy 1979 rPGlYleuProLYsAlaGlnSerGlYSerIlELeuSeRValHisSerGlnProAlaAsPT 1999
Db 6416 GGGGCTCCCAAAGCTCAgTCAgGCTCCGTCTGTCCGTTCACtCCcAGcCCAGcAGATA 6475
Qy 1999 hrSerCysIlELeuGlnleuProLYsAspValHisTYrLeuLeuGlnProHisGlYAlaP 2019
Db 6476 CCAGCTACATCCTGCAGCTTCCCAAAGATGCAcCTCATCTGCTCCAGcCCCAcAGcGCC 6535
Qy 2019 roThrTrpGlYAlaIlEProLYsleuProProProGlYARgSerProleuAlaGlnArGP 2039
Db 6536 CAACCTGGGGCAcCATcCCCAAACtGcCCcCAcGAGcGCTcCCcTTGGCTCAGAGGc 6595
Qy 2039 roLeuARgARgGlNAlaAlaIlEArgThraSPserleuAspValGlnGlYleuGlYSeRa 2059
Db 6596 CACTCAGGCGCCAGGCAATAAGACTGACTCTTGACGTTcAGGGTCTGGGcAGcCC 6655
Qy 2059 rGglUAspLeuLeuSerGlUValSerGlYProSerCysProleuThraRgSerSerSeRP 2079
Db 6656 GGGAAAGACTGTGTCAGAGGTAGTGGGCCCTCCcCCcCGCCCTGGcCCGGGcCTACTCTT 6715
Qy 2079 heTrpGlYglYSerSerIlEglnValGlnARgSerGlYIlEglnSerLYsValSerL 2099
Db 6716 TCTGGGGCCAGTCAAGTACCAGGACAGCAGCACTCCGcAGcCCAGcCAAGATCTCCA 6775
Qy 2099 YehIsIlEArgLeuProAlaProCysProGlYleuGlUProSerTrpAlaLYsAsPProp 2119

Db 6776 AGCACA TGACCCCGCCAGCCCTTGGCCAGGCCCCAGAACCCA CTGGGCGAAGGCCCTC 6835
Qy 2119 roGlUThrARgSerSerleuGlUleuAspThrGlUleuSerTrpIlEsERGlYAspLeuL 2139
Db 6836 CAGAGACCAGAGCACTTAGAGTTGGACA CGGAGCTGAGCTGAGATTTCAGAGACCTCC 6895
Qy 2139 eu--ProSerSerGlnglUglUProleuPheProARgAspLeuLYsLYsCysTYrSerY 2158
Db 6896 TGCCCCCTGGCGGCGAGAGAGGCCCCATCCcCAcGGAGcCTGAAGAAGTGTACAGCG 6955
Qy 2158 aGlUThrGlnSerCysARgARgARgProGlYPheTrpLeuAspGlUglnARgARhIsS 2178
Db 6956 TGGAGGCCCAgAGCTGCCAGCGCCGGCTACGTCCTGGCTGATGAGCAGAGAGACT 7015
Qy 2178 eRlIEAlaValSerCysLeuAspSerGlYSerGlnProARgLeuCysProSerProSers 2198
Db 7016 CTATCGCCGTCAgCTGCTGACAGCGGCTCCAAcCCCAcCTGGGcACAGACCCCTCTA 7075
Qy 2198 eRleuGlYglYglnProleuGlYglYProGlYSerARgProLYsLYsLeuSerProP 2218
Db 7076 ACCTTGGGGCGCAcCTCTTGGGGGCGCGGAGCGGCCCAAGAAAAAACTCAGCCCGC 7135
Qy 2218 roSerIlEsERlEAsPProProGlUSeRGlnglYSerARgProProCysSerProGlYV 2238
Db 7136 CTAGTATCACCATAGACCCCCCGAGAGCCAAGTCTCTCGGACCCCGCCAGCCCTGT 7195
Qy 2238 aLCysLeuARgARgARgAlaProAlaSerAspSerLYsAsPProSerValSerSerProl 2258
Db 7196 TCTGCCTCCGAGAGGGGCTCCGTCCAGGCACTCCAAGATCCCTTGcCTTGcCCCCC 7255
Qy 2258 euAspSerThrAlaAlaSerProSerProLYsLYsAspThrleuSerleuSerGlYleuS 2278
Db 7256 CTGACAGCATGGCTGCCTCGCCCTCCcCAAAGAAAGATGTGTGAGTCTCTCGGTTAT 7315
Qy 2278 eRSerAsPProThraSPMeTAsPPro 2286
Db 7316 CCTCTGACCCAGCAGACCTGGAACCCC 7341

RESULT 9
AAx83481
ID AAx83481 standard; cDNA, 6750 BP.
XX
AC AAx83481;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCav11a) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Homo sapiens.
XX
PN W09929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
DR P-PSDB; AAY14586.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 31-40; 138bp; English.
XX
CC This sequence represents the coding region for a human T-type voltage-

CC gated calcium (Ca) channel alpha-1-G designated hCav1a. Voltage gated
CC channels are membrane bound glycosylated proteins formed of several
CC subunits. The large alpha subunits form a pore in the membrane that is
CC selective for a given ionic species. Each alpha subunit contains 4
CC domains (I, II, III and IV) and each domain contains 6 putative
CC transmembrane helical segments (S1-S6). T-type Ca channels are activated
CC at a lower voltage than L- or N-type channels. Characteristics of T-type
CC channels include short current time, slow activation kinetics near
CC threshold, fast inactivation kinetics and slow tail current. The
CC sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel
CC genes from humans and rats. Each of the novel Ca-channels contains a
CC putative IVS4 region comprising the amino acid sequence AAY14598. Cells
CC expressing the T-type voltage-gated calcium channel proteins can be used
CC to screen for drugs which affect calcium channels. Methods are also
CC disclosed for treating a disease or disorder associated with a deficiency
CC in a native T-type calcium channel nucleic acid, e.g. to treat
CC cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6750 BP, 1290 A; 2170 C; 1984 G; 1306 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6750
Score: 10970.00 Matches: 2111
Percent Similarity: 94.99% Conservative: 32
Best Local Similarity: 93.57% Mismatches: 105
Query Match: 91.20% Indels: 8
DB: 2 Gaps: 4

US-09-611-257A-24 (1-2287) x AAX83481 (1-6750)

QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
DB 2 TGACAGGAGGAGGATGGAGCGGCGCCGAGGAGTCCGGACAGCCCCGGAGCTTCATGC 61
QY 54 SerSerThrThrCysProGlyPro-GlyAlaAlaGlyAla-GlySerThrGluLysAsp 73
DB 62 GGCTCAACGACCTGTGCGGGGGCCGGGGGGGGCGCCGGGGGGGGGTCAGCAGAAAAGGACC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValAlaP 93
DB 122 CGGGCAGCGCGGACTCCGAGGCGGAGGGGTGCGCCGTACCGCGCTGGCCCCGGTGGTTT 181
QY 93 hepTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 113
DB 182 TCTTCTACTGAGCCAGGACAGCCGCCCGGAGCTGGTCTCCGACGCTGTAAACC 241
QY 113 roTyrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
DB 242 CCTGGTTGAGCGGCATCAGCATGTGGTCATCTTCTCACTGCGTGACCCCTGGGCATGT 301
QY 133 hepArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhea 153
DB 302 TCCGGCCATGCGAGACATCGCTGTGACTCCAGCGCTGCCGATCCTGCAGGCCCTTTG 361
QY 153 sPAspPheIlePheAlaPhePheAlaValGluMetValIleLysMetValAlaLeuGlyI 173
DB 362 ATGACTTCACTTTGCTTCTTTCCTTGGAGATGGTGAAGATGGTGGCTTGGGCA 421
QY 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
DB 422 TCTTTGGGAAAAAGTGTACCTGGGAGACACTTGAAACCGGCTTGACTTTTCACTGTC 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
DB 482 TCGCAGGGATGCTGAGTACTCGCTGGACCTGCAGACGTCAGCTTCTCAGCTGTCA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
DB 542 CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCCAACATGCGCATCTTG 601
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
DB 602 TCACGTTGCTGTGATACGCTGCGCATGCTGGGCAACGTCCTGCTGCTTCTTTCG 661

QY 253 alpPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
DB 662 TCTTCTTCACTTCGGGCATCGTCGGCGTCCAGCTGTGGGACAGGCTGCTTCGAAACCGAT 721
QY 273 yspPheLeuProGluAsnPheserLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
DB 722 GCTTCCTACCTGAGAAATTTCAGCCTCCCGCTGAGCGTGGACCTGGAGCGCTATTACAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
DB 782 CAGAGAACGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGCGATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyGlyProProCysSerLeuA 333
DB 842 CCTGCAGAACGCTGCCACGCTGCGCGGGGACGGGGGGCGGTGGCCCACTTGGGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
DB 902 ACTATGAGGCTTACACAGCTCCAGCAACACCACCTGTGTCAACTGGAAACGACTACTACA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnDheaAspAsnIleG 373
DB 962 CCACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGGCATCAACTTGAACAACATTG 1021
QY 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetT 393
DB 1022 GCTATGCTTGATCGCCATCTTCCAGGTCAACGCTGGAGGGCTGGGTGCAATCATGT 1081
QY 393 yrPheValMetAspAlaHisSerPheTyrAsnPhelIeTyrPheIleLeuLeuIleIleV 413
DB 1082 ACTTTGTATGATGATGCTCATTTCTTCTCAATTTCACTACTTCATCTCTCATCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheserGluT 433
DB 1142 TGGGTCTCTTCTTCAATGATCAACCTGTGCTGTGGTGAATTGCCACGCGATTCTCAGAGA 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
DB 1202 CCAAGCAGCGGAAAGCCAGCTGATCGGAGCAGCGTGGCGGTCTCTTCCAACGCCA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGlyGluLeuLeuLysTyrLeuV 473
DB 1262 GCACCTGGCTAGCTTCTCTGAGCCCGGACGCTGATGAGAGCTGCTCAAGTACCTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
DB 1322 TGTACATCTTCTGTAAGGACCCCGAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys 513
DB 1382 GGGTTGGGCTGCTCAGCAGCCACGACCCCTCGGGGGGCCAGGAGACCCAGCCACGAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
DB 1442 GCTGCTCTCGCTCCACCGCGCCTTATCCGTCCACCACTGTGCAACCAACCAACCA 1501
QY 533 ishHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
DB 1502 ATCACCACTACCTACCTGGGCAATGGAGCGCTCAGGGCCCCCGGGCGAGCCGAGGA 1561
QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProt 573
DB 1562 TCCAGGACAGGATGCCAATGGGTCCCGCGGCTCATGTGCCACCAACCTGACGCGCTG 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
DB 1622 CCTTCTCGGGGGCCCCCTGTGTGGCGCAGAGTGTGTGACACAGCTTCTTACCATGCGACT 1681
QY 593 yshHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
DB 1682 GCCACTTAAGACCAGTCCGCTGCGCAGGCGCCCTCCCAAGTCCCATTTGAAGGCATCCG 1741

QY	613	lyArGThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI	633
Db	1742	GCAGAGCTGTGGCGAGCGGAAGGTGTATCCACCGTGACACAGCCCTCCACCGAGA	1801
QY	633	leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuHis	653
Db	1802	CGCTGAAGAGAGAAGGCGCTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACCA	1861
QY	653	erPheAsnIleProProGlyProPheSerSerMetHisLysLeuGluThrGlnSerT	673
Db	1862	GCCTCAACATCCACCCGGGGCCCTACAGCTCCATGCACAGAGCTGTGAGACACAGAGTA	1921
QY	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
Db	1922	CAGGTGCCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAAGCAGACAGTGGAG	1981
QY	693	laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA	713
Db	1982	CCTGTGCTCAGACAGCTGCCCTACTGTGCCGGGGCCGAGGAGGTGAGCTCG	2041
QY	713	laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733
Db	2042	CCGACCGTGAATGCTGACTCAGACAGCGAGGAGAGTTATGAGTTACACAGAGATGCC	2101
QY	733	lnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA	753
Db	2102	AGCACAGCGACCTCCGGGACCCCAACAGC--CGCGGCAACGAGCCCTGGGCCAGATG	2158
QY	753	laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV	773
Db	2159	CAGAGCCAGCTCTGTGTGGCTTCTTGAGGCTAATCTGTGACACCTCCGAAAGATTG	2218
QY	773	alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM	793
Db	2219	TGGACAGCAGACTTGTGGCCGGGAATCATGATCGCCATCCTGGTCAACACACTCAGCA	2278
QY	793	etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
Db	2279	TGGGCATCGAATACCAGCAGCAGCCGAGGAGCTTACCAAGCCCTAGAAATCAGCAACA	2338
QY	813	leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp	833
Db	2339	TCGTCTTCACGACCTCTTTTGCCTGGAGATGCTGTGAAGCTGCTGTGTATGGTCCCT	2398
QY	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT	853
Db	2399	TTGGCTACATCAAGAAATCCCTACAACATCTTCGATGGTGCATTTGTGTCATCAGCGTGT	2458
QY	853	rpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA	873
Db	2459	GGGAGATCGTGGCCAGCAGGGGGGGCGGCTGTCCGTGCTGGGACCTCCGCGCTGATGC	2518
QY	873	rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893
Db	2519	GTGTGCTGAAGCTGGTGGCTTCTTCGCGGCGCTGCAGCGGCAGCTGGTGTGCTCATGA	2578
QY	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheS	913
Db	2579	AGACCATGGAACAACGTGGCCACCTTCTGCATGTGCTTATGCTCTTCATCTTCATCTTCA	2638
QY	913	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL	933
Db	2639	GCATCCTGGGCATGCATCTTTCGGCTGCAAGTTTGCCTGTAGCGGGATGGGACACCC	2698
QY	933	euProAspArgLysAsnAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953
Db	2699	TGCCAGACCGGAAGATTTTGACTCCTTGCTCTGGGCCATCGTCACTGTCTTCAAGATCC	2758
QY	953	euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA	973
Db	2759	TGACCCAGGAGGAGCTGGAACAAGTCTCTACAATGGTATGGCTCCACAGTGTCTGTGG	2818
QY	973	laAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV	993

Db	2819	CGGCCCTTAATTTCATTGCCCCATGACCTTCGGCAACTACGTGCTCTTCAATTGCTGG	2878
Qy	993	aAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluP	1013
Db	2879	TCCGCAATTCGTGTGAGGGCTTCCAGCGCGAGGAGATGCCAACAGAGTCCGAAATCAGAGC	2938
Qy	1013	roAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuV	1033
Db	2939	CCGATTTCCTTCTCAACCCAGCCTGGATGGTGATGGGGACAGGAAGAGTGTGCTTGGCTTGG	2998
Qy	1033	aAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisT	1053
Db	2999	TGTCCCTGGGAGAGCACCCGGAGCTGCGAAGAGCCTGCTGCCGCTCTCATCATCCACA	3058
Qy	1053	hrrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuG	1073
Db	3059	CGGCCGCCACCCCATGTGCTGCTGCCAAGACACACAGCAGCGCTTGGGGAGGCGCTGG	3118
Qy	1073	lySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyValAlaHisHisG	1093
Db	3119	GCCCTGCGTGGCGCCGACACAGCAGCGGGTCCGACAGACCTTGGGGCGGCGC--CACG	3175
Qy	1093	lunMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS	1113
Db	3176	AGATGAAGTCAACGCCAGCGCCGAGCTCTCCGCACAGCCCCCTGGAGCGCTGCAAGCA	3235
Qy	1113	erTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA	1133
Db	3236	GCTGACCAACGAGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCCTGAAGCGGA	3295
Qy	1133	rgSerProSerGlyGlyLysArgArgSerLeuLeuSerGlyGluGlyGlnGlySerGlnAspG	1153
Db	3296	GAAGCCCAAGTGGAGAGCGGCGGTCTCTGTGTGGGAGAAGGCCAGAGAGCCAGGATG	3355
Qy	1153	lunGluGluSerSerGluGluLysSerArgAlaSerProAlaGlySerAspHisArgHisArgG	1173
Db	3356	AAGAGGAGAGCTCAGAAAGAGAGCGGGCCAGCCTCGGGCAGTGACCATGCCACAGGG	3415
Qy	1173	lySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG	1193
Db	3416	GGTCCCTGGAGGGGAGGCCAAGAGTTCTTTGACCTGCACAGACACACTGCAGGTGCCAG	3475
Qy	1193	lyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL	1213
Db	3476	GGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTGAGCACCAGACTGCATGGCA	3535
Qy	1213	ysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA	1233
Db	3536	AGTCGGCTTCAGGGCGCCTGGCCCGGGCCCTCGCGCCTGATGACCCCCCACTGGATGGGG	3595
Qy	1233	spAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS	1253
Db	3596	ATGACGCCGATGACGAGGGCAACCTGAGCAAAAGGGAAAGGGTCCGCGCTGGATCCGAG	3655
Qy	1253	erArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrlIlePheProProG	1273
Db	3656	CCCGACTCCCTGCTGCTGCTGCCTCGAGCGAGACTCCTGGTCACTACATCTTCCCTCCTC	3715
Qy	1273	lnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV	1293
Db	3716	AGTCCAGGTTCCGCTCTCTGTGTCAACCGATCATCACCCACAAGATGTTGACACAGTGG	3775
Qy	1293	alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP	1313
Db	3776	TCCTTGTATCATCTTCTTAACGTGATCAACCATGCCATGGAGCGCCCAAAATTGACC	3835
Qy	1313	roHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrlIlePheThrAlaValPheL	1333
Db	3836	CCACAGCGCTGAACGCATCTTCTTGACCTCTCCAATTACATCTTACCGCAGTCTTTC	3895
Qy	1333	euAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrl	1353

Db 3896 TGGCTGAATGACAGTGAAGGTGGTGCACTGGGCTGTGCTTCGGGGAGCAGCGCTACC 3955
QY 1353 euArgSerSerTrpAsnValIleuAspGlyLeuLeuValIleSerValIleAspIleL 1373
Db 3956 TGGGAGCAGTTGGAACGTGCTGGAACGGGCTGTGCTCATCTCCGTCATCGACATTTC 4015
QY 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393
Db 4016 TGGTGTCATGCTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGCTCGGC 4075
QY 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413
Db 4076 TGCTGGGGAACCTGCGCCGCTCAGGGTGATCAGCCGGGCGCAGGGCTGAAGCTGTGG 4135
QY 1413 aIGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaP 1433
Db 4136 TGGAGACGCTGATGTCCTCACTGAAAACCATCGGCACATTGTAGTCATCTGTGCTCCT 4195
QY 1433 hepheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453
Db 4196 TCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAGGGAAGTTTTCGTGTGCC 4255
QY 1453 lngIlgIuAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgT 1473
Db 4256 AGGGCGAGGATACCAAGAACATCAACATAATCGACTGTGCCGAGGCCAATTACCGGT 4315
QY 1473 rpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493
Db 4316 GGGTCGGGCACAAGTACAACTTGACAACTTGCGCAGGCCCTGATGTCCTGTCTGTTT 4375
QY 1493 euAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513
Db 4376 TGGCTCCAAAGGATGTTGGGTGACATCATGTAAGGGCTGGATGCTGTGGGGCTGG 4435
QY 1513 spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL 1533
Db 4436 ACCAGCAGCCCATCATGAACCAACCAACCCCTGATGCTGTCTACTTCATCTCTCTGC 4495
QY 1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL 1553
Db 4496 TCATGTGGCTTCTTGTCTTGAACATGTTGTGGTGTGTGGTGAGAACTTCCACA 4555
QY 1553 ybCyAsArgIlnHisGlnGluGluGluAlaArgArgArgGluLysArgLeuArgA 1573
Db 4556 AGTGTGGGACGACCAAGAGAGAGAGAGGCCCGCGCGGAGAGAGAGAGCGCTACGAA 4615
QY 1573 rglLeuGlnLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProT 1593
Db 4616 GACTGGAGAAAAGAGAGAGAGATGAAGAGACAGATGGCTGAAGCCCACTGCAAACTT 4675
QY 1593 yrrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrL 1613
Db 4676 ACTACTCCGACTACTCCCGCTTCCGGCTCTCGTCCACCACTTGTGACCAAGCCACTACC 4735
QY 1613 euAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisT 1633
Db 4736 TGGACCTCTTCATCACAGGTGTCAATCGGGCTGAACGTGTCAACCATGGCCATGGAGCACT 4795
QY 1633 yrrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValI 1653
Db 4796 ACCAGCAGCCCCAGATTCTGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCA 4855
QY 1653 lePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnA 1673
Db 4856 TCTTTGTCTTGAGTCAAGTTTCAAACTTGTGGCTTGTGTTTCCGTGCTTCCAGG 4915
QY 1673 spArgTrpAnglnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuG 1693
Db 4916 ACAGGTGAACCACTGACCTGGCCATTGTGCTGTCTCATGCGCATCAAGCTGG 4975
QY 1693 lngIuIleGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgV 1713
Db 4976 AGGAATCGAGGTCAACGCCCTGCTGCCCATCAACCCCACTCATCCGCATCATGAGGG 5035

QY 1713 alLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuL 1733
Db 5036 TGCTGGCATTGCCCCAGGTGCTGAAGCTGCTGAAGATGGCTGTGGCATGCGGGCCTGC 5095
QY 1733 euHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuL 1753
Db 5096 TGGACACGGTGATGAGGCCCTGCCCCAGGTGGGGAACCTGGACTTCTCTTCATGTTGT 5155
QY 1753 euPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluT 1773
Db 5156 TGTTTTCATCTTGGAGCTCTGGGCTGAGCTCTTTGAGACCTGAGTGTGACGAGA 5215
QY 1773 hrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheL 1793
Db 5216 CACACCCCTGTGAGGGCTGGGCGCTCATATGCCACTTTCGGAACCTTGGCATGGCCTTCC 5275
QY 1793 euThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerA 1813
Db 5276 TAACTCTCTCCAGTCTCCACAGGTGACAAATTGGAATGGCATTATGAGACACACCTCC 5335
QY 1813 rGAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValS 1833
Db 5336 GGGACTGTGACCAAGAGTCCACTGTCTACACACGGTCATCTCGCTTACTACTTGTGT 5395
QY 1833 erPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysH 1853
Db 5396 CTTTCGTGTGACGGCCAGTTCGTGCTAGTCAACGTGTGATCGCGCTGTGATGAAGC 5455
QY 1853 iSLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluL 1873
Db 5456 ACCTGAGGAGAGACAAAGAGAGGCCAAGAGAGAGGCCGAGCTAGAGGCTGAGCTGAGC 5515
QY 1873 euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrp 1893
Db 5516 TGGAGATGAAGACCTTCAAGCCCCCAGCCCCCACTTCGCCACTGGGCAAGCCCCCTTCTG 5575
QY 1893 roGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThra 1913
Db 5576 CTGGGCTGAGGGCCCGACAGCCCCGACAGCCCCCAAGCCTGGGGCTTGCAACCCAGCGG 5635
QY 1913 laHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProG 1933
Db 5636 CCGAGCGAGATCAGCCTCCCACTTTTCCCTGGAGCACCCACGATGACAGCCCCACCCA 5695
QY 1933 lngIuValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSera 1953
Db 5696 CGAGCTGCCA-----GAGCACACTTACTGACTGTGCGGAGTCTGGGGTCAAGCC 5746
QY 1953 rgtThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgS 1973
Db 5747 GAACGCACTCTTGCCCAATGACAGCTACATGTGTGGCATGGGAGCACTGCCGAGGGGC 5806
QY 1973 erLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValH 1993
Db 5807 CCTTGGACACAGGGCTGGGGGCTCCCAAGCTCAGTCAAGGCTCCGTCTGTCCGTTCC 5866
QY 1993 iSserGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuL 2013
Db 5867 ACTCCAGCCAGCAGATACAGCTTACATCTCGAGCTTCCCAAGATGACCTCATCTGC 5926
QY 2013 euGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGluArgS 2033
Db 5927 TCCAGCCCCACAGCGCCCAACTGGGGCACCACTCCCAAACTGCCCCCAAGAGCGCT 5986
QY 2033 erProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspv 2053
Db 5987 CCCCCTTGGCTCAGAGGCCACTCAGGCGCCAGGACCAATAAGACTGACTCTTGAGCG 6046
QY 2053 aGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProL 2073
Db 6047 TTCAAGGCTCTGGCAGCCGGGAAGACTGTGTCAGAGGTGAGTGGGCCCTTCCCGCCCC 6106


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Qy      2073 eutHrArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyI 2093
Db      6107 TGGCCCCGGGCTACTCTTTCTTGGGGCCAGTCAAGTACCAGGCACAGCAGCACTCCGCA 6166
Qy      2093 legInSerLySValSerLyShisIleArgLeuProAlaProCysProGlyLeuGlnProS 2113
Db      6167 GCCACAGCAAGATCTCCAAAGACACATGACCCCGGACGCCCTTGCCAGGCCAGAACCA 6226
Qy      2113 eRTpAlaLyAspProProGluThrArgSerSerLeuGlnLeuAspThrGlnLeuSerT 2133
Db      6227 ACTGGGGCAAGGGCCCTCCAGAGACCAGAACGACGTTAGATTGGACACGAGCTGAGCT 6286
Qy      2133 xPileSerGlyAspLeuLeu--ProSerSerGlnGlnGluProLeuPheProArgAspL 2152
Db      6287 GGATTTCAAGAGACTCCTGCCCCCTGGCGGCCAGAGGAACCCCATCCCCACGGGACC 6346
Qy      2152 euLySlyScySTyrSerValGluThrGlnSerCysArgArgProGlyPheTrpLeuA 2172
Db      6347 TGAAGAAGTGCTACAGCGCTGAGGGCCAGAGCCAGAGCTGCCAGCGCCGCTACGTCCTGCTGG 6406
Qy      2172 sPGLuGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgL 2192
Db      6407 ATGAGCAGAGAGACACTCTATCGCCGTGAGCTGCTGGACAGCGGCTCCCAACCCACC 6466
Qy      2192 euCysProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProL 2212
Db      6467 TGGGCACAGACCCCTCTAACCTTGGGGGCCAGCCTTGGGGGGCGCTGGAGCGGCCCA 6526
Qy      2212 ySLySLySLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgP 2232
Db      6527 AGAAAAAACTCAGCCCGCCTAGTATCACCATAGACCCCCCGAGAGCCAAAGTCTCTCGGA 6586
Qy      2232 roProCysSerProGlyValCysLeuArgArgArgAlaProAlaSerAspSerLyAspP 2252
Db      6587 CCCCCGCCAGCCCTGTATCTGCCTCCGGAGGAGGCTCCGTCCAGGACTCCAGAGATC 6646
Qy      2252 roSerValSerSerProLeuAspSerThrAlaAlaSerProSerProLySLyAspThrL 2272
Db      6647 CCTTGGCCTCTGGCCCCCTGACAGCATGGCTGCTGCCCCCTCCCAAGAAAGATGTGC 6706
Qy      2272 euSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286
Db      6707 TGAGTCTCTCCGGTTATCTCTGACCCAGACGACTGGAACCC 6750

RESULT 10
AAx83483
ID      AAx83483 standard; cDNA; 6804 BP.
XX
AC      AAx83483;
XX
DT      07-DEC-1999 (first entry)
XX
DE      Human T-type voltage-gated Ca channel alpha-1-G (hCav1c) cDNA.
XX
KW      Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KM      activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS      Homo sapiens.
XX
PN      MO9929847-A1.
XX
PD      17-JUN-1999.
XX
PF      30-OCT-1998; 98WO-US023161.
XX
PR      05-DEC-1997; 97US-00985809.
XX
PA      (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI      Perez-Reyes E, Cribbs LL;
XX
DR      WPI; 1999-394972/33.
DR      P-PSDB; AAY14588.

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[illegible]

Db 542 CAGTCCGCTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCCATCCTTG 601
Qy 233 aLThrLeuLeuLeuAspThrLeuPrometLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACGTTGCTGCTGGATACGCTGCCCATGCTGGGCAACGCTCCTGCTGCTTCTTCG 661
Qy 253 aPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTCATCTTCGGCATCGTCGGCTCCAGCTGTGGGCAAGGCTGCTTCGGAACCGAT 721
Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCCTACCTGAGAAATTTCAGCCTCCCTGAGCGTGACCTGGAGCGCTATTACAGA 781
Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGGCATGCGGT 841
Qy 313 erCyAsnSerValProThrLeuArgGlyGlyGlyGlyProProCySerLeuA 333
Db 842 CCTGCAAGACGCTGCCACGCTGGCGGGGACGGGGGCGGTGCCACCTTGCGGTCTGG 901
Qy 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGGCTTACAACAGCTCCAGCAACACCACCTGTGTCAACTGGAAACGATACTACA 961
Qy 353 hrAsnCySerAlaGlyGluHisAsnProPheGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGACAACTTCMAAGGCGCCATCAACTTGACACATTG 1021
Qy 373 lYTrAlaTrpIleAlaIlePheGlnValIleThrLeuGlnGlyTrpValAspIleMetT 393
Db 1022 GCTATGCTCGATCGCCATCTTCCAGGTTCATCAGCTGAGGGCTGGTGCACATCATGT 1081
Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIev 413
Db 1082 ACTTGTGATGGATGCTCATCTCTTCAATTCATCTTCACTCCTCCTCATCATCG 1141
Qy 413 aLgLySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCTTCTTCATGATCAACTGTGCTGTGTGATGCCACGCACTTCTCAGAGA 1201
Qy 433 hrLyGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGAAAGCCAGCTGATCGGGAGCAGCGTGTGCGGTTCTGTCCAAGCCA 1261
Qy 453 erThrLeuLaserPheSerGluProGlySerCysTyrGlnGluLeuLeuYsTyrLeuV 473
Db 1262 GCACCCGTGCTAGCTTCTCTGAGCCCGGACAGCTGCTATGAGAGCTGCTCAAGTACTG 1321
Qy 473 aLTrpIleLeuArgLyAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCCTTCGTAAGGACGCCGAGGCTGGCTCAGGTCTCTGGGACAGCAAGTGTG 1381
Qy 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCCAAGCACTCCGGGGCCAGAGAACCCAGCCACAGCA 1441
Qy 513 erCyThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTGCTCCACCGCGCTTATCGTCCACCACTGTGTGACCAACCAACCAACC 1501
Qy 533 iHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisH 553
Db 1502 ATCACCAACCACTACCACTGGGCAATGGAGCGCTCAGGGCCCCCGGGCCAGCCCGAGA 1561
Qy 553 legLAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProt 573
Db 1562 TCCAGGACAGGATGCCAATGGTCCCGCGGCTCATGTGCCACCACTCGACGGCTG 1621
Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593

Db 1622 CCTCTCCGGGGCCCCCTGTGTGCGCAGAGTCTGTGCACAGCTTCTACATGCCGACT 1681
Qy 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTGAGGCATCCG 1741
Qy 613 lYArgThrValGlySerGlyLySValTyrProThrValHisThrSerProProGluI 633
Db 1742 GCAGACTGTGGGACGGGGAAGGTATCCACCGTGACACCAAGCCCTCCACCGGAGA 1801
Qy 633 lLeuLyAspLyAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653
Db 1802 CGCTGAAGAGAAAGCACTAGTAGAGGTGGTCCAGCTCTTGAGGCCCAACCTCACCA 1861
Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLySLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCCAAGCTCCGCGGCCCTACAGCTCCATGCACAAGCTGTGGAGACAGAGTA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLySIlleSerSerProCySerLyAlaAspSerGlyA 693
Db 1922 CAGTGCCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGTTGAAGCAGACAGTGAG 1981
Qy 693 lAcYsGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGCTCAGACAGACTGCCCTACTGTGCCCCGGGCGGGGACGGGAGGTGAGCTCG 2041
Qy 713 lAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCTGAATGCTGTACTCAGACAGCAGGCGAGTTATGATGTACACAGGATGCC 2101
Qy 733 lHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGCAGCTCCGGGACCCCAAGC---CGCGGCAACGAGCTGGGCCAGATG 2158
Qy 753 lAcGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLySileV 773
Db 2159 CAGAGCCAGCTGTGTGCTGGCTTCTGAGGCTAATCTGTGACACCTTCGAAAGATTG 2218
Qy 773 aLAspSerLySTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGACAGCAAGTACTTGGCCGGGGAATCATGATGCCATCCTGTGTCACACATCAGCA 2278
Qy 793 etGlyIleGluTyrHisGlnGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCAATCGAATACCAAGCAGCCCGAGAGCTTACCAAGCCCTAGAAATCAACAACA 2338
Qy 813 lValPheThrSerLeuPheAlaLeuGluMetLeuLeuLySLeuLeuValTyrGlyProP 833
Db 2339 TCGCTTCACACAGCCTTTCCTCCCTGAGATGCTGTGAAGCTGCTGTGTATGTCCCT 2398
Qy 833 heGlyTyrIleLyAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
Db 2399 TTGGCTATCATCAAGATCCCTACACAATCTTCAGTGTGTCATTCAGCGTGT 2458
Qy 853 rpGluIleValGlyGlnGlnGlyGlyLyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGGAGATCGTGGGCCAGCAGGGGGGGCGGCTGTGCGTGTGCGGACCTTCGCGCTGATGC 2518
Qy 873 rgValLeuLySLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2519 GTGTGTGAAGCTGTGTGCTTCTCGCGGCTGCGGCTGACGCGGCAAGCTGTGTGTCTCATGA 2578
Qy 893 ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
Db 2579 AGACCAATGACAACAGTGGCCACTTGTGCATGTGTTATGCTCTTCACTTCATCTTCA 2638
Qy 913 erIleLeuGlyMetHisLeuPheGlyCysLySPhelAserGluArgAspGlyAspThrL 933
Db 2639 GCATCCTGGGCATGCATCTTTCGGCTGCAAGTTGCTCTGAGCGGAGTGGGACACCCC 2698
Qy 933 euProAspArgLyAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953
Db 2699 TGCCAGACCGGAAGATTGTGACTCTTGTGCTGTGGCCATCGTCACTGTCTTCAGATCC 2758

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QY 973 1aAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuV 993
Db 2819 CGGCCCTTATTTCATTGCTCCCTCATGACCTTGGCAACTACGTGCTCTTCAATTGCTGG 2878
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Db 2879 TCGCCATTCTGTGAGAGGCTTCCAGCGGAGGAGATGCCAACAAAGTCCGAATCAGAGC 2938
QY 1013 roAspPhePheSerProSerValAspGlyAspArgLysLysArgLeuAlaLeuV 1033
Db 2939 CCGATTCTTCTTCACCCAGCCTGATGTGATGGGGAACAGAAAGATGCTTGGCCTTGG 2998
QY 1033 aAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisT 1053
Db 2999 TGTCCCTGGAGAGACACCCGGAGCTCGCGAAGAGCCTGTGCTCCGCTCTCATCATCCACA 3058
QY 1053 hrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuG 1073
Db 3059 CGGCCGCCACACCCATGTGCTGCTGCCAAGAGCACAGCACGGGCTTGSGCGAGCGCTGG 3118
QY 1073 LysSerGlySerArgArgThrSerSerSerGlySeraAlaGluProGlyAlaAlaHisHisG 1093
Db 3119 GCCCTGCGTCGCGCGCACAGACAGCAGCGGGTCGGCAGAGCCTGGGCGGCC--CACG 3175
QY 1093 LuMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS 1113
Db 3176 AGATGAAGTCAACGCCCAAGCGCCGACAGCTCTCGCACAGCCCCCTGGAGCGCTGCAAGCA 3235
QY 1113 eTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgA 1133
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QY 1133 rgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnLysSerGlnaspG 1153
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QY 1153 luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG 1173
Db 3356 AAGAGGAGAGCTCAGAGAGGAGCGGGCCAGCCCTCCGGCAGTGACATCGCCACAGGG 3415
QY 1173 LysSerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProG 1193
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QY 1193 LysLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213
Db 3476 GGTGCATCGCACTGCACGTGGCCGAGGCTGTCTTGTAGCACACAGACTGCAATGGCA 3535
QY 1213 ySerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyA 1233
Db 3536 AGTCGGCTTCAGGCGCGCTGGCCCCGGCCCTGCGCCTGATGACCCCCCACTGGATGGGG 3595
QY 1233 spAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgS 1253
Db 3596 ATGACGCCGATGACGAGGCAACCTGAGCAAAAGGGAACGGGTCCGCCGTGATCCGAG 3655
QY 1253 eArArgLeuProAlaCysCysArgGlyArgAspSerTrpSeraIaTyrIlePheProProG 1273
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QY 1273 InSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValV 1293
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QY 1293 alLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspP 1313
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QY 1313 roHisSeraIaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheL 1333
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QY 1333 euAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrL 1353
Db 3896 TGGCTGAATGACAGTGAAGGTGGGCACTGGGCTGTGCTTCGGGAGCAGGCGTAAC 3955
QY 1353 euArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleL 1373
Db 3956 TGGGAGCAGTTGGAACGTGCTGGACGGGCTGTGGTGCTCATCTCCGTCATCGACATT 4015
QY 1373 euValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgL 1393
Db 4016 TGGTGTCATGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGCTGCGGC 4075
QY 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValV 1413
Db 4076 TGCTCGGACCTTGCGCCGCTCAGGGTGAATCAGCCGGCGCAGGGGCTGAAGCTGGTGG 4135
QY 1413 alGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaP 1433
Db 4136 TGGAGACGCTGATGTCTCTCACTGAACCCATCGGCAACATTTAGTCATCTGTGCT 4195
QY 1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysG 1453
Db 4196 TCTTCATCATTTTCGGCATCTTGGGGTGACGCTTCAAAGGGAAGTTTTCGTGTGCC 4255
QY 1453 lngLysGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgT 1473
Db 4256 AGGGCGAGGATACAGGAACATCACCAATAATCGGACTGTGCCGAGCGCAGTTACCGGT 4315
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Db 4316 GGGTCCGGCACAAGTACAACTTTGACAACTTGGCCAGGCCCTGATGTCCCTGTTCGTTT 4375
QY 1493 euAlaSerLysaspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValA 1513
Db 4376 TGGCCTCCAAGATGTTGGTGAGACATGATGAGATGGGCTGATGCTGTGGCGCTGG 4435
QY 1513 spGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuL 1533
Db 4436 ACCAGCAGCCCATCATGAACCAACACCCCTGGATGCTGCTGTACTTCACTCGTCTGCC 4495
QY 1533 euIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisL 1553
Db 4496 TCATTGTGCGCTTCTTGTCTGACATGTTTGTGGTGTGGTGGAGAACTTCCACA 4555
QY 1553 ysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeuArgA 1573
Db 4556 AGTGTGGCAGCACCAAGAGGAGAGAGGCCCGCGCGGAGGAGAGAACGCCCTACGAA 4615
QY 1573 rgLeuGluLysLysArgArgSerLysGluLysGlnMetAla----- 1586
Db 4616 GACTGGAGAAAAGAGAAAGTAGTAGAGAGAAAGCATGGCTGATCTAATGCTGGAGCATG 4675
QY 1587 -----GluAlaGlnCysLysProTyrTyrS 1595
Db 4676 TAATTGCTTCCGCGAGCTCAGCCAGCGCTGCTCAGAAAGCCAGTGCAAACTTACTACT 4735
QY 1595 eArAspTyrSerArgPheArgLeuLeuValHisLysLeuCysThrSerHisTyrIleAspL 1615
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QY 1615 euPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisGlyArgIng 1635
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Db 4856 AGCCCCAGATTTCTGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCACTTTG 4915
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Db 4916 TCTTGAGTCAAGTTTCAAACTGTGGCCTTGGTTCCGTCCGTTCCTTCAGAGACAGGT 4975
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Db 4976 GGAACCAAGCTGACCTGGCCATGTGCTGTCCATCATGGGCATCACGCTGAGAGAAA 5035
Qy 1695 IeGluValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValIleu 1715
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Qy 1775 rOcYseGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThr 1795
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Qy 1815 ysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPhe 1835
Db 5396 GTGACCAAGAGTCCACCTGTACAACAACGGTCATCTCGCTATCTACTTGTGTCCTTCG 5455
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Db 5456 TGCTGAGGGCCCAAGTTCGTGTGTCATCAACGTGTGATCGCGTGTGATGAAGCACCTGG 5515
Qy 1855 IuGluSerAsnLysGluAlaIleGluGluGluAlaGluLeuGluAlaGluLeuGluLum 1875
Db 5516 AGGAGAGCAACAAGAGAGGCCAAGAGAGAGCCGAGCTAGAGCTGAGCTGAGCTGGAGA 5575
Qy 1875 etLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTyrProGly 1895
Db 5576 TGAAGACCTTCAGCCCCCAGCCCCCACTGCGCACTGGGCAGCCCTTCTCTGGCTGGGG 5635
Qy 1895 alGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrAlaHisI 1915
Db 5636 TCGAGGGCCCCGACAGCCCCGACAGCCCCAAGCCTGGGGCTGTGCACCCAGCGGCCACG 5695
Qy 1915 IeGlyAlaIleSerGlyPheSerLeuGluHisProThrMetValProHisProGluGlu 1935
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Db 5756 TGCCA-----GGACCAGACTTAAGTGAAGTGTGCGGAAGTCTGGGGTCAAGCCGAA 5806
Qy 1955 isSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeu 1975
Db 5807 ACTCTCTGCCCAATGACAGCTACATGTGTGCGCATGGAGCACTGCCGAGGGGGCCCTGG 5866
Qy 1975 IyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSer 1995
Db 5867 GACACAGGGGCTGGGGCTCCCAAAGCTCAGTCAAGGCTCGTCTGTCCGTTACTCCC 5926
Qy 1995 InProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGln 2015
Db 5927 AGCCAGCAGATACCACTACATCCTGACGTTCCCAAAGATGCACCTCATCTGCTCCAGC 5986
Qy 2015 roHisGlyAlaProThrTyrGlyAlaIleProLysLeuProProGlyArgSerPro 2035

Db 5987 CCCACAGCGCCCAACCTGGGGCACCATCCCAAACTGCCCCACAGAGAGCCTCCCTT 6046
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Db 6047 TGGCTCAGAGGCCACTCAGAGCGGCCAGGACGAATAAGACTGACTCTTGAGCGTTCAAG 6106
Qy 2055 IyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThra 2075
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Qy 2194 roSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProLysLys 2214
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Db 6587 AACTCAGCCCGCTAGTATCACCATAGACCCCCCGAAGACCAAGTCTCGGAACCCGC 6646
Qy 2234 ysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspProSer 2254
Db 6647 CCAGCCTGTATCTGCTTCGGAGAGAGGGCTCGTCCAGCACTCCAAGATCCCTTGG 6706
Qy 2254 alSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSer 2274
Db 6707 CCTCGGCCCCCCTGACAGCATGGCTGCTGCGCTCCCAAGAAAGATGTGTGAGTC 6766
Qy 2274 euSerGlyLeuSerSerAspProThrAspMetAspPro 2286
Db 6767 TCTCGGTTATCTCTGACCCAGCAGACCTGACCCC 6804
RESULT 11
AAK83482
ID AAK83482 standard; cDNA; 6783 BP.
XX
AC AAK83482;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCavT1b) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Homo sapiens.
XX
PN WO929847-A1.
XX
PD 17-JUN-1999.
XX

PF 30-OCT-1998; 98WO-US023161.
XX 05-DEC-1997; 97US-00985809.
XX (LOYO) UNIV LOYOLA CHICAGO.
PA
XX Perez-Reyes E, Cribbs LL;
XX
XX
XX WPI; 1999-394972/33.
DR P-PSDB; AAY14587.
XX
XX
XX New T-type voltage-gated calcium channels.
PS Disclosure; Page 40-49; 138pp; English.
XX
XX This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCavT1b. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (SI-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

CC
XX
SQ Sequence 6783 BP; 1294 A; 2182 C; 1990 G; 1317 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 6783
Score: 10923.50 Matches: 2105
Percent Similarity: 94.31% Conservative: 33
Best Local Similarity: 92.85% Mismatches: 110
Query Match: 90.82% Indels: 19
DB: 2 Gaps: 5

US-09-611-257A-24 (1-2287) x AAX83482 (1-6783)

QY 34 TrpThrArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACGAGGAGGAGGATGGACGGGGCCGAGGAGTCGGGACAGCCCGGAGACTTCATGC 61
QY 54 SerSerThrThrCysProGlyPro-GlyAlaIaIaGlyAla-GlySerThrGluLysAsp 73
Db 62 GGCTCAACGACCTGTCGGGGGGCCGGGGGGCGGGGGCCGGGGTCAGCAGAAAAAGGACC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCCGGTGT 181
QY 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuAArgThrValCysAsn 113
Db 182 TCTTCTACTTGAGCCAGACAGCCGCCCGAGCTGGTGTCTCCGACGGGTCTGTAACC 241
QY 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CCTGGTTTGAGCGCATCAGCATGTGTGCATCTTCTCAACTGCGTGACCTGGGCATGT 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCCGGCCATGCGAGACATCGCCTGTGACTCCACGGCTGCCGATCCTGCAGGCTTTG 361
QY 153 spAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTCATCTTGTCTTCTTTGCGGTGAGATGTGTGAAGATGTGGCTTGCGCA 421

QY 173 lePheGlyLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
Db 422 TCTTTGGAAAAAGTGTACCTGGGAGACACTTGAAACGGCTTGACTTTTCATCGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGGATGTGGAGTACTCGCTGGACCTGCAGAACGTACACTTCTCAGCTGTGAGA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGTGCGACCGCTCAGGGCATTAAACGGGTGCCAGCATGCGCATCTTG 601
QY 233 alThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACGTGTGCTGGATACGCTGCCCATGTGGCAACGTCCTGCTGCTTCTTCG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTCATCTTCGGCATCGTCGGCTCCAGCTGTGGCGAGGCTGCTCGAACCGAT 721
QY 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCCTACCTGAGAAATTTCAGCCTCCCCCTGACGCTGACCTGGACCGCTATTACAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGATGAGAGCCCTTATCTGCTCCAGCCAGCCGAGAACCGCATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAGCGTCCACGCTGCGGGGAGCGGGGGCGGTGGCCACCTTGCGGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGCGCTTACAACAGCTCCAGCAACACCTGTGTCACTGGAACCACTACTACA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGACACACCCCTTCAAGGGCGCCATCACTTGACAACATTG 1021
QY 373 lYThrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
Db 1022 GCTATGCTGATGCCATCTTCCAGTTCATCAGCTGGAGGCTGGTGACATCATGT 1081
QY 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACTTGTGATGATGCTCATTCCTTCAAAATTTCATCTACTTCATCTCCTCATCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGTGATGTCACGCAATTCTCAGAGA 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGAAAGCCAGCTGATGCGGAGACAGCGTGCCTTCTCCAAAGCCA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCTGCGTACCTTCTCTGAGCCCGGCACTGCTATGAGGACTGCTCAAGTACCTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCTTGTGAAGCAGCCCGGAGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGTGGGCTGTCAGCAGCCAGCACCCTCGGGGGCCAGAGAACCCAGCCAGCAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GCTGCTCTGCTCCACCGCGCCTATCCGTCCACCACCTGTGTGCAACCAACCAACC 1501

Qy	533	ISHISHISHIeTYrchiSleuGlyAsnGlyThrIleAArgValProAArgIAsSerProGluI	553
Db	1502	ATCACCACCACTACCACTGGGCAATGAGACGCTACAGGGCCCCCGGGCCAGCCCGGAGA	1561
Qy	553	IeGlnAspArgAspAlaAsnGlySerArgArgIleuMetLeuProProProSerThrProT	573
Db	1562	TCCAGGACAGGGATGCCAATGGGTCCCGCCGGCTCATGCTGCCACCACCTTCAGCGCTG	1621
Qy	573	hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyHisAlaAspC	593
Db	1622	CCCTCTCCGGGGCCCCCTGTGTGGCGCAGAGTCTGTGCACAGCTTCTACATGCCACT	1681
Qy	593	YSHISleuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerg	613
Db	1682	GCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCATCTGAGGCATCCG	1741
Qy	613	lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI	633
Db	1742	GCAGGACTGTGGGCGAGCGGAAGGTGTATCCACCGTGCACACAGCCCTCCACCGAGA	1801
Qy	633	IeLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrIleuThrs	653
Db	1802	CGCTGAAGGAGAGGCACTAGTAGAGGTGCTGCCAGCTCTGGGCCCCCAACCTTCACCA	1861
Qy	653	eRPhEAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSert	673
Db	1862	GCCTCAACATCCCAACCCGGGCCCTACAGCTCCATGCACAAAGCTGCTGAGACACAGATA	1921
Qy	673	hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA	693
Db	1922	CAGGTCCCTGCCAAAGCTTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGGAG	1981
Qy	693	IaCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera	713
Db	1982	CCTGTGTCCAGACAGCTGCCCTTACTGTGCCCGGGCCAGGAGGTGAGCTCG	2041
Qy	713	IaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG	733
Db	2042	CCGACCGTGAAATGCTGACTCAGACAGCAGGACAGTTATGATTACACACAGATGCC	2101
Qy	733	IlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA	753
Db	2102	AGCACAGCGACCTCCGGGACCCCAACAGC--CGGCGGCAACGAGCCTGGGCCAGATG	2158
Qy	753	IaGluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIleV	773
Db	2159	CAGAGCCCAAGCTCTGTGCTGGCCTTCTGAGGCTAATCTGTGACACCTTCCGAAGATTG	2218
Qy	773	aIaSpSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerm	793
Db	2219	TGGAACAGCAAGTACTTTGGCCGGGGAATCATGATCGCCATCCTGCTCAACACACTGACA	2278
Qy	793	eGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
Db	2279	TGGGCATCGAATACCAACGAGCAGCCGAGAGCTTACCAAGCCCTAGAAATCAGCACA	2338
Qy	813	IeValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp	833
Db	2339	TGCTCTTACCAAGCCTCTTGGCCCTGGAGATGCTGCTGAAGCTGTTGTATGTCCT	2398
Qy	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT	853
Db	2399	TTGGCTACATCAAGAAATCCCTCAACATCTTGATGGTGTATGTGTCATCAGCGTGT	2458
Qy	853	trGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetA	873
Db	2459	GGGAGATCGTGGGCCAGCAGGGGGCGGCTGTGCTGTGGGGAACCTTCGCTGATGC	2518
Qy	873	rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL	893
Db	2519	GTGTGCTGAAGCTGTGTGCGCTTCTGTCCGGCGCTGCAGCGGACGCTGTGTGCTCATGA	2578
Qy	893	yvThrMetCAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913

Db	2579	AGACCATGGAACAGTGGCCACCTTCTGCAATGCTGCTTATGCTCTTCACTTCACTTCA	2638
Qy	913	erlleuGlYMeHisleuPheGlyCyelYsPheAlaSerGluArgAspGlyAspThrL	933
Db	2639	GCATCTGGGCATGCACTCTTCTGGCTGCAGATTGCTCTGAGCGGATGGGACACCC	2698
Qy	933	eUProAspArgLYsAsnPheAspSerleuLeuTrpAlaileValThrValPheGlnIleL	953
Db	2699	TGCCAGACCAGGAAGATTGACTCTTGCTCTGGGCCATCGTCACTGCTTTCAGATCC	2758
Qy	953	euThrgIngluAspTrpAsnLYsValleuTYrAsnGlyMetAlaSerThrSerSerTrpA	973
Db	2759	TGACCCAGAGGACTGGAAACAAGTCCCTTACATGTATGGCTCCACGTCGTCTGGG	2818
Qy	973	laAlaleuTYrPheileAlaleuMetThrPheGlyAsnTYrValleuPheAsnleuY	993
Db	2819	CGGCCCTTATTTCATTGCTCCCTCATGACCTTCGGCACTACGTGCTCTCAATTGCTGG	2878
Qy	993	AlAlaileuValGluGlyPheGlnAlaGluGlyAspAlaThrLYsSerGluSerGluP	1013
Db	2879	TGCGCATCTGTGTGAGGGCTTCCAGGCGGAGAGATGCCAACAAAGTCCGAATCAGAGC	2938
Qy	1013	roAspPhePheSerProSerValAspGlyAspGlyAspArgLYsLYsArgLeuAlaLeuV	1033
Db	2939	CCGATTCTTCTTCAACCCAGCTGATGTGATGGGACAGGAAGAAGTGTGGCTTGG	2998
Qy	1033	AlAlaleuGlyGlnHisAlaGluLeuArgLYsSerleuLeuProProleuIleIleHisT	1053
Db	2999	TGTCCCTGGAGAGCACCCCGAGCTGCGGAGAGACCTGCTGCCGCTCTCATCATCCACA	3058
Qy	1053	hrAlaAlaThrProMetSerHisProLYsSerSerSerThrGlyValGlyAlaIleuG	1073
Db	3059	CGGCGGCACACCATGTGCTGCTGCCAAGACACCAACGCGGCTGGGCGAGCGCTGG	3118
Qy	1073	LYserGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisISG	1093
Db	3119	GCCCTGCGTGGCGCGCACACAGCAGCGGGTGGGAGAGAGCTGGGGCGGCC--CACG	3175
Qy	1093	luMetLYsCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS	1113
Db	3176	AGATGAAGTCAACCGCCGACGCGCCGACAGCTCTCCGCAACAGCCCTGAGCGTGCAMGCA	3235
Qy	1113	erTrpThrSerArgArgSerSerArgAsnSerleuGlyArgAlaProSerleuLYsArgA	1133
Db	3236	GCTGACCAAGCAGAGCGCGCTTCCAGCCGGAACAGCTTCGGCCGTGCAACCAAGCTGAAGCGGA	3295
Qy	1133	rgSerProSerGlyGluArgArgSerleuLeuSerGlyGluGlyGlnGluSerGlnAspG	1153
Db	3296	GAAGCCCAAGTGAGAGCGCGCTCCCTGTTGTGGGAGAAAGGCCAGAGAGCCAGGATG	3355
Qy	1153	luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG	1173
Db	3356	AAGAAGAGAGCTCAGAAGAGAGAGCGGGCCAGCCCTGCGGCAGTGACCATCGCCACAGGG	3415
Qy	1173	LYserleuGluArgGluAlaLYsSerSerPheAspIleuProAspThrleuGlnValProG	1193
Db	3416	GGTCCCTGGAGCGGAGGCCAAGATTCTTTCCTTGACCTGACACACACTGCAGGTGCCAG	3475
Qy	1193	LYleuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL	1213
Db	3476	GGCTGCATCGCACTGCCAGTGAGCGGAGGGTCTGCTTGTAGACACAGGACTGCAATGGCA	3535
Qy	1213	YsSerAlaSerGlyArgLeuAlaArgThrleuArgThrAspAspProGlnleuAspGlyA	1233
Db	3536	AGTCGGCTTCAGGCGGCTGGCCCGGGCCCTGCGGCTGATGACCCCCACTGATGGGG	3599
Qy	1233	sPaAspAspAsnAspGluGlyAsnleuSerLYsGlyGluArgIleGlnAlaTrpValArgS	1253
Db	3596	ATGACGCCGATGACGAGGGCAACTGAGCAAAAGGGGACGGGTCCGCGGTGATCCGAG	3655
Qy	1253	eaArgleuProAlaCysCysArgGluArgAspSerTrpSerAlaTYrIlePheProProG	1273

Db 3656 CCCGACTCCCTGCTTGCTGCCTCGAGCGAGACTCCTGCTCAGCCCTACATCTTCCCTCCTC 3715
QY 1273 InSeArpHeArGlEuLeuCyShiSArgIleIleThRhISLySMeCPheASpHiSValV 1293
Db 3716 AGTTCAGGTTCCGCTCTGCTGTCAACCGATCATACCCACAAGATGTTGACACGCTGG 3775
QY 1293 aLleuValIleIlePheLeuASnCySileThRIleAlMeGlUAxgProLySileASpP 1313
Db 3776 TCCTTGTCATCATCTTCTTAACTCGATCACCATGCGCATGAGCGGCCCAAAATTGACC 3835
QY 1313 roHISserAlaGlUAxgIlePheLeuThrLeuSerASnTYrIlePheThrAlaValPheL 1333
Db 3836 CCCACAGCGCTGAACCGCATCTTCTTGACCCCTCTCCAATTACATCTTCACCGCAGTCTTTC 3895
QY 1333 euAlaGlUmetThrValLySValValAlaLeuGlyTrpCySpheGlyGluGlnAlaTYrL 1353
Db 3896 TGGCTGAATGACAGTGAAGGTGGTGACACTGGGCTGGTCTTCGGGGAGCAGGCGTACC 3955
QY 1353 euArgSerSerTrpASnValLeuASpGlyLeuLeuValLeuIleSerValIleASpIleL 1373
Db 3956 TGCAGACAGTTGGAACGTGCTGACGCGGCTGTTGGTGTCTCATCTCCGTCATCGACATTC 4015
QY 1373 euValSerMetValSerASpSerGlyThrLySileuGlyMetLeuArgValLeuArgL 1393
Db 4016 TGGTTCATAGTCTCTGACAGCGGCACCAAGATCTGGGCATGCTGAGGGTGCTGCGGC 4075
QY 1393 euLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLySLeuValV 1413
Db 4076 TGCTGGCGAACCTGCGCCGCTCAGGGTGATGATCAGCCGGCGCAGGGGCTGAAGCTGTGG 4135
QY 1413 aLGlUthrLeuMetSerSerLeuLySProIleGlyASnIleValValIleCySCysAlaP 1433
Db 4136 TGGAGACGCTGATGTCTCTACTGAAACCCCATCGGCAACATTGTAGTCTGTGCTGCT 4195
QY 1433 hePheIleIlePheGlyIleLeuGlyValGlnLeuPheLySgLYLySPhePheValCySg 1453
Db 4196 TCTTCATCATTTTCGGCATCTTGGGGGTGACGCTCTCAAGGGAAGTTTTCGTGTGCC 4255
QY 1453 InGlyGlUASpThrArgASnIleThrASnLySserASpCysAlaGlnAlaSerTYrArgT 1473
Db 4256 AGGGCGAGGATACAGAAATCAACCAATAAATCGACTGTGCCGAGGCCAGTTACCGGT 4315
QY 1473 rpValArgHisLySTyrASnPheASpASnLeuGlyGlnAlaLeuMetSerLeuPheValL 1493
Db 4316 GGGTCCGGCACAAGTACACTTTGACAACTTGCCAGGCCCTGATGTCCCTGTTGCTTT 4375
QY 1493 euAlaSerLySASpGlyTrpValASpIleMetTYrASpGlyLeuASpAlaValGlyValA 1513
Db 4376 TGGCTCCCAAGGATGTTGGGTGACATCATGTACGATGGGCTGATGCTGTGGGCGTGG 4435
QY 1513 spGlnGlnProIleMetASnHisASnProTrpMetLeuLeuTYrPheIleSerPheLeuL 1533
Db 4436 ACCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTACTTCACTCTGTTCCCTGC 4495
QY 1533 euIleValAlaPhePheValLeuASnMetPheValGlyValValGlnASnPheHisL 1553
Db 4496 TCATTGTGGCTTCTTGTCTGAACATGTTGTGGTGTGGTGGAGAACTTCACACA 4555
QY 1553 ySCysArgGlnHisGlnGluGluGlnGlyAlaArgArgArgGlyGluLySArgLeuArgA 1573
Db 4556 AGTGTGGGACGACACAGAGGAAGAGAGGCCGCGGCGGAGAGAGAGCGCTACGAA 4615
QY 1573 rgleuGluLySlySArgArg-----SerLySg 1582
Db 4616 GACTGGAGAAAAGAGAGAGAAATCTAATGCTGAGCATGTAAATTGCTTCCGGCAGCTCAG 4675
QY 1582 LuLySglnMetAlaGlyAlaGlnCysLySProTYrTYrSerASpTYrSerArgPheArgL 1602
Db 4676 CCAGCGCTGCGTCAGAAGCCCAAGTGCAAACCTTACTACTCCGACTACTCCGCTTCCGGC 4735
QY 1602 euLeuValHisHisLeuCySThrSerHisTYrLeuASpLeuPheIleThrGlyValIleG 1622
Db 4736 TCTCTGCTCCACCACTGTGTGACCAAGCCACTACTGGAACCTTCTTCATCAAGGTGTATCG 4795

QY 1622 LyLeuASnValValThrMetAlaMetGlnHisTYrGlnGlnProGlnIleLeuASpGluA 1642
Db 4796 GGCTGAACGTGGTTCACCATGGCCATGGAGCACTACCAAGCAGCCCCAGATTCTGTGATGAGG 4855
QY 1642 laLeuLySileCyASnTYrIlePheThrValIlePheValPheGluSerValPheLySL 1662
Db 4856 CTCTGAAGATCTGCACTACATCTTCACTGTCACTTGTGTGGAAGTCAGTTTTCAAAC 4915
QY 1662 euValAlaPheAlaPheArgArgPhePheGlnASpArgTrpASnGlnLeuASpLeuAlaI 1682
Db 4916 TTGTGGCTTTGGTTTCCGTGGGTTCTTCCAGGACAGGTGAAACCAAGCTGACCTGGCCA 4975
QY 1682 leValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlyValASnLeuSerLeuP 1702
Db 4976 TTGTGCTGCTGTGCATCATGGGCATGAGCTGAGGAATCGAGGTCAACGCTCGCTGC 5035
QY 1702 roIleASnProThRIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLySL 1722
Db 5036 CCATCAACCCCAACCATCATCCGCATCATGAGGGTGCTGGCGCATTGCCGAGTGCTGAAGC 5095
QY 1722 euLeuLySMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProG 1742
Db 5096 TGCTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGGACACGSGTATGACAGGCCCTGCC 5155
QY 1742 InValGlyASnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyV 1762
Db 5156 AGGTGGGAACCTGGGAACCTTCTCTTCAATGTGTGTTTTCATCTTTGCAAGCTCTGGGCG 5215
QY 1762 aLGlUleuPheGlyASpLeuGluCyASpGluThrHisProCySGluGlyLeuGlyArgH 1782
Db 5216 TGAGACTCTTTGGAGACCTGGAGTGTGACGAGACACACCCTGTGAGGGCCTGGGCGCTC 5275
QY 1782 iSAlaThrPheArgASnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyA 1802
Db 5276 ATGCCACCTTTCGGAACCTTGAGATGGCTTCTTAACCTCTTCGAGTCCACAGGTG 5335
QY 1802 spASnTrpASnGlyIleMetLySASpProSerArgASpCyASpGlnGluSerThrCysT 1822
Db 5336 ACAATTGGAATGGCATTTATGAAGACACCCTCCGGACTGTGACCAGAGTCCACCTGCT 5395
QY 1822 yRASnThrValIleSerProIleTYrPheValSerPheValLeuThrAlaGlnPheValL 1842
Db 5396 ACAACACGTCATCTCGCTATCTACTTTGTGTCTTCTGTGCTGACGGCCCAAGTTCGTGC 5455
QY 1842 euValASnValValIleAlaValLeuMetLySHisLeuGluGluSerASnLySglnAlaL 1862
Db 5456 TAGTCAACGTGTGATGCGCGGTGTGTAAGACACCTGGAGAGAGCAACAAGAGGCCA 5515
QY 1862 ySGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLySThrLeuSerProGlnP 1882
Db 5516 AGGAGAGGCCGAGCTAGAGGCTGAGCTGAGCTGAGATGAAGACCTCAGCCCCCAGC 5575
QY 1882 roHISserProLeuGlySerProPheLeuTrpProGlyValGluGlyValASnSerThra 1902
Db 5576 CCCACTCGCACTGGGACAGCCCTTCTGCTGGCTGGGTCGAGGGCCCCGACAGCCCCG 5635
QY 1902 spSerProLySProGlyAlaProHisThrThraHisIleGlyAlaAlaSerGlyPheS 1922
Db 5636 ACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCACCGAGATCAGCCTCCCACTTTT 5695
QY 1922 erLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyProA 1942
Db 5696 CCCTGAGCACCCACGATGACAGCCCCACCCACGAGAGTGCCA-----GGACCAG 5746
QY 1942 sPLeuLeuThrValArgLySserGlyValSerArgThrHisSerLeuProASnASpSerT 1962
Db 5747 ACTTACTAGCTGTGGAAGTCTGGGTCAAGCCGAACGCACTCTGTGCCCAATGACAGCT 5806
QY 1962 yRMetCysArgASnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTYrPGLyLeuP 1982
Db 5807 ACATGTGTGCGCATGGGAGACACTGCGGAGGGGCCCTGGGACACAGGGGCTGGGGCTCC 5866

OY 1982 rolyalaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysI 2002
DB 5867 CCAAGCTCAGTCAGGCTCCGCTTGTCCGTTCACTCCCAAGCAGACAGATACCACTACA 5926
OY 2002 lEleuGlnLeuProLyAspValHisTyrLeuGlnProHisGlyAlaProThrTrpG 2022
DB 5927 TCCTGCAGCTTCCCAAGATGCACTCATCTGCTCCAGCCCCACAGCGGCCCACTGGG 5986
OY 2022 lYAlaIleProLySLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgA 2042
DB 5987 GCACCATCCCAAACTGCCCCCAAGACGAGCGCTCCCTTTGGCTCAGAGGCCACTCAGGC 6046
OY 2042 rGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspL 2062
DB 6047 GCCAGGCAATAAGACTGACTCTTGAGCGTTCAGGGTCTGGGACCGGGAAGACC 6106
OY 2062 euleuSerGluValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyG 2082
DB 6107 TGCTGGCAGAGGTGAGTGGGCCCTTCCCGCCCTGGGCCCGGCTACTCTTTCTGGGGCC 6166
OY 2082 lYSerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLyValSerLyHisIleA 2102
DB 6167 AGTCAAGTACCAGGACAGACAGCACTCCGACGCCACAGCAAGATCTCCAAGCACAATGA 6226
OY 2102 rGleuProAlaProCysProGlyLeuGlnProSerTrpAlaLyAspProProGluThra 2122
DB 6227 CCCCCGCGACCCCTTGCCAGGCCAGAAACCAACTGGGCCAAGGCCCTCCAGACCA 6286
OY 2122 rGSerSerLeuGlnLeuAspThrGlnLeuSerTrpIleSerGlyAspLeuLeu---ProS 2141
DB 6287 GAAGCAAGCTTAGAGTTGAGACACGGAGCTGAGCTGATTTCAAGAGACCTCCGCCCCCTG 6346
OY 2141 erSerGlnGluGluProLeuPheProAlaArgAspLeuLySlyCysTyrSerValGluThrg 2161
DB 6347 GCGGCCAGAGAGACCCCATCCCAACGGGACCTGAAGAGTCTAAGCGTGGAGGCC 6406
OY 2161 lnsrCyAsrArgArgProGlyPheTrpLeuAspGlnGlnArgHisSerIleAlay 2181
DB 6407 AGAGCTGCAGCGCCGCTACGCTCTGCTGATGAGCAGAGAGACACTTATCTGCGG 6466
OY 2181 alSerCySLeuAspSerGlySerGlnProAlaGlyCysProSerProSerSerLeuGlyG 2201
DB 6467 TCAGCTGCCTGGACAGCGGCTCCCAACCCACCTGGGACAGACCCCTTAACCTTGGGG 6526
OY 2201 lYglnProLeuGlyGlyProGlySerArgProLySlySlyLeuSerProProSerIleS 2221
DB 6527 GCCAGCCTTTGGGGGGGCGTGGAGCGGCCCAAGAAAAAACTCAAGCCCGCTAGATCA 6586
OY 2221 erIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysLeuA 2241
DB 6587 CCATAGACCCCCCGAGAGCCAAAGTCTCGGACCCCGCCAGCCCTGGTATCTGCTCC 6646
OY 2241 rGArgArgAlaProAlaSerAspSerLySAspProSerValSerSerProLeuAspSert 2261
DB 6647 GGAGGAGGGCTCCGTCAGCGACTCCAAAGATCCCTTGGCTCTGGCCCCCTGACAGCA 6706
OY 2261 hrAlaAlaSerProSerProLySlyAspThrLeuSerLeuSerGlyLeuSerSerAspP 2281
DB 6707 TGGCTGCCTCGCCCTCCCAAGAAAGATGTGCTGAGTCTCTCGGTTTATCTGACCC 6766
OY 2281 roThrAspMetAspPro 2286
DB 6767 CAGCAGACCTGACCCC 6783

RESULT 12
AAx83484
ID AAx83484 standard; cDNA, 6729 BP.

XX
AC AAx83484;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCav1d) cDNA.

XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Homo sapiens.
XX
PN WO929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
DR P-PSDB; AAX14589.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 58-67; 138pp; English.
XX
CC This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCav1d. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAx83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAV14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6729 BP; 1283 A; 2168 C; 1975 G; 1303 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 0 Length: 6729
Score: 10919.50 Matches: 2103
Percent Similarity: 94.68% Conservative: 33
Best Local Similarity: 93.22% Mismatches: 105
Query Match: 90.78% Indels: 15
DB: 2 Gaps: 5
US-09-611-257A-24 (1-2287) x AAx83484 (1-6729)
OY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
DB 2 TGAGCAGAGAGAGATGAGCGGGCGCCGAGGATCGGACAGCCCCGGAGCTTCATGC 61
OY 54 SerSerThrThrCysProGlyPro-GlyAlaAlaGlyAla-GlySerThrGlnLyAspP 73
DB 62 GGCTCAAGACCTGTGGGGGCGGGGGCGCGCCGGGGCGGGGTCAAGCAAAAGAAC 121
OY 73 roGlySerAlaAspSerGluAlaGlnGlyLeuProTyrProAlaLeuAlaProValAlP 93
DB 122 CGGCGAGCGCGGACTCCGAGGCGGAGGGGCTGCCCTAACCGGCGTGGCCCCGCTGTT 181
OY 93 hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113
DB 182 TCTTCTACTTAGACCAAGACAGACGCGCCGCGAGCTGTGTCTCCGACGCTGTAAACC 241
OY 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133

Db 242 CCTGTTTGAGCGCATCAGCATGTTGGTTCATCTTCTCAACTGCCGTGACCTGGGCATGT 301
Qy 133 hearGProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheA 153
Db 302 TCCGGCCATGCAGAGACATCGCCTGTGACTCCAGCGCTGCCGATCTGCAGGCGCTTTG 361
Qy 153 sPAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTCATCTTCTCTTCTTTGCCGTGAGATGGTGTGAAGATGGTGGCCTTGGGCA 421
Qy 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
Db 422 TCTTTGGGAAAAAGTGTTACTTGAGACAATTGGAACCGGCTTGACTTTTCATCGTCA 481
Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGGATGCTGAGTACTCGCTGGAACCTGCAGACGTCAAGCTTCAAGCTGTCAAGA 541
Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTGCCAGCGCTCAGGGCCATTAAACGGGTGCCCAAGCATGCCATCTTG 601
Qy 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACGTTGCTGCTGATACGCTGCCATGCTGGGCAACGTCTGCTGCTTCTTCTTG 661
Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTCATCTTCGGCATCTGCGCGTCCAGCTGTGGCAGGGGCTGCTTCGGAAACCGAT 721
Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCCTACCTGAGAATTTCAGCCTCCCGCTGAGCTGAGCCTGAGCGCTATTACCA 781
Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGGATGAGAGCCCCCTTCATCTGCTCCAGCCACGCGAGAACGGCATGCGGT 841
Qy 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAAAGCGTGCCCAAGCTGCCGCGGGAGCGGGGCGGTGGCCCACTTGCGGTCTGG 901
Qy 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGGCTTACAACAGCTCCAGCAACACCACTGTGTCAACTGGAAACCACTACTACA 961
Qy 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGCCATCAACTTGAACAACATTG 1021
Qy 373 lYTyraIatTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 393
Db 1022 GCTATGCCTGGATCGCAATCTTCCAGGTCAATCAAGGGCTGGAGGGCTGGTCGACATCATGT 1081
Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACTTTGTGATGATGCTCATCTTCTTACAATTTCATCTACTTCATCTCCTCATCATCG 1141
Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCTTCTTCATGATCAACCTGTGCTGGTGTGATTGGCCACGCAATTCTCAGAGA 1201
Qy 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGGAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTTCCTGTCCAACGCCA 1261
Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeuV 473
Db 1262 GCACCTGTGCTAGCTTCTCTGAGCCCGGAGCTGTATGAGGAGCTGTCAAAGTACCTGG 1321
Qy 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493

Db 1322 TGTACATCTTTCGTAAGGAGCAGCCCGAGGCTGGCTCAGGTTCTTCGGGAGCAGGTGTGC 1381
Qy 493 rGAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGTTGGGTGCTTCAGACAGCCAGCAGCCCTTCGGGGCCAGAGAACCCAGCCAGCAGA 1441
Qy 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHis 533
Db 1442 GCTGCTCTCGCTCCACCGCGCGCTTACCGTCCACCACTGTGTGCAACCAACCACCA 1501
Qy 533 lSH 553
Db 1502 ATCACCACCACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCGAGAG 1561
Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProt 573
Db 1562 TCCAGGACAGGGATGCCAATGGGTCCCGCGGCTCATGCTGCCAACCACTCGACGCTG 1621
Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CCTCTCCGGGGCCCCCTGTGGCGAGAGTGTGTGACAGCTTCTACCATGCGCACT 1681
Qy 593 ysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCATCTGAGGCATCCG 1741
Qy 613 lYArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
Db 1742 GCAGAGCTGTGGGAGCGGGAAGGTATCCACCGTGACACCAACCTCCACCGGAGA 1801
Qy 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653
Db 1802 CGCTGAAGAGAGAGCACTAGTAGAGTGGCTGCCAGCTGTGGGCCCCCAACCTCAACA 1861
Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCCAACCGGGGCCCTACAGCTCCATGCACAAAGCTGTGAGACACAGACTA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGGTGCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGTAAGAAGCAGACAGTGAAG 1981
Qy 693 lACysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGTCCAGACAGCTGCCCTACTGTGCCGGCGGGGAGAGGTGAGCTCG 2041
Qy 713 lAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGTGAATGCTGACTCAGACAGCGAGCAGTTATAGTTACACACAGATGCC 2101
Qy 733 lNHlSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCAGCGCACTCCGGGAGCCCCACAGC--CGGGCGAACGAGAGCTGGGCCAGATG 2158
Qy 753 lAGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCAGCTGTGTGCTGGCTTGTGAGGCTTAATCTGTACACCTTCCGAAAGATTG 2218
Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGACAGCAAGTACTTTGGCCGGGAATCATGATGCCATCTGTGTCAACACACTCAGCA 2278
Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACACAGAGCAGCCGAGGAGCTTACCAACGCCCTAGAAATCAGACA 2338
Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
Db 2339 TCGTCTTACCAAGCCTTGTGCCCTGAGATGCTGTGAAGCTGCTGTGTATAGTCCCT 2398
Qy 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
Db 2399 TTGGCTACATCAAGAATCCCTACACACATCTTCGATGTGTTCATTGTGTATCAGCGTGT 2458

QY 853 rpGlulIeValGlYnglNglyGlYleuSerValIeuArgThrPheArgIeuMetA 873
|||||
Db 2459 GGGAGATGCTGGGCCAGCAGGGGGGGCGCTGTCCGTGTCGGGACCTTCCGCTGATGC 2518
QY 873 rgValIeuYsIeuValArgPheIeuProAlaIeuGlnArgGlnIeuValIeuMetL 893
|||||
Db 2519 GTGTGCTGAAGCTGTGTCGCTTCTTGCCGGCGCTGCAGCGGCAGCTGGTGTGTCATGA 2578
QY 893 ysthrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePheS 913
|||||
Db 2579 AGACCATGCAACAGTGGCCACCTTCTGCATGTGCTTATGCTTTCATCTTCA 2638
QY 913 erIleuGlYmetHisIeuPheGlyCysYsPheAlaSerGluArgAspGlyAspThrL 933
|||||
Db 2639 GCATCCTGGGCATGATCTTCCGCTGCAGATTGCTTGACGGGATGGGACACC 2698
QY 933 euProAspArgIyAsnPheAspSerIeuIeuTrpAlaIleValThrValPheGlnIleL 953
|||||
Db 2699 TGCCAGACCGAAGAATTGTACTCTTGCTTGCCCATGTCATGCTTTCAGATCC 2758
QY 953 eutHrgInglYAspTrpAsnIySValIeuTyrAsnGlyMetAlaSerThrSerSerTrpa 973
|||||
Db 2759 TGACCCAGAGSACTGGAACTAAGTCTCTACAATGATGCTCCACGTCGTCGGG 2818
QY 973 IaAlaIeuTyrPheIleAlaIeuMetThrPheGlyAsnTyrValIeuPheAsnIeuIuV 993
|||||
Db 2819 CGGCCCTTTATTTCATTGCTCCCTCATGACCTTCGGCACTACGTGCTTCAATTGCTGG 2878
QY 993 aIAlaIeIeuValGlYglYpHeGlnAgIuGlyAspAlaThrYsSerGluSerGluP 1013
|||||
Db 2879 TCGCCATTCTGGTGAGGGCTTCCAGCGGAGAGATGCCAACAACTCCGAATCAGAGC 2938
QY 1013 roAspPhePheSerProSerValAspGlyAspGlyAspArgIySArgIeuAlaIeuV 1033
|||||
Db 2939 CCGATTCTCTCAACCCAGCCTGATGGTATGGGACAGAGAAAGTGTGGCTTGG 2998
QY 1033 aIAlaIeuGlYglYhIhIsAlaGluIeuArgIySerSerIeuIeuProIeuIleIhIsT 1053
|||||
Db 2999 TGTCCCTGGGAGAGACACCCGGAGCTGGCAGAGACCTGCTGCCCTCTCATCATCACA 3058
QY 1053 hrAlaAlaThrProMetSerHisProIySerSerSerThrGlyValGlyAlaIeug 1073
|||||
Db 3059 CGGCCGCCACACCATGTGCTGCTGCCAAGACACACAGCACGGGCTGGGCGAGCGCTGG 3118
QY 1073 lySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisIsG 1093
|||||
Db 3119 GCCCTGCTGCGCGCCGACACAGCAGCGGGTGGCAGAGCCTGGGGCGGCC--CACG 3175
QY 1093 lUmetIySsCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerS 1113
|||||
Db 3176 AGATGAAGTCAACGCCACAGCGCCGCACTCTCCGACACAGCCCTGGAGCGCTGACAACA 3235
QY 1113 erTrpThrSerArgArgSerSerArgAsnSerIeuGlyArgAlaProSerLeuIySArgA 1133
|||||
Db 3236 GCTGGACCAAGCGCGCTCCAGCCGGAACAGCCTCGGCCGTGCAACCAAGCGGA 3295
QY 1133 rgSerProSerGlyGluArgArgSerIeuIeuSerGlyGluGlynglIuSerGlnAspG 1153
|||||
Db 3296 GAAAGCCCAAGTGAGAGCGGCGGTCTCTGTGTCGGGAGAGGCCAAGAGCCAGGATG 3355
QY 1153 luGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgG 1173
|||||
Db 3356 AAGAGAGAGCTCAAGAGAGAGCGGGCCAGCCTGCGGGCAGTGAACATCGCCACAGGG 3415
QY 1173 lySerIeuGluArgGluAlaIySerSerPheAspIeuProAspThrIeuGlnValProG 1193
|||||
Db 3416 GGTCCCTGAGCGGGAGGCCAAGAGTCTTTGACCTGCACAGACACACTGCAGGTGCCAG 3475
QY 1193 lyIeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyL 1213
|||||
Db 3476 GGCTGCATCGCACTGCCAGTGGCGGAGGGTCTGCTTCTGAGCACCAAGACTGCAATGCGA 3535

QY 1213 ySserAlaSerGlyArgIeuAlaArgThrIeuArgThrAspAspProGlnIeuAspGlyA 1233
|||||
Db 3536 AGTCGGCTTCAGGCGCGCTCGGCCCGGCGCTGATGACCCCCCACTGATGGGG 3595
QY 1233 sPaAspAspAsnAspGluGlyAsnIeuSerIyGlyGluArgIleGlnAlaTrpValArgS 1253
|||||
Db 3596 ATGACGCCCATGACGAGGGCAACTGAGCAAGGGGAACGGGTCCGGCTGATCCGAG 3655
QY 1253 exArgIeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProG 1273
|||||
Db 3656 CCCGACTCCCTGCTGCTGCTGAGCGAGACTCTGGTCAAGCTTACATCTTCCCTCCTC 3715
QY 1273 InSerArgPheArgIeuIeuCysHisArgIleIleThrHisIySmetPheAspHisValV 1293
|||||
Db 3716 AGTCCAGGTTCCGCTCTGTGTCAACGATATCACCCACAAGATGTTGACCAAGTGG 3775
QY 1293 alIeuValIleIlePheIeuAsnCysIleThrIleAlaMetGluArgProIySleAspP 1313
|||||
Db 3776 TCCTTGTATCATCTTCTTAATGATCATCACCATGGAGCGCCCAAAATTGACC 3835
QY 1313 roHisSerAlaGluArgIlePheIeuThrIeuSerAsnTyrIlePheThrAlaValPheL 1333
|||||
Db 3836 CCCACAGCGCTGAACGCATCTTCTGACCTTCCAAATTACATCTTACCCGAGTCTTTC 3895
QY 1333 euAlaGluMetThrValIySValValAlaIeuGlyTrpCysPheGlyGluGlnAlaTyrL 1353
|||||
Db 3896 TGGCTGAATGACAGTGAAGGTGGTGCACTGGGCTGGTCTTCCGGGAGCAGCGCTAAC 3955
QY 1353 euArgSerSerTrpAsnValIeuAspGlyIeuIeuValIeuIleSerValIleAspIleL 1373
|||||
Db 3956 TGCGGAGAGTTGGAACGTGCTGAGCGGGCTGTGGTCTCATCTCCGTCATCGACATTTC 4015
QY 1373 euValSerMetValSerAspSerGlyThrIySileuGlyMetIeuArgValIeuArgL 1393
|||||
Db 4016 TGGTGTCCATGCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTGTGGGC 4075
QY 1393 euIeuArgThrIeuArgProIeuArgValIleSerArgAlaGlnGlyIeuIySleuValV 1413
|||||
Db 4076 TGCTGCCGACCCCTGCGCCGCTCAAGGTGATCAGCGCGGCAGGGCTGAAGCTGTGG 4135
QY 1413 alGluThrIeuMetSerSerIeuIySProIleGlyAsnIleValValIleCysCysAlaP 1433
|||||
Db 4136 TGAGAGCCTGATGTCTCTACTGAACCCATCGGCAACATTGTAGTATCTGTGTGCCCT 4195
QY 1433 hepHeIleIlePheGlyIleIeuGlyValGlnIeuPheIySGLyIySPheneValCysG 1453
|||||
Db 4196 TCTTCATATTTTCCGATCTTGGGGGTGCAGCTTTCAAAGGGAAGTTTTCGTGTGCC 4255
QY 1453 lngIyGluAspThrArgAsnIleThrAsnIySerAspCysAlaGluAlaSerTyrArgT 1473
|||||
Db 4256 AGGCGGAGGATACAGAACTACCAATAAATCGGACTGTGCCGAGCCAGTTAACCGGT 4315
QY 1473 rpValArgHisIySlyTyrAsnPheAspAsnIeuGlyGlnAlaIeuMetSerIeuPheValL 1493
|||||
Db 4316 GGGTCCGGCAAGTACACTTTGAACAACCTTGCCAGGCCCTGATGTCCCTGTGTTT 4375
QY 1493 euAlaSerIySAspGlyTrpValAspIleMetTyrAspGlyIeuAspAlaValGlyValA 1513
|||||
Db 4376 TGGCTTCAAGGATGTTGGGTGACATCATGTACGATGGGCTGATGCTGTGGCGCTGG 4435
QY 1513 spGlnGlnProIleMetAsnHisAsnProTrpMetIeuIeuTyrPheIleSerPheIeuL 1533
|||||
Db 4436 ACCAGCAGCCCATATGAACCAACACCCCTGATGCTGTGTACTTCATCTCGTTCCTGC 4495
QY 1533 euIleValAlaPhePheValIeuAsnMetPheValGlyValValGluAsnPheHisL 1553
|||||
Db 4496 TCATTTGGCTTCTTGTCTGTGAACATGTTGTGGGTGTGGTGAAGACTTCCACA 4555
QY 1553 ySsCysArgGlnHisGlnGluGluGluGluAlaArgArgArgGluGluIySArgIeuArgA 1573
|||||
Db 4556 AGTGTCCGAGCAACAGAGAGAGAGAGGCCCGCGCGGGAGAGAGAACGCGCTCAAGAA 4615
QY 1573 rgIeuGluIySlySArgArgSerIySglulYsGlnMetAlaGluAlaGlnCysIySProT 1593

Db 4616 GACTGGAGAAAAAGAGAGG-----AAAGCCAGGTGCAAACTTT 4654
QY 1593 YRTYRSERASPTYRSERARGPHEARGLEULEUVALHISHISLEUCYSTHRSERHISTYRL 1613
Db 4655 ACTACTCCGACTACTCCCGCTTCGGCTCCGTCCACCACTTGTCAGCCAGCCACTACC 4714
QY 1613 euaAspLeuPheIleThrglyValIleGlyLeuAsnValValThrmecAlaMetGluHisT 1633
Db 4715 TGGACCTCTTCATCACAGGTGTCTATCGGCTGAACGTGTGTCACCATGGCCATGGAGCACT 4774
QY 1633 YrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrlIlePheThrValI 1653
Db 4775 ACCAGCAGCCCCAGATTCGGATGAGGCTCTGAAGATCTGCAACTACTTCACTGTCA 4834
QY 1653 IePheValPheGluSerValIlePheLysLeuValAlaPheAlaPheArgArgPhePheGlnA 1673
Db 4835 TCCTTTGCTCTTGGAGTCAGTTTCAAACTGTGGCCTTTGGTTCCGTCGGTCTTCCAGG 4894
QY 1673 sPArGTpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuG 1693
Db 4895 ACAGGTGGAACAGCTGGAGCTGGCCATTGTGCTGCTGTCCATCATGGGCATCACGCTGG 4954
QY 1693 IuGluIleGluValAsnLeuSerLeuProIleAsnProThrlIeIleArgIleMetArgV 1713
Db 4955 AGGAATCGAGGTCAACGCGCTCGCTGCCCATCAACCCCATCATCCGATCATGAGGG 5014
QY 1713 aLLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuL 1733
Db 5015 TGCTGGGCATTGCCCGAGTGTGAAGCTGTGAAGATGGCTGTGGGCAATGGCGGCGCTGC 5074
QY 1733 euhIsthrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuL 1753
Db 5075 TGGACACGCGTGATGCAGGCGCTGCCCCAGAGTGGGGAACCTGGACTTCTCTCATGTTGT 5134
QY 1753 euphePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluT 1773
Db 5135 TGTTTTTCATCTTTGCAGCTCTGGGCGCTGGAGCTCTTTGGAGAACCTGGAGTGTGACGAGA 5194
QY 1773 hrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheL 1793
Db 5195 CACACCCCTGTGAGGGCCTGGGCGCTCATGCCACTTTTCGGAACCTTTGGCATGGCCTTCC 5254
QY 1793 eutHrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerA 1813
Db 5255 TAACTCTCTTCGAGTCTCCACAGGTGACAAATGGCAATGGCATTATGAAGAACACCCCTCC 5314
QY 1813 rgAspCysAspGlnGluSerThrCysTyrrAsnThrValIleSerProIleTyrrPheValS 1833
Db 5315 GGGACTGTGACCAAGAGTCCAGCTGTACAACAACAGGTTCATCTGCCCTACTACTTGTGT 5374
QY 1833 erPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysH 1853
Db 5375 CCTTCGTCTGACGCGCCAGTTCTGTCTAGTCAACGTGTGTATCGCCGTCTGATGAAGC 5434
QY 1853 iSLeuGluGluSerAsnLysGluAlaLysGluGluValaGluLeuGluValaGluLeuGluL 1873
Db 5435 ACCTGGAGGAGAGCAACAAGGAGGCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTGGAGC 5494
QY 1873 euGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrp 1893
Db 5495 TGGAGATGAAGACCTTCAGCCCCCAGCCCCCAGCTGGCAGAGCCCTTCTCTGCGC 5554
QY 1893 roGlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThra 1913
Db 5555 CTGGGCTCGAGGGCCCCGACAGCCCCGACAGCCCCCAAGCTTGGGCTCTGCACCCAGCGG 5614
QY 1913 IaHisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrmecValProHisProg 1933
Db 5615 CCCACGCGAGATCAGCCTCCCACTTTTCCCTGGAGACCCCAAGATGCAGCCCAACCCA 5674
QY 1933 IuGluValProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerA 1953

Db 5675 CGGAGCTGCCA-----GGACCAGACTTACTGACTGTGCGGAAGTCTGGGGTCAGCC 5725
QY 1953 rgThrHisSerLeuProAsnAspSerTyrrMetCysArgAsnGlySerThrAlaGluArgS 1973
Db 5726 GAACGCACTCTCTGCCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCCGAGGGCC 5785
QY 1973 erLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValH 1993
Db 5786 CCCTGGGACACAGGGGCTGGGGGCTCCCAAAGCTCAGTCAGGCTCCGCTTGTCCGTTCC 5845
QY 1993 iSSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrrLeuL 2013
Db 5846 ACTCCAGCCAGCAGATACCAAGCTATCTTCAGCTTCCCAAAGATGCACCTCATCTGC 5905
QY 2013 euGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyLys 2033
Db 5906 TCCAGCCCCACAGCGCCCCCAACCTGGGGCAACATCCCCAAACTGGCCCCCAGAGAGCT 5965
QY 2033 erProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspV 2053
Db 5966 CCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGCAGCAATAGAGACTGACTCCTTGAGC 6025
QY 2053 aGlnGlnLysLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProL 2073
Db 6026 TTCAGGGTCTGGGCAAGCCGGAAGACCTGTCGACAGAGTGAGTGGCCCTCCCGGCC 6085
QY 2073 eutHrArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyI 2093
Db 6086 TGGCCCCGGCTACTCTTCTGCGGGCCAGTCAAGTACCAGGACACAGCAGCAGACTCCCGCA 6145
QY 2093 IeGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProS 2113
Db 6146 GCCACAGCAAGATCTCCAAGCACAATGACCCCGCCAGCCCTTTGCCCAAGGCCCAAGACCA 6205
QY 2113 erTrpAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerT 2133
Db 6206 ACTGGGGCAAGGCGCTCCAGAGACCAAGACAGCTTAGAGTTGGAACAGGAGCTGAGCT 6265
QY 2133 rPIleSerGlyAspLeuLeu--ProSerSerGlnGluGluProLeuPheProArgAspL 2152
Db 6266 GGATTTCAAGAGACTCTGCCCCCTGGCGGCCAGAGAGAGCCCCCATCCCAAGGAGACC 6325
QY 2152 euLysLysCysTyrrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuA 2172
Db 6326 TGAAGAAGTGTACAGCGTGAGGCCCCAGAGCTGCCAGCGCGGCTTACGTCCTGGCTGG 6385
QY 2172 spGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgL 2192
Db 6386 ATGAGCAGAGGAGACACTTATCGCCGTCAAGCTGCTGGACACGCGCTCCCAACCCCAACC 6445
QY 2192 euCysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgProL 2212
Db 6446 TGGGCACAGACCCCTCTTAACCTTGGGGGCCAGCCTCTTGGGGGGGCTGGAGCCGGCCCA 6505
QY 2212 ySLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArgP 2232
Db 6506 AGAAAAAACTCAGCCCGCTAGTATCACATAGACCCCCCGAGAGCCCAAGGTCTCTGGA 6565
QY 2232 roProCysSerProGlyValCysLeuArgArgAlaProAlaSerAspSerLysAspP 2252
Db 6566 CCCCCGCCAGCCCTGTATGTCTGCTCCGAGGAGGAGGCTCCGTCCAGCACTCCAAGGATC 6625
QY 2252 roSerValSerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrL 2272
Db 6626 CCTTGGCCTCTGGCCCCCTTGACAGCATGCGCTGCTCGCCCTCCCAAGAAAGATGTGC 6685
QY 2272 euSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286
Db 6686 TGAGTCTCTCGGTTTATCTCTGACCCAGCAGACCTGGACCCC 6729

RESULT 13
AAF31684
ID AAF31684 standard; cdna; 6892 BP.

XX AAF31684;
AC
XX
DT 09-APR-2001 (first entry)
XX
DE Human alpha-IG T-type calcium channel cDNA.
XX
KW Human; antiarrhythmic; anticonvulsant; hypotensive; cardiant; nootropic;
KW T-type calcium channel subunit; cardiac hypertrophy; cardiac arrhythmia;
KW hypertension; sleep disorder; epilepsy; alpha-IG T-type calcium channel;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200102561-A2.
XX
PD 11-JAN-2001.
XX
PF 04-JUL-2000; 2000WO-CA000794.
XX
PR 02-JUL-1999; 99US-00346794.
XX
PA (NEUR-) NEUROMED TECHNOLOGIES INC.
XX
PI Snutch TP, Baillie DL;
XX
DR MPI; 2001-12311/13.
DR P-PSDB; AAB66481.
XX
XX
PT Novel T-type calcium channel alpha-1 subunit gene useful for treating
PT cardiac hypertrophy, cardiac arrhythmia, hypertension, sleep disorder and
PT epilepsy.
XX
XX Example 3; Fig 6; 103pp; English.
XX
CC The present sequence is given in a specification providing sequences and
CC partial sequences for three types of mammalian (human and rat) T-type
CC calcium channel subunits. An expression cassette has been generated which
CC comprises a nucleotide sequence encoding a T-type calcium channel alpha_1
CC subunit operably linked to control sequences to effect its expression.
CC The novel calcium channel nucleic acids and proteins are useful for
CC treating conditions characterised by undesirable levels of T-type calcium
CC channel activity such as cardiac hypertrophy, cardiac arrhythmia,
CC hypertension, sleep disorder and epilepsy
XX
XX
SQ Sequence 6892 BP; 1315 A; 2223 C; 2017 G; 1337 T; 0 U; 0 Other;
XX
XX
Alignment Scores:
Pred. No.: 0 Length: 6892
Score: 10916.00 Matches: 2109
Percent Similarity: 93.42% Conservative: 34
Best Local Similarity: 91.94% Mismatches: 113
Query Match: 90.75% Indels: 38
DB: 5 Gaps: 6
US-09-611-257A-24 (1-2287) x AAF31684 (1-6892)
QY 19 AlaArgProSerSerAspProProGlyProAlaGluAlaArgGlyTrpThrArgArgArg 38
DB 7 GCTTGCCCTCTCCGATCGCCCGGGGCCCGGCTGGCCAGAGGATGGAAGAGGAGG 66
QY 39 MetGluArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrThrCys 58
DB 67 ATGAGCGGGCGCGAGAGTCCGGACAGCCCGAGACTTCATGCGGCTCAACGACCTGT 126
QY 59 ProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspS 78
DB 127 CGGGGGCGGGCGGGCGGGCGGGCGGGTCAAGAAAGACCCGGGCGAGCGGACT 186
QY 78 erGluAlaGluGlyLeuProTyrProAlaLeuAlaProValPhePheTyrLeuSerG 98
DB 187 CCGAGGGCGGAGGGGCTGCCGTACCCGGCGCTGCCCGGTGTCTTCTACTTGAGCC 246

QY 98 lnaSPSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgV 118
DB 247 AGACAGCCGCCCGGAGAGCTGTGTCTCCGACAGGTCTGTAAACCCCTGTGAGCGCA 306
QY 118 aISerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluA 138
DB 307 TCAGCATGTTGTCATCTTCTCAACTGCGGTGACCCCTGGCATGTTCGGCCATGCGAGG 366
QY 138 spIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePhea 158
DB 367 ACAATCGCTGTGACTCCAGCGCTGCCGATCTGCAGAGCCCTTGATGACTTCATCTTTG 426
QY 158 lAphePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysC 178
DB 427 CCTTCTTGCCGTGAGATGTTGTTGAGATGTTGCTTGCGCATCTTTGGAAAAAGT 486
QY 178 yETyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuG 198
DB 487 GTTACCTGGAGACACTTGGAACCGGCTTGACTTTTCATCGTCATCGCAGGATGCTGG 546
QY 198 lUTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuA 218
DB 547 AGTACTCGCTGGACCTGCAGAAAGTCAAGCTTCAAGCTGTCAAGACAGACGTCGTGCTGC 606
QY 218 rGProLeuArgAlaIleAsnArgValProSerMetCArgIleLeuValThrLeuLeuA 238
DB 607 GACCGCTCAGGGCCATTAACGGGTGCCAGCATGCGCATCTTGTACAGTTGCTGCTGG 666
QY 238 sPTThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheG 258
DB 667 ATACGCTGCCATGTGTGGCAAGTCTGTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTG 726
QY 258 lYIleValGlyValGluLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluA 278
DB 727 GCATCGTCGGCGCTCCAGCTGTGGGCGAGGCTGCTCGGAACGATGCTTCTTACCTGAGA 786
QY 278 snPheSerLeuProLeuSerValAspLeuGluProTyrTrpGlnThrGluAsnGluAspG 298
DB 787 ATTTCAGCTCCCTCCCTGAGCGGTGACCTGAGCGGCTATTACAGACAGAGACGAGATG 846
QY 298 lUSeRProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValP 318
DB 847 AGAGCCCTTCATCTGTCTCCAGCCACCGCAGAACGCGCATGCGGTCTGCGAAGCGGTGC 906
QY 318 roThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrA 338
DB 907 CCACGCTCGCGGGGAGCGGGCGGTGCCACCTTGCCTGTGACTATGAGCGCTTACA 966
QY 338 snSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTrpAsnCysSerAlaG 358
DB 967 ACAGCTCCAGCAACACCACTGTGTCAACTGGAACAGTAATAACCACTGTCTCAGCGG 1026
QY 358 lYgluHisAsnProPheIleGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleA 378
DB 1027 GGGAGCACAAACCTTCAAGGGGCCCATCACTTGAACAATTGGCTATGCTGGATCG 1086
QY 378 lAilePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspA 398
DB 1087 CCATCTTCAGGTATCATCGCTGGAGGGCTGGGTCCACATCATGTACTTGTGATGATG 1146
QY 398 lAhISerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheM 418
DB 1147 CTCATTCCTTCACAATTTCATTACTTCACTTCTTCATCATCGTGGCTCTTCTTCA 1206
QY 418 etIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluS 438
DB 1207 TGATCAACCTGTGCTGTGTGATGTCACAGCAGATTCTCAGAGACCAAGCAGCGGAAA 1266
QY 438 erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458
DB 1267 GCCAGCTGATCGGGAGCAGCGGTGCGGTCTCTGTCCAAGCAGCACCTGTGCTAGCT 1326
QY 458 heSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgL 478

Db 1327 TCTTGAGCCCCGGCAGCTGCTATGAGGAGCTGCTCAAGTACCTGGTGTACATCCTTCGTA 1386
QY 478 ysaIaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuS 498
Db 1387 AGGCAGCCCCGACAGGCTGGCTCAGGTCCTCTCGGGCAGCAGGTGTGGGGTTGGGCTTCA 1446
QY 498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518
Db 1447 GCAGCCAGCACCCTCGGGGGCCAGAGACCAGCCAGCAGCAGCTGCTCGCTCC 1506
QY 518 iSaArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyrH 538
Db 1507 ACCGCCGCTATCCGTCCACCACTGGTGACACCAACCAACCAACCACTACC 1566
QY 538 iSLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspA 558
Db 1567 ACCTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGGACAGGGATG 1626
QY 558 laAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP 578
Db 1627 CCAATGGGTCCCGCAGGCTCATGTGCTCCACCACTTCGACGCTCGCCCTTCGGGGGCC 1686
QY 578 roProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProV 598
Db 1687 CCGCTGGTGCGCAGAGTCTGTGCACAGCTTCAACATGCCGACTGCCACTTAGAGCCAG 1746
QY 598 aArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlys 618
Db 1747 TCCGTGCGCAGCGCCCCCTCCAGGTCCCCCACTGAGGCATCCGGCAGACTGTGGCA 1806
QY 618 erGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysA 638
Db 1807 GCGGGAAGGTATATCCCAACCGTGACACACAGCCCTCCACCGGAGACGCTGAAGAGAG 1866
QY 638 laLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProp 658
Db 1867 CACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCAACCAAGCTCAACATCCAC 1926
QY 658 roGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisS 678
Db 1927 CCGGGCCCTACAGCTCCATGCAAAAGCTGTGGAGACACAGAGTACAGGTGCTGCCAA 1986
QY 678 erSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspS 698
Db 1987 GCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGACAGACAGTGAGCCTGTGTCCAGACA 2046
QY 698 erCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetP 718
Db 2047 GCTGCCCTACTGTGCCCGGGCCGGGACGGGAGGTGGAGCTCGCCGACCGTGAATGC 2106
QY 718 roAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuA 738
Db 2107 CTGACTCAGACAGCGAGGCAGTTTATGAGTTCAACAGATGCCACGACAGCACTCC 2166
QY 738 rGaSPProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerServ 758
Db 2167 GGGACCCCCACAGC--CGGCGGCAACGAGGCTGGGCCCAAGATGCAGAGCCCAAGCTCTG 2223
QY 758 alLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrP 778
Db 2224 TGCTGGCTTCTGAGGCTAATCTGTGACACCTTCGAAAGATTGTGACAGCAAGTACT 2283
QY 778 heGlyArgGlyIleMetIleAlileuValAsnThrLeuSerMetGlyIleGluTyrH 798
Db 2284 TTGGCCGGGGAATCATGATCGCATCTGTCAACACACTCAGCATGGGCATCGAATACC 2343
QY 798 iSeGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerL 818
Db 2344 ACGAGCAGCCCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACATCGTCTTCAACAGCC 2403
QY 818 euPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysA 838

Db 2404 TCTTGGCCCTGGAGATGCTGCTGAAGCTGCTGTGTATGTGTCCTTGGGCTACATCAAGA 2463
QY 838 snProTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGlyG 858
Db 2464 ATCCCTACACATCTTGATGGTGCATTTGTGTATCAGCGTGTGGAGATCGTGGCC 2523
QY 858 lngGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuV 878
Db 2524 AGCAGGGGGGGCCTGTGCGGTGTGGGACCTTCGCCCTGATGCGTGTGTGAAGCTGG 2583
QY 878 alArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnV 898
Db 2584 TGGCTTTCCTGCGCGCGCTGCAGCGGACAGCTGTGTGCTCATGAAGACCATGACAAG 2643
QY 898 alAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMeth 918
Db 2644 TGGCACCTTCTGCATGTGCTTATGCTCTTCATCTTCAAGCATCCTGGGCATGC 2703
QY 918 iSLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysA 938
Db 2704 ATCTCTTGGCTGCAAGTTTGTGCTTGAGCGGGATGGGACACCCTGCCAGACCGGAAGA 2763
QY 938 snPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnLysPT 958
Db 2764 ATTTGACTCTGCTCTGGGCCATCGTCACTGTCTTCAAGATCCTGACCAGAGGACT 2823
QY 958 rPaSnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheI 978
Db 2824 GGAACAAGTCTCTACAATGGTATGGCTCCACGTCGTCTGGCGGCCCTTATATTCA 2883
QY 978 leAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValG 998
Db 2884 TTGCCCTCATGACCTTCGGCACTACGTGCTCTTCAATTGTGTGTGCGCCATTGCTGTGG 2943
QY 998 lueGlyPheGlnAlaGlu----- 1003
Db 2944 AGGCTTCCAGCGGAGGAATCAGCAAAACGGGAAGATGCCAGTGGACAGTTAAGCTGTA 3003
QY 1004 -----GlyAspAlaThrLysSerGluSerGluProAspP 1015
Db 3004 TTCAGCTGCTGTGCACTCCAGGGGGAGATGCCAACAACTCCGAATCAGAGCCGATT 3063
QY 1015 hePheSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaL 1035
Db 3064 TCTTCTACCCAGCCTGGATGTGATGGGGAACAGAAAGATGCTTGGCCTTGTGTCCC 3123
QY 1035 euGlyGluHislaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaA 1055
Db 3124 TGGGAGAGCACCCGGAAGCTGCGGAAGACCTGTGCCGCTCATCATCCACAGGCGG 3183
QY 1055 laThrProMetSerHisProLysSerSerSerThrGlyValGlyLualaLeuGlySerg 1075
Db 3184 CCACACCCATGTGCTGCCCAAGAGCACACAGACGGGCGCTGGGCGGAGGCGCTGGCCCTG 3243
QY 1075 lySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetL 1095
Db 3244 CGTGGCGCCGACACAGCAGCAGCGGTCGGCAGAGCCTGGGCGGCC--CACGAGATGA 3300
QY 1095 ysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpT 1115
Db 3301 AGTCACGCCCGCAGCGCCGACAGCTTCGCCACAGCCCCCTGAGCGCTGCAAGCAGCTGA 3360
QY 1115 hrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerP 1135
Db 3361 CCAGCAGGCGCTCCAGCCCGGAACAGCTTCGGCCGTGCACCCAGCCTGAAGCGGAAGGCC 3420
QY 1135 roSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluG 1155
Db 3421 CAAGTGAGAGCGGCGTCCCTGTTGTGGGAGAAAGGCCAGAGACCATGAAGAGG 3480
QY 1155 luserSerGluGluAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerL 1175
Db 3481 AGAGCTCAGAAAGAGAGCGGGCCAGCCCTGCGGGCAGTGACCATCGCCACAGGGGGTCCC 3540

QY 1175 euGluaRgLuAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuH 1195
|||||
Db 3541 TGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCAGACACTGCAGCTGCCAGGGCTGC 3600
QY 1195 iSArgThrAlaSerGlyArgSerSerAlaSerGlnHiSegInAspCysAsnGlyLysSera 1215
|||||
Db 3601 ATCGCACTGCCAGTGGCCGAGGGTCTGCTTGTAGACACCAAGACTGCAATCGCAAGTCCG 3660
QY 1215 laSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspa 1235
|||||
Db 3661 CTTCAGGGGGCTGGCCCGGGCCCTGGCCCTGATGATGACCCCCCACTGGATGGGATGAAG 3720
QY 1235 sPAsnAspGluGlyAsnLeuSerLysGlyGlyArgGlnAlaTrpValArgSerArgL 1255
:::
Db 3721 CCGATGACGAGGGCAACCTGAGCAAGGGGAACGGGTCCGCGGTGATCCGAGCCGAC 3780
QY 1255 euProAlaCysCysArgGluArgAspSerTrpSerAlaTyrTrilePheProProGlnSera 1275
|||||
Db 3781 TCCCTGCCCTGCTAACCTCGAGCGAGACTCCTGTCAACCTACATCTTCCCTCCTCAGTCCA 3840
QY 1275 rGpHeArgLeuLeuCysHisArgTleileThrHisLysMetPheAspHisValValLeuV 1295
|||||
Db 3841 GGTTCGGCTCCTGTGTCAACCGGATCATCACCAAGATGTTGACCAAGGTGGTCTTG 3900
QY 1295 aLleilePheLeuAsnCysSileThrileAlaMetGluArgProLysileAspProHis 1315
|||||
Db 3901 TCATCATCTTCTTAACGTGATCATCATCGCATGGAGCGCCCAAAATTGACCCCCACA 3960
QY 1315 exAlaGluArgilePheLeuThrLeuSerAsnTyrilePheThrAlaValPheLeuAlaG 1335
|||||
Db 3961 GCGGTGAACGATCTTCTGACCCCTCTCCAATTACATCTTCAACGAGTCTTTCTGGCTG 4020
QY 1335 luMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlnAlaTyrLeuArgS 1355
|||||
Db 4021 AAATGACAGTGAAGGTGGTGCACCTGGCTGTGCTCGGGAGCAGGGCTACCTGCGGA 4080
QY 1355 erSerTrpAsnValLeuAspGlyLeuLeuValLeuileSerValileAspIleLeuValS 1375
|||||
Db 4081 GCAGTTGGAACGTGTCGACGGGCTGTGCTCATCTCCGTATCGACATTCGTGGTGT 4140
QY 1375 erMetValSerAspSerGlyThrLysTleileuGlyMetLeuArgValLeuArgLeuLeuA 1395
|||||
Db 4141 CCATGGTCTTGACAGCGGCACCAAGATCTGGGCATGCTGAGGGTGTGCGGCTGCTGC 4200
QY 1395 rGThrLeuArgProLeuArgValileSerArgAlaGlnGlyLeuLysLeuValValGluT 1415
|||||
Db 4201 GGACCCGTGCGCCGCTCAGGGGTGATCAGCCGGCGCAGGGGCTGAAGCTGTGTGGAGA 4260
QY 1415 hrLeuMetSerSerLeuLysProileGlyAsnileValValileCysCysAlaPhePheI 1435
|||||
Db 4261 CGCTGATGTCTCTCACTGAACCCCATCGCAACATTGTAGTCACTGTGCTGCTTCTTCA 4320
QY 1435 leilePheGlyileLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyG 1455
|||||
Db 4321 TCATTTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGAAATTTCGTGTGCCAGGGCG 4380
QY 1455 luAspThrArgAsnileThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValA 1475
|||||
Db 4381 AGGATACCAAGAACATCACCAATAATCGACTGTGCCGAGGCCAGTTAACCGGTGGGTCC 4440
QY 1475 rGHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaS 1495
|||||
Db 4441 GGCACAAGTACAACCTTGACAACCTTGCCAGGCCCTGATGTCCCTGTTTGCCCT 4500
QY 1495 erLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnG 1515
|||||
Db 4501 CCAAGATGTTGGGTGACATCATGTACGATGGGCTGATGTGTGGCGTGACACAGC 4560
QY 1515 lnProileMetAsnHisAsnProTrpMetLeuLeuTyrPheileSerPheLeuLeuileV 1535
|||||
Db 4561 AGCCCATCATGAACACCAACCCCTGAGTGTGCTGACTTCACTCGTTCCGTGCTCATTTG 4620

QY 1535 alAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysA 1555
|||||
Db 4621 TGGCTTCTTGTCTGTACAATGTTGTGGGTGTGGTGGAGAACTTCCACAAGTGA 4680
QY 1555 rGlnHisGlnGluGluGluAlaArgArgArgGluLysArgLeuArgArgLeuG 1575
|||||
Db 4681 GGCAGCACCAAGAGGAAGAGAGGCCCGCGCGGAGAGAGAGCGCTCAAGAACTGG 4740
QY 1575 luLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrS 1595
:::
Db 4741 AGAAAAAGAGAGG-----AAAGCCAGTGCAAACCTTACTACT 4779
QY 1595 exAspTyrSerArgPheArgLeuLeuValHisileuCysThrSerHisTyrLeuAspL 1615
|||||
Db 4780 CCGACTACTCCGCTTCGGGCTCCTGTCACCACTTGTGCACCAAGCACTACCTGACC 4839
QY 1615 euPheileThrGlyValileGlyLeuAsnValValThrMetAlaMetGlnHisTyrGlnG 1635
|||||
Db 4840 TCTTCATCACAGGTGTCATCGGGCTGAACGTGTGCATGCCATGGACCACTACAGC 4899
QY 1635 lnProGlnileLeuAspGluAlaLeuLysileCysAsnTyrilePheThrValilePheV 1655
|||||
Db 4900 AGCCCAAGATTCTGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCATCTTGG 4959
QY 1655 alPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgT 1675
|||||
Db 4960 TCTTGGAGTCAGTTTCAAACCTTGTGGCTTTGGTTTCCGTGCGTTCTTCCAGACAGGT 5019
QY 1675 rPAsnGlnLeuAspLeuAlaileValLeuLeuSerileMetGlyileThrLeuGluGluI 1695
|||||
Db 5020 GGAACCACTGGAACCTGGCATTTGTGCTGTGTCATCATGGGCATCAGCTGAGGAAA 5079
QY 1695 leGluValAsnLeuSerLeuProileAsnProThrileleArgileMetArgValLeuA 1715
|||||
Db 5080 TCGAGTCAACGCTCGCTGCCCATCAACCCCACTCATCCGCATCAGAGGGTGTGC 5139
QY 1715 rGileAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisT 1735
|||||
Db 5140 GCATTGCCGAGTGTGTAAGCTGTGAAGATGGCTGTGGCATGCGGGCGTGTGGACA 5199
QY 1735 hrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheP 1755
|||||
Db 5200 CGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTGTGTTT 5259
QY 1755 heilePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisP 1775
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Db 5260 TCATCTTTGCAAGCTGTGGCGGTGAGCTCTTGGAGACCTGAGTGTGACGACACACC 5319
QY 1775 roCysGlnGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrL 1795
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Db 5320 CCTGTAGGGGCTGGGCGGTATGCCACCTTTCGGAACCTTGGCATGGCTTCTTAACCC 5379
QY 1795 euPheArgValSerThrGlyAspAsnTrpAsnGlyileMetLysAspProSerArgAspC 1815
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QY 1815 ysAspGlnGluSerThrCysTyrAsnThrValileSerProileTyrPheValSerPheV 1835
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Db 5440 GTGACCAAGAGTCCACCTGTCTACAACACGGTCACTCGCCTATCTTACTTGTGCTTCCG 5499
QY 1835 alLeuThrAlaGlnPheValLeuValAsnValValileAlaValLeuMetLysHisLeuG 1855
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|||||
Db 5560 AGAGAGCAACAAGAGGCCAAGAGAGAGGCCGAGCTAGAGGCTGAGCTGAGCTGAGAGA 5619
QY 1875 etLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyV 1895
|||||
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QY 1895 alGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrAlaHisI 1915

||||| :||| ||||||||| ||| |||||
Db TCAGAGGCCCCGACAGCCCCGACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCACG 5739
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Qy 2214 ySerLeuProProSerSerIleSerIleAspProProGluSerGlnGlySerArgProProc 2234
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Qy 2254 aLerSerProLeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerL 2274
.

Db 6751 CCTCTGCCCCCTGACAGCATGGCTGCCTCGCCCTCCCAAGAAAGATGTGCTGAGTC 6810
Qy 2274 euSerGlyLeuSerSerAspProThrAspMetAspPro 2286
Db 6811 TCTCCGTTTATCTCTGACCCAGACAGACCTGAGACCCC 6848
RESULT 14
ADQ89063
ID ADQ89063 standard; cDNA; 7648 BP.
XX
AC ADQ89063;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human urological disorder related protein 4421 encoding cDNA SEQ.15.
XX
KW urological disorder; uropathic; cytostatic; urinary incontinence;
KW benign prostatic hyperplasia; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..7134
FT /*tag= a
FT /product= "urological disorder related protein 4421"
XX
PN WO2004065576-A2.
XX
PD 05-AUG-2004.
XX
PF 14-JAN-2004; 2004WO-US000750.
XX
PR 15-JAN-2003; 2003US-0440318P.
PR 04-FEB-2003; 2003US-0444783P.
PR 27-MAR-2003; 2003US-0457901P.
PR 08-MAY-2003; 2003US-0468775P.
PR 19-MAY-2003; 2003US-0471614P.
PR 16-JUN-2003; 2003US-0478742P.
PR 18-JUL-2003; 2003US-048529P.
PR 30-JUL-2003; 2003US-0491156P.
PR 02-SEP-2003; 2003US-0499594P.
PR 26-SEP-2003; 2003US-0506332P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Karichei V, Silos-Santiago I, Eliasof SD;
XX
DR WPI; 2004-562167/54.
DR P-PSDB; ADQ89064.
XX
PT Use of polypeptides related to urological disorders, e.g. 44390, 54181,
PT 211 or for identifying a compound capable of treating a urological
PT disorder or identifying and treating a subject having a urological
PT disorder.
XX
PS Claim 1; SEQ ID NO 15; 542pp; English.
XX
CC The present invention describes the use of polypeptides related to
CC urological disorders for identifying a compound capable of treating a
CC urological disorder, identifying a subject having a urological disorder,
CC or treating a subject having a urological disorder. Also described: (1) a
CC method for identifying a compound capable of treating a urological
CC disorder; (2) a method for identifying a subject having a urological
CC disorder; and (3) a method for treating a subject having a urological
CC disorder. The compound has uropathic and cytostatic activities. The
CC polypeptides related to urological disorders are useful for identifying a
CC compound capable of treating a urological disorder, identifying a subject
CC having a urological disorder, or treating a subject having a urological
CC disorder. Disorders include urinary incontinence and benign prostatic
CC hyperplasia. The present sequence encodes a human urological disorder
CC related protein, which is used in the exemplification of the present
CC invention.
XX

Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 10845.50 Matches: 2105
Percent Similarity: 89.72% Conservative: 33
Best Local Similarity: 88.33% Mismatches: 110
Query Match: 90.17% Indels: 135
DB: 13 Gaps: 7

US-09-611-257A-24 (1-2287) x ADQ89063 (1-7648)

QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
DB 2 TGGACGAGAGGAGGATGGAGCGGCGCGAGAGTCCGGACAGCCCCGGAGCTTCATGC 61
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
DB 62 GGCTCAACGACCTGTCGGGGGGCGGGGGCGCGCGGGGGGTCAAGCAAGAAAGGACC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
DB 122 CGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCGGGCGCTGGCCCCGGTGGTTT 181
QY 93 hePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 113
DB 182 TCTTCTACTGAGCCAGAGACAGCCGCGCGAGCTGGTGTCTCCGACGCTGTAAACC 241
QY 113 roTyrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
DB 242 CCTGGTTTGACGCGCATCAGCATGTGTGCATCTTCTCAACTGCGTGACCCCTGGGCATGT 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhea 153
DB 302 TCCGGCCATGCGAGACATCGCTGTGACTCCAGCGCTCGGGATCCTGACAGGCTTTG 361
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DB 362 ATGACTTCAATCTTTCCTTCTTGGCGTGAGATGGTGAAGATGGTGGCTTGGGCA 421
QY 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
DB 422 TCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAACCGGCTTGACTTTTCAATCGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
DB 482 TCGCAGGGATGCTGAGTACTCGCTGCACCTGCAGACCTTCTCAGCTGTACAGA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
DB 542 CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCACATGCGCATCTTG 601
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
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QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
DB 662 TCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGAGGGCTGCTTCGGAACGAT 721
QY 273 ysPheLeuProGluAsnPheserLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
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QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
DB 782 CAGAGAAAGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGCGCATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyGlyProProCysSerLeuA 333
DB 842 CCTGCAGAAAGCGTCCACGCTGCGCGGGAGCGGGGCGGTGCCCACTTGCGGTGTGG 901
QY 333 sPTyrgluThrTyraBnsSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353

DB 902 ACTATGAGGCGCTACACAGCTCCAGCAACACCACCTGTGTCACTGAGAACCACTACTACA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
DB 962 CCACTGCTCAGCGGGAGACACAACCCCTTCAAGGGCGGCATCACTTGACAACAATTG 1021
QY 373 lYTyraAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrTrpValAspIleMet 393
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DB 1382 GGGTTGGGCTGCTCAGCAGCCACACCCCTCGGGGGGCCAGGAGACCAGCCACGAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
DB 1442 GCTGCTCTGCTCCACCGCGCTATCCGTCCACCACTGTGTGACACCACCAACCACC 1501
QY 533 iSHisHisIstYrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
DB 1502 ATCACCACTACCACTCGGGCAATGGAGCGTCAAGGCCCCCGGGCCAGCCGGAGA 1561
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DB 1622 CCTCTCCGGGGCCCCCTGTGGTGGCGCAGAGTGTGTGCACAGCTTCTACCATGCGGACT 1681
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DB 1682 GCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCTCCAGGTCCCATGTGAGGCGATCCG 1741
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QY 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThS 653
DB 1802 CGCTGAAGAGAGAAGCACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
DB 1862 GCCTCAACATCCACCCGGGCTTACAGCTTCATGCACAAGCTGCTGGAGACACAGAGTA 1921
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Db 1982 CCTGTGTCACAGACAGTGCCTTACTGTGCCGGGCGGGGACAGGGAGGTGAGCTCG 2041
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Db 2819 CGGCCCTTATTTCAATTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTGCTGG 2878
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Db 3776 TCCCTCCTCAGTCAAGTTCGCGCTCTGTGTACCCGATCATCACCCACAAGATGTTG 3835
QY 1290 spHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL 1310
Db 3836 ACCACGTGTCTTGTATCATCTTCTTAAGTGCATCACCATCGCATGAGCGCCCA 3895
QY 1310 ysIleAspProHisSeraLagluArgIlePheLeuThrLeuSeraSniTyrIlePheThra 1330
Db 3896 AAATTGACCCCCACAGCGCTGAACGCATCTTCTGACCCCTTCCAATTACATCTTACCG 3955
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Db 3956 CAGTCTTCTGCTGAATGACAGTGAAGGTGTGGCACTGGGCTGTGCTTCGGGGAGC 4015
QY 1350 lnaAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSeraValI 1370
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QY	1410	ysleuValValGluThrleuMetSerSerleuysProIleGlyAsnIleValIleC	1430
Db	4196	AGCTGGTGGAGACGCTGATGTCCTCACTGAACCCATCGGCAACATTGATCATCT	4255
QY	1430	ysCysAlaPhePheIleIlePheGlyIleleuGlyValGlnleuPheGlyLysPheP	1450
Db	4256	GCTGTGCCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAGGAAGTTT	4315
QY	1450	heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS	1470
Db	4316	TCGTGTGCCAGGCGGAGATACCAGAACATCACCAATAATCGACTGTGCCGAGGCCA	4375
QY	1470	erTyrArgTrpValArgHisLysTyrAsnPheAspAsnleuGlyGlnAlaMetSerL	1490
Db	4376	GTTACCGGTGGTCCGGACAAGTACAACTTTGACAACCTTGGCCAGGCCGTGATGCC	4435
QY	1490	eupheValleuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaV	1510
Db	4436	TGTTCTGTTTGGCCTCCAAAGATGGTTGGGTGACATCATGTAGATGGGCTGGATGCTG	4495
QY	1510	alGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleS	1530
Db	4496	TGGGCGTGACACGACGCCCATCATGAAACCACAACCCTGGATGCTGCTGACTTCATCT	4555
QY	1530	erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA	1550
Db	4556	CGTTCCTGCTCATGTGTGGCCTTCTTGTCTGAACAATGTTGTGGGTGTGGTGAGAGA	4615
QY	1550	snPheHisLysCysArgGlnHisGlnGlnGluGluGluAlaArgArgArgGluLysA	1570
Db	4616	ACTTCCACAAGTGTCCGACACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4675
QY	1570	rgLeuArgArgLeuGluLysLysArgArg-----	1579
Db	4676	GCCTACGAAGACTGGAGAAAAGAGAAGAAATTAATGCTGGACGATGAATGCTTCCG	4735
QY	1580	--SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA	1599
Db	4736	GCAGCTCAGCAGCGCTGCGTCAGAAAGCCAGTGCAACCTTACTACTCCGACTACTCCC	4795
QY	1599	rgPheArgLeuLeuValHisHisleuCysThrSerHisTyrLeuAspLeuPheIleThrg	1619
Db	4796	GCTTCCGGCTCCTCGTCCACCACTTGTGCACCAAGCCACTAAGCTTTCATCATCAG	4855
QY	1619	lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL	1639
Db	4856	GTTGCATCGGGCTGAACGTGTGCATCATGCGCATGAGCACTAACGACAGCCCCAGATTCC	4915
QY	1639	euaSpGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV	1659
Db	4916	TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCATCTTGTCTTGAGTTCAG	4975
QY	1659	alPheLysleuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuA	1679
Db	4976	TTTTCAAACTTGTGGCCTTGTGTTCCGTCGGTCTTCCAGACAGGTGGAACCAAGCTGG	5035
QY	1679	spleuAlaIleValleuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL	1699
Db	5036	ACCTGGCCATTGTGCTGTGTTCATCATGCGGCATCAGCCTGGAGGAAATCGAGGTCAACG	5095
QY	1699	eusSerleuProIleAsnProThrIleIleArgIleMetArgValleuArgIleAlaArgV	1719
Db	5096	CCTTCGCTGCCCATCAACCCCAACCATCATCCGCATCATGAGGCTGCGCATTGGCCGAG	5155
QY	1719	alleuLysleuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA	1739
Db	5156	TGCTGAAGCTGCTGAAGATGGCTGTGGGCATGCGGGCGCTGCGAGACGCGTATGCAGG	5215
QY	1739	laLeuProGlnValGlyAsnleuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA	1759
Db	5216	CCCTGCCCCAAGGTGGGAACTGGACTTCTTTCATGTGTGTTTTCATCTTTGCAG	5275
QY	1759	laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL	1779

Db	5276	CTCTGGCGCTGAGCTCTTTGGAGACCTTGAGTGTGACGAGACACACCCCTGTGAGGGCC	5335
Qy	1779	eUGlyArghIsaIaThrPheArgAsnPhcGIyMeCAlaPheLeuThrLeuPheArGValS	1799
Db	5336	TGGGCGCTCATGCGCACTTTCGGAACTTTGGCATGGCCTTCCTAACCCCTTCCGAGCT	5395
Qy	1799	eThrGIyAspAsnTrpAsnGIyIleMeLyAspProSerArGAspCyAspDGIyIus	1819
Db	5396	CCACAGGTGACAAATTGGAATGGCATTATGAAAGACACCCCTCCGGGACTGTGACCAGAGT	5455
Qy	1819	eThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG	1839
Db	5456	CCACCTGTACACACGCGTCATCTCGCCTATCTATTGTGTCTTGTGTGCTGACGGCC	5515
Qy	1839	InPheValLeuValAsnValValIleAlaValLeuMeLyShISLeuGIyIuSerAsnL	1859
Db	5516	AGTTCGTCTAGTCAACGTGTGATCGCCGTGCTGATGAAGCACCTGAGAGAGCAACA	5575
Qy	1859	ysGIyAlaLySGIyAlaGIyLeuGIyAlaGIyLeuGIyAlaGIyLeuGIyMeLyThrLeuS	1879
Db	5576	AGGAGGCCAAGAGAGAGCGGAGCTAGAGGCTGAGCTGAGAGTGAAGACCTCA	5635
Qy	1879	eRProGIyProHisSerProLeuGIySerProPheLeuTrpProGIyValGIyIyVala	1899
Db	5636	GCCCCAGCCCCACTCGCCACTGGGAGAGCCCTTCTCTGGCTGGGGTGAAGGCGCCG	5695
Qy	1899	snSerThrAspSerProLySProGIyAlaProHisThrThrAlaHisIleGIyAlaIas	1919
Db	5696	ACAGCCCCGACAGCCCAAGCCTGGGGCTTGACACCAGCGGCCACGAGATCAGCCT	5755
Qy	1919	eRGIyPheSerLeuGIyHisProThr-----	1927
Db	5756	CCCACCTTTCCCTGGAGCACCCACGAGACAGGACGTGTTGACACCATATCCCTGTGA	5815
Qy	1927	-----	1927
Db	5816	TCCAGGCGCTCCCTGAGTGGAGAGCTGAAGCTGATGACGAGCTGGAGGCCAGGGGCC	5875
Qy	1927	-----	1927
Db	5876	AGCCCTCTGCCTTCCCTCTGCCCCCAGCCTGGAGGCTCCGACCCACAGATCCCTTAG	5935
Qy	1927	-----	1927
Db	5936	CTGAGATGAGGCTCTGTCTCTGACGTACAGATTTGTGTGAACCGTCTGCTCTAG	5995
Qy	1927	-----	1927
Db	5996	CTCTGACGGATGACTCTTTGCTGTATGACATGCACACACTCTTACTTAGTGCCTTGAGA	6055
Qy	1928	-----MetValProHisProGIyGIyValProValProLeuGIyProAspLeuLeuThrV	1946
Db	6056	GCAATATGACAGCCCCCAGCCACGAGAGTGCCA-----GGAACAGACTTACTGACTG	6106
Qy	1946	AlaRGIySserGIyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA	1966
Db	6107	TGCGGAAGTCTGGGGTACGCCGAACGCACTCTGCCCCAATGACAGCTACATGTGTGGC	6166
Qy	1966	snGIySerThrAlaGIyArgSerLeuGIyHisArgGIyTrpGIyLeuProLySAlaGIyS	1986
Db	6167	ATGGGAGCACTGCGGAGGGCCCTGGGACACAGGGGCTGGGGGCTCCCAAAGCTCAGT	6226
Qy	1986	eRGIySerIleLeuSerValHisSerGIyProAlaAspThrSerCysIleLeuGIyLeuP	2006
Db	6227	CAGGCTCCGCTGTGTCCGTTCACTCCACAGCAGAGATACCACTACATCTGCAGCTTC	6286
Qy	2006	roLySAspValHisTyrIleuLeuGIyProHisGIyAlaProThrTrpGIyAlaIleProL	2026
Db	6287	CCAAAGATGACACCTCATCTGTCTCCAGCCCCACAGCGGCCCAACCTGGGGACCATCCCA	6346
Qy	2026	ysLeuProProProGIyArgSerProLeuAlaGIyIleArgProLeuArgArgIleAlaIai	2046

Db 6347 AACTGCCCCCACCAGACGCTCCCTTTGGCTCAGAGGCCACTCAGCGCCACGAGCAAA 6406
QY 2046 lAArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGluV 2066
Db 6407 TAAAGACTGACTCCTTGAGCGTTACAGGCTCGGGCAGCCGGAAAGACTGCTGCAGAGG 6466
QY 2066 aISerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSerIleG 2086
Db 6467 TGAAGTGGGCCCTCCCGCCCTTGCGCCGGCCCTACTCTTTCTGGGGCCAGTCAAGTACC 6526
QY 2086 lNValGlnGlnArgSerGlyIleGlnSerIleValSerIleHisIleArgLeuProAlaP 2106
Db 6527 AGGCACACAGCAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCAGCCC 6586
QY 2106 rOCysProGlyLeuGluProSerTrpAlaIleAspProProGluThrArgSerSerLeuG 2126
Db 6587 CTTGCCCCAGGCCAGAACCCCACTGGGGCAAGGGCCCTCCAGAGACCAAGACAGCTTAG 6646
QY 2126 luleuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu--ProSerSerGlnGluG 2145
Db 6647 AGTTGACACAGGAGCTGAGCTGAGATTTCAGAGACCTCCTGCCCCCTGGCGCAGAGAG 6706
QY 2145 lUProLeuPheProArgAspLeuLysLysCysIleTrpSerValGluThrGlnSerCysArg 2165
Db 6707 AGCCCCCATCCCCACGGGACCTGAAGAAGTGTACAGCGTGAGGCCACAGAGCTGCCAGC 6766
QY 2165 rGArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeu 2185
Db 6767 GCCGGCCTTACGTCTCGGTGATGAGCAGAGAGACACTCTATCGCCCTCAGCTGCTGG 6826
QY 2185 sPSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlyGlnProLeuG 2205
Db 6827 ACAGCGGCTCCCAACCCCACTGGGCACAGACCCCTTAACCTTGGGGGCCCAACCTCTTG 6886
QY 2205 lYGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProp 2225
Db 6887 GGGGGCCTGGAGCCGGCCCAAGAAAAAATCAGCCCGCTAGTATCACATAGACCCCC 6946
QY 2225 rOGlySerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlaP 2245
Db 6947 CCGAGAGCCAAAGTCTCTGGACCCCGCCAGCCCTGTATCTGCTCGGAGAGGGCTC 7006
QY 2245 rOAlaSerAspSerIleAspProSerValSerSerProLeuAspSerThrAlaIleAsp 2265
Db 7007 CGTCCAGCGACTCCAGAGATCCCTTGCCCTTGCCCCCTGACAGCATGGCTGCC 7066
QY 2265 rOSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMet 2285
Db 7067 CCTCCCCAAAGAAAGATGTGCTGAGTCTCTCCGTTTATCTCTGACCCAGACAGACCTGG 7126
QY 2285 sPPro 2286
Db 7127 ACCCC 7131

RESULT 15
ADSI6298
ID ADSI6298 standard; DNA; 7648 BP.

AC ADSI6298;
XX 02-DEC-2004 (first entry)
XX Human voltage-dependent alpha 1G subunit calcium channel (CACNA1G) DNA.
DE Voltage-dependent ion channel; drug candidate;
KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
KW anticonvulsant; antiarrhythmic; human; alpha 1G subunit; ds.
OS Homo sapiens.
XX
XX US2004175761-A1.
PN
XX 09-SEP-2004.
PP

XX 01-MAR-2003; 2003US-00377139.
PF
XX 01-MAR-2003; 2003US-00377139.
PR
XX (MACK/) MACKINNON R.
PA (MACK/) MACKINNON A L.
PA (JIAN/) JIANG Y.
PA (RUTA/) RUTA V.
XX
PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
XX WPI; 2004-642122/62.
DR REFSEQ; NM_018896.
XX
PT Screening drug candidates that target voltage dependent ion channel
PT protein, involves contacting screening protein with chemical compound,
PT which is drug candidate and determining whether chemical compound binds
PT to screening protein.
XX
PS Disclosure; SEQ ID NO 10; 61pp; English.
XX

CC The invention relates to the composition of matter suitable for use in
CC identifying chemical compounds that bind to voltage-dependent ion channel
CC proteins. The composition comprises a screening protein that consists of
CC an ion channel voltage sensor domain of the ion channel protein
CC immobilised on a solid support. The invention is useful for identifying
CC chemical compounds (drug candidate) that bind to voltage-dependent ion
CC channel proteins. The drug candidate of the invention is utilised for
CC treating a condition mediated by aberrant electrical activity that
CC initiates uptake or release of neurotransmitters and contraction of
CC muscles. The drug candidate of the invention is also utilised for
CC treating epilepsy and arrhythmia. The present sequence is a voltage-
CC dependent calcium channel DNA.
XX

SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 10845.50 Matches: 2105
Percent Similarity: 89.72% Conservative: 33
Best Local Similarity: 88.33% Mismatches: 110
Query Match: 90.17% Indels: 135
DB: 13 Gaps: 7

US-09-611-257A-24 (1-2287) x ADSI6298 (1-7648)

QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACGAGGAGGAGATGAGCGGGCCGAGAGTGGGACAGCCCGAGCTTCATGC 61
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
Db 62 GGCTCAACGACTGTGCGGGCCGGGGCCGGCGGGGGTCCAGCAAGAAAGAAC 121
QY 73 rOGlySerAlaAspSerGluAlaGlnGlyLeuProTyProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGACTCCGAGGGCGGAGGGCTGCCGTACCCGCGCTGGCCCGGTGTT 181
QY 93 hePheTyrlLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 113
Db 182 TCTTCTACTTGAGCCAGGACAGACGCCCGCGGAGCTGTGTCTCCGACAGGTCTTAAC 241
QY 113 rOTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CCTGTTGAGCGCATCAGCATGTGTGATCTTCTCAACTGCGTGACCTGGGCATGT 301
QY 133 heArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhea 153
Db 302 TCCGGCCATGCGAGGACATCGCCTGTGACTCCAGCGCTGCCGATCCTGCAGGCCCTTG 361
QY 153 sPAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173

Db 362 ATGACTTCATCTTGTGCGCTTTCTTTGCCGTGAGATGCTGTAAGATGCTGCGCTTGGGCA 421
QY 173 lPheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
Db 422 TCTTTGGGAAAAAGTGTACTGCGGAGACACTTGGAACCGGCTTGACTTTTTCATCTGCTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGAGATGCTGGAGTACTCGCTGGACCTGCAGAAAGTCAGCTTCTCAGCTGTGAGGA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGATGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCACAGCATGCGCATCCTTG 601
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACGTTGCTGCTGGATACGCTGCCCATGCTGGGCAACGTCCTGCTGCTTCTTGCG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGCAGGGGCTGCTTCGGAACCGAT 721
QY 273 YsPheLeuProGluAsnPheserLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCCTACCTGAGAATTTCAGCCTCCCTCGAGCGTGGAACCTGGAGCGCTATTACAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAAGAGATGAGAGCCCTTCATCTGCTCCAGCCAAGGAGAACGGCATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAAGCCTGCCACCGCTGCCGGGGACGGGGCGGTGGCCCACTTGCGGTCTGG 901
QY 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGGCTTCAACAAGCTCCAGCAACACCACTGTGTCAACTGGAAACAGTACTACA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGACAAACCCCTTCAAGGCGCCATCAACTTGACAACATTG 1021
QY 373 lYTrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393
Db 1022 GCTATGCGGTGATCGCCATCTTCCAGTTCATCAGCTGAGGGCTGGGTGACATCATGT 1081
QY 393 YrpheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACTTGTGATGATGCTCATCTCTTCTTAACAATTCATCTACTTTCATCTCTCATCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGATTGCCACGCAAGTTCTCAGAGA 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGGAAGCCAGCTGATGCGGAGACAGCGTGTGCGGTTCTGTCCAACGCCA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGlnGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCTGGCTAGCTTCTCTGAGCCCGGCACTGCTATGAGAGCTGCTCAAGTACTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCTTCTGTAAGGACGCCGCGAGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCACGACCCCTCGGGGGCCAGGAGACCCAGCCAGCAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisIleHisH 533
Db 1442 GCTGCTCTGCTGCCACCGCGCTATCGTCCACCACCTGTGTGACCAACCAACCAACC 1501

QY 533 iSHISHISITyRHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ATCACCAACCACTACCACTGGGCAATGGAGCCTCAGGGCCCCCGGGGCCAGCCGGAGA 1561
QY 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
Db 1562 TCCAGGACAGGAGATGCCAATGGGTCCCGCAGGCTCATGTGCAACCACTCGACGCCCTG 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CCTCTCCGGGGCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTAACATGCCGACT 1681
QY 593 YsHisLeuGluProValArgCysGlnAlaProProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCTCCAGGTCCCAATCTGAGGATCCG 1741
QY 613 lYArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGluI 633
Db 1742 GCAGACTGTGGGACGGGGAAGTGTATCCACCGTGACACACCAAGCCTCCACCGAGA 1801
QY 633 leLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653
Db 1802 CGCTGAAGAGAGAGCACTAGTAGAGGTGCTGCCAGCTCTGGGCCCCCAACCTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCGTCAACATCCACCGGGGCCCTACAGCTCCATGCACAAGCTGTGAGACACAGAGTA 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGGTGCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGACAGACAGTGAG 1981
QY 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera 713
Db 1982 CCTGTGCTCAGACAGCTGCCCCCTACTGTGCCGGGCGGGGACGGGAGGTGAGCTCG 2041
QY 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACGTGAATGCTGTGACTCAGACAGCAGGAGGATTATGAGTTACACAGAGATGCC 2101
QY 733 lnhISerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCAGACGACCTCCGGGACCCCAACAGC--CGGGGCAACGAGCCTGGGCCACAGATG 2158
QY 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCCAAGCTCTGTGCTGCGCTTCTGAGGCTTAATCTGTGACACCTTCCGAAGAATTG 2218
QY 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerm 793
Db 2219 TGGACAGCAAGTACTTTGGCGGGGAATCATGATGCCATCTGTGTACACACATCAGCA 2278
QY 793 etGlyIleGluTyrHisGlnGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCAATCGAATACACAGCAGCCCGAGAGCTTAACCAACGCCCTAGAAATCAGCAACA 2338
QY 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
Db 2339 TCGTCTTCAACAGCCTTCTTGCGCTGGAGATGCTGTGAAGCTGTTGTATGGTCCCT 2398
QY 833 heGlyTyrIleLeuAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
Db 2399 TTGGCTACATCAAGAATCCCTTCAACATCTTCGATGTGTATGTGTCATCAGCGTGT 2458
QY 853 xpgLuleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGGAGATCGTGGGCCAGCAGGGGGGGCGGCTGTGCTGCTCGGACCTTCCGCTGATGC 2518
QY 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2519 GTGTGCTGAAGCTGTGCGCTTCTGCGCGGCTGACGCGGACAGCTGTGTGTCTCATGA 2578

QY	893	YSThRMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
Db	2579	AGACCATGACAAACGTCGCCACCTTCTGCATGCTGTATGCTCTTCATCTTCATCTTCA	2638
QY	913	erIleLeuGIymethIleuPheGIYcysLysPheAlaSerGIuArgAspGIYAspThrL	933
Db	2639	GCATCTGGGCATGATCTCTTCGGCTGCAGATTGGCTTGTAGCGGGATGGGACACC	2698
QY	933	eUProAspArgLysAsnAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953
Db	2699	TGCCAGACCGGAAGAAATTGACTCCTTGCTCTGGGCCATCGTCACTGTCTTACAGATCC	2758
QY	953	eUThrGIuGIuAspTrpAsnLysValLeuTYrAsnGIYMetAlaSerThrSerSerTrpA	973
Db	2759	TGACCCAGAGAGACTGGACAAGTCCCTACATGGTATGGCTCCACGTCGTCTCGG	2818
QY	973	IaAlaLeuTYrPheIleAlaLeuMetThrPheGIYAsnTYrValLeuPheAsnLeuL	993
Db	2819	CGGCCCTTATTTCATTGCCCTCATGACCTTCGGCACTACGTCTCTCAATTGTCTGG	2878
QY	993	aAlaIleLeuValGIuGIYpHeGlnAlaGIu-----	1003
Db	2879	TGCCATTCTGTGGAGGCTTCAGGCGAGAAATCAGCAAA CGGAAGATGCGAGTG	2938
QY	1004	-----GlyAspAlaThrLysSerG	1010
Db	2939	GACAGTTAAGCTGTATTCAGCTGCTGTGCACTCCAGGGGGAGATGCCAACAAAGTCCG	2998
QY	1010	IuSerGIuProAspPhePheSerProSerValAspGIYAspGIYAspArgLysLysArgL	1030
Db	2999	AATCAGAGCCCGATTCTCTCAACCCAGCCTGGATGGTATGGGACAGAGAAGAGTGCT	3058
QY	1030	eUAlaLeuValAlaLeuGIYGIuHisAlaGIuLeuArgLysSerLeuLeuProProLeuI	1050
Db	3059	TGGCCTTGTTGTCCTCGGAGAGACACCCGAGCTGCGGAAGACCTGCTGCCCTCTCA	3118
QY	1050	IeIleHisThrAlaIaIaThrPrometSerHisProLysSerSerSerThrGIYValGIY	1070
Db	3119	TCATCCACACGGCCGCCACACCCATGTGCTGCCCAAGACACACGACGCGCTGGGCG	3178
QY	1070	IuAlaLeuGIYSerGIYSerArgArgThrSerSerSerSerGIYSerAlaGIuProGIYAla	1090
Db	3179	AGGCGTGGCCCTGCGTCGCCGCCACACGACGACGCGGTGGCAGAGCCTGGGGCG	3238
QY	1090	IaHisIGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerA	1110
Db	3239	CC---CACGAGATGAATGTCACGCCACAGCGCCGACGCTCTCCGACAGCCCTGAGCG	3295
QY	1110	IaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGIYArgAlaProSerL	1130
Db	3296	CTGCAAGCAGCTGGACCAAGCAGCGCTCCAGCCGGAACAGCCTCGGCCGTGACACCCAGCC	3355
QY	1130	eUlysArgArgSerProSerGIYGIuArgArgSerLeuLeuSerGIYGIuGIYGIuL	1150
Db	3356	TGAAGCGGAGAACCCCACTGAGAGCGGCGGTCCCTGTGTCCGGAAGGCCACAGAGA	3415
QY	1150	eRGIuAspGIuGIuLysSerSerGIuGIuAspArgAlaSerProAlaGIYSerAspHisA	1170
Db	3416	GCCAGATGAAGAGAGAGACTCAGAAGAGAGCGGGCCAGCCCTGCGGGCAGTGACCATC	3475
QY	1170	rGHISArgGIYSerLeuGIuArgGIuAlaLysSerSerPheAspLeuProAspThrLeuG	1190
Db	3476	GCCACAGGGGGTCCCTGGAGCGGAGGCCAAGATTCTTTGACTGACAGACACACTGC	3535
QY	1190	IuValProGIYLeuHisArgThrAlaSerGIYArgSerSerAlaSerGIuHisGIuAspC	1210
Db	3536	AGGTGCCAGGCGCTGCATCGCACTGCCAGTGCGCGAGGCTGTCTTGAGCACACGACT	3595
QY	1210	YsAsnGIYLysSerAlaSerGIYArgLeuAlaArgThrLeuArgThrAspAspProGIuL	1230
Db	3596	GCAATGGCAAGTCGGCTTCAGGGCGCCTGGCCCCGGCCCTGCGGCTGATGACCCCCCAC	3655
QY	1230	eUAspGIYAspAspAsnAspGIuGIYAsnLeuSerLysGIYGIuArgIleGlnAlaT	1250

Db	3656	TGATGGGGATGACGCCGATGACGAGGGCAACTGAGCAAAAGGGAACGGGTCCGCGCT	3715
QY	1250	rpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIleP	1270
Db	3716	GGATCCGAGCCCGACTCCCTCGCTGCTGCTCGAGCGAGACTCTGGTCAAGCTTACATCT	3775
QY	1270	heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA	1290
Db	3776	TCCCTCTCTAGTCCAGGTTCCGCCCTCTGTGTCAACCGATCATCACCACAAGATGTTCCG	3835
QY	1290	sPHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL	1310
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QY	1470	erTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGIYGlnAlaLeuMetSerL	1490
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QY	1510	alGIYValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleS	1530
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Qy 1619 lYValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL 1639
Db 4856 GTGTCAATCGGGCTGAACGTGTGTCAACCATGGCCATGGAGCACTAACAGACGCCAGATTTC 4915
Qy 1639 euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV 1659
Db 4916 TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACCTGCATCTTGTCTGGAGTCAG 4975
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Qy 1839 lnpheValIleuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnL 1859
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Qy 1879 erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValA 1899
Db 5636 GCGCCCAAGCCCACTCGCCACTGGGAGCCCTTCTCTGCGCTGGGGTGAAGGCGCCCG 5695
Qy 1899 snSerThrAspSerProLysProGlyValaProHisThrThraHisIleGlyAlaAlaAs 1919
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Qy 1919 erGlyPheSerLeuGluHisProThr----- 1927
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Db 6347 AACTGCCCCACACGAGAGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGCAACAA 6406
Qy 2046 lArGThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluV 2066
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Db 6467 TGAGTGGGCCCCCTCCCGCCCTGGCCCCGCTACTTCTTGAGGCGCAAGTCAATCCC 6526
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Db	7007	CGTCCAGCGACTCCAAAGATCCCTTGCCCTCTGGCCCCCTGACAGCATGGCTGCTCGC	7066
QY	2265	roSerProLySlyAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetA	2285
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QY	2285	spPro	2286
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Job time : 3043.18 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2005, 18:10:57 ; Search time 721.312 Seconds
(without alignments)
5188.000 Million cell updates/sec

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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11066.5	92.0	7741	3	US-09-426-998-4 Sequence 4, Appli
2	10948.5	91.0	6822	3	US-09-426-998-3 Sequence 3, Appli
3	10739	89.3	7405	4	US-09-935-016-3859 Sequence 3859, Ap
4	6241	51.9	7898	4	US-08-984-709A-49 Sequence 49, Appl
5	6103	50.7	3993	4	US-09-398-522-51 Sequence 51, Appl
6	5420	45.1	6816	3	US-09-404-650-1 Sequence 1, Appli
7	5420	45.1	6816	4	US-09-935-541-1 Sequence 1, Appli
8	5420	45.1	6855	3	US-09-404-650-3 Sequence 3, Appli
9	5420	45.1	6855	4	US-09-935-541-3 Sequence 3, Appli
10	5407	45.0	6503	3	US-09-404-650-12 Sequence 12, Appl
11	5407	45.0	6503	4	US-09-935-541-12 Sequence 12, Appl
12	2055	17.1	70308	4	US-09-949-016-15601 Sequence 15601, A

13	1974	16.4	1669	3	US-08-984-709A-51	Sequence 51, Appli
14	1745.5	14.5	7362	1	US-08-455-543A-7	Sequence 7, Appli
15	1745.5	14.5	7362	2	US-08-193-078B-7	Sequence 7, Appli
16	1745.5	14.5	7362	2	US-08-223-305C-7	Sequence 7, Appli
17	1745.5	14.5	7362	2	US-08-149-097D-7	Sequence 7, Appli
18	1745.5	14.5	7362	3	US-08-949-386-7	Sequence 7, Appli
19	1745.5	14.5	7362	3	US-08-450-562-7	Sequence 7, Appli
20	1745.5	14.5	7362	3	US-08-984-709A-7	Sequence 7, Appli
21	1745.5	14.5	7362	3	US-08-450-272-7	Sequence 7, Appli
22	1745.5	14.5	7362	4	US-08-450-273-7	Sequence 7, Appli
23	1743.5	14.5	7376	3	US-09-268-163-3	Sequence 3, Appli
24	1740.5	14.5	7266	3	US-08-713-118-1	Sequence 1, Appli
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26	1739.5	14.5	7364	3	US-09-268-163-5	Sequence 5, Appli
27	1727	14.4	7175	1	US-08-455-543A-8	Sequence 8, Appli
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38	1703	14.2	5975	1	US-08-314-083B-1	Sequence 1, Appli
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41	1699.5	14.1	6114	4	US-09-495-714C-5	Sequence 5, Appli
42	1693	14.1	7011	3	US-09-268-163-9	Sequence 9, Appli
43	1691	14.1	5975	1	US-08-336-257A-3	Sequence 3, Appli
44	1683.5	14.0	5962	6	5386025-5	Patent No. 5386025
45	1683.5	14.0	5962	6	5386025-5	Patent No. 5386025

ALIGNMENTS

RESULT 1
US-09-426-998-4
; Sequence 4, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHAIG T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHAIG-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 4
; LENGTH: 7741
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-4

Alignment Scores:

Pred. No.: 0
Score: 11066.50
Percent Similarity: 93.81%
Best Local Similarity: 92.38%
Query Match: 92.01%
DB: 3
Length: 7741
Matches: 2134
Conservative: 33
Mismatch: 112
Indels: 31
Gaps: 5

US-09-611-257A-24 (1-2287) x US-09-426-998-4 (1-7741)

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QY	63	Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGlu	82
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QY	102	roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuY	122
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QY	122	alllleuleuAsnCysValThrleuGlyMetPheArgProCysGluAspIleAlaCysA	142
Db	791	TCATCTTCTCACTCGCTGACCCCTGGGATGTTCCGGCCATGCGAGACATCGCCTGTG	850
QY	142	spSerGluArgCysArgIleleuGluAlaPheAspAspPheIlePheAlaPhePheAlaV	162
Db	851	ACTCCAGCGCTGCCGATCCCTGACAGGCCCTTTGATGACTTCATCTTGCCCTTTGGCG	910
QY	162	alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTrpLeuGlyA	182
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Db	1091	CCATTACCGGGTCCCGACCATGCGCATCTTGTACGTTGCTGTGATACGCTGCCCA	1150
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QY	382	alllethrleuGlUGLYTrpValasplleMETTyrPheValmeCAspAlahisSerPheT	402
Db	1571	TCATACGCTGGAGGGCTGGGTGCACATCATGTACTTGTGATGATGCTCATTCCTTCT	1630
QY	402	YrAsnPhelIeTyrPheIleleuLeuIleIleValGlySerPhePheMeCileasnuLeuC	422
Db	1631	ACAATTTCATCTACTTCATCTCCCTCATCATCGTGGGCTCCTTCTTCATGATCAACCTGT	1690
QY	422	YsleuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnleuMeT	442
Db	1691	GCCTGGTGTGATTGCCACGACGATTTCTCAGAGACCAAGCAGCGGAAGCAGCTGATGC	1750
QY	442	rgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProg	462
Db	1751	GGGAGCAGCGTGTGCGGTCTCCTGTCCACGCCACGACCCTGGCTAGCTTCTGAGCCCG	1810
QY	462	lySerCysTyrGluGluLeuLeuYsTyrIleuValTyrIleleuArgLysAlaAlaArg	482
Db	1811	GCAGCTCTATGAGGAGCTGCTCAAGTACCTGTGTATCATCTTCGTAAGCAGCCCGCA	1870
QY	482	rgleuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSerProVal	502
Db	1871	GGCTGGCTCAGTCTCTCGGGCAGCAGGTGTGCGGGTGGGTGCTCAGACCCAGCAC	1930
QY	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1931	CCCTCGGGGGCCAGAGACCCAGCCAGCAGCAGCTGCTCTCGTCCCAACGCCCTTAT	1990
QY	522	ervalHisHisleuValHisHisHisHisHisHisHisTyrHisleuGlyAsnG	542
Db	1991	CCGTCCACCACTGTGTGCACACCACCAACCATCACCACTACCACTGGGCAATG	2050
QY	542	lyThrleuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySer	562
Db	2051	GGACGCTCAGGGCCCCCGGGCCAGCCCGAGATCCAGGACAGGATGCCAATGGTCCC	2110
QY	562	rgArgleuMeCLeuProProProSerThrProThrProSerGlyGlyProProArgGly	582
Db	2111	GCAGGCTCATGCTGCCACCACTTCAGCGCTGCCCTCTCCGGGGCCCCCTGTGGCG	2170
QY	582	laGluSerValHisSerPheTyrHisAlaAspCysHisleuGluProValArgCysGln	602
Db	2171	CAGAGTCTGTGCACAGCTTCTTACCATGCGACTGCTCACTTAGAGCCAGTCCGCTGCAGG	2230
QY	602	laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2231	CGCCCCCTCCAGGTCCCATCTGAGGATCCGGCAGACTGTGGGCAGCGGGAAGTGT	2290
QY	622	yrProThrValHisThrSerProProProGluIleleuLysAspLysAlaLeuValGluV	642
Db	2291	ATCCCAACCGTGACACACAGCCCTCCACCGGAGACGCTGAAGAGAGACACTAGTAGAGG	2350
QY	642	alaIaProSerProGlyProProThrIleuThrSerPheAsnIleProProGlyProPheS	662
Db	2351	TGGCTGCCAGCTCTGGGCCCCCAACCTTCACCAAGCTCAACATCCCAACCCGGCCCTACA	2410
QY	662	erSerMeHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2411	GCTCCATGCACAAAGCTGCTGGAGACACAGATACAGGTGCTGCAAAAGCTTTGCAAGA	2470
QY	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	2471	TCTCCAGCCCTTGCTTGAAAGCAGACAGTGAAGCTGTGTCCAGACAGTGCCTTACT	2530
QY	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValmeCProAspSerAsps	722
Db	2531	GTGCCCGGGCGGGGCGAGGAGGTGAGCTCGCCGACGTGAATGCTGACTCAGACA	2590
QY	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS	742
Db	2591	GCGAGGCAATTATGAGTTCAACAGGATGCCACAGCAGCAGCCTCCGGGACCCCCACA	2650
QY	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValleuAlaPheT	762

Db 2651 GC---CGGGGCAACGAGCGCTGGGCCAGATGCAGAGCCAGCTCTGTGGCTTCT 2707
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Db 2768 TCATGATGCCATCTGTGTCAACACTCAGCATGGGCATCGAATACCAAGAGCAGCCCG 2827
QY 802 lUgIleuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG 822
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QY 1002 lAgLu----- 1003
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QY 1439 lLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgA 1459
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QY      2218 roSerIleSerIleAspProProGIuSerGIuLySerArgProProCySerProGIyV 2238
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QY      2238 aLCysLeuArgArgArgAlaSerProSerProLySLyAspThrLeuSerLeuSerGIyLeuS 2258
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Db      7196 TCTGCTCCGGAGAGGGCTCCGTCAGCGACTCCAAAGGATCCCTTGGCCTCTGGCCCCC 7255
QY      2258 euAspSerThrAlaAlaSerProSerProLySLyAspThrLeuSerLeuSerGIyLeuS 2278
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QY      2278 erSerAspProThrAspMetAspPro 2286
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RESULT 2
US-09-426-998-3
; Sequence 3, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426,998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 3
; LENGTH: 6822
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3
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Alignment Scores:
Pred. No.: 0 Length: 6822
Score: 10948.50 Matches: 2111
Percent Similarity: 94.03% Conservative: 32
Best Local Similarity: 92.63% Mismatches: 105
Query Match: 91.03% Indels: 31
DB: 3 Gaps: 5
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US-09-611-257A-24 (1-2287) x US-09-426-998-3 (1-6822)

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QY      34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
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QY      54 SerSerThrThrCysProGIyProGIyAla-AlaGIyAla-GlySerThrGIuLyAspP 73
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Db      62 GGCTCAACGACCTGTCCGGGGCCGGGGCCGGGGCGGGGTCAAGCAAGAAAGGAGACC 121
QY      73 roGIySerAlaAspSerGIuAlaGIuGIyLeuProTyTProAlaLeuAlaProValValP 93
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Db      122 CGGGCAGCGCGGACTCCGAGCGGAGGGGTGCTCCGTACCCGGCGCTGGCCCGGTGTTT 181
QY      93 hePheTyRLeuSerGIuAspSerArgProArgSerTyTPCysLeuArgThrValCysAsnP 113
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Db      182 TCTTCTACTTGAGCCAGACAGCCGCCCGGAGAGCTGTGTCTCCGACGGTCTGTAAAC 241
QY      113 roTrpPheGIuArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGIyMetP 133
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QY      133 heArgProCySGluAspIleAlaCysAspSerGIuArgCysArgIleLeuGIuAlaPheA 153
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Db      302 TCCGGCCATGCGAGGACATCGCTGTGACTCCAGCGCTGCCGATCTGCAGGCGCTTGG 361
QY      153 sPAspPheIlePheAlaPhePheAlaValaGIuMetValValLyMetValAlaLeuGIyI 173
       |||||
Db      362 ATGACTTCATCTTTCCTTCTTGGCGTGAGATGGTGTGAAGATGTGGCCTTGGCA 421
QY      173 lePheGIyLySLyCysTyRLeuGIyAspThrTPAsnArgLeuAspPheIleValI 193
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Db      422 TCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAACGGCTTGACTTTTCATCGTCA 481
QY      193 leAlaGIyMetLeuGIuTyRSerLeuAspLeuGIuAsnValSerPheSerAlaValArgT 213
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Db      482 TCGCAGGATGCTGGAGTACTCGCTGACCTGCAGACGTCAAGCTTCTCAGCTGTCAAGA 541
QY      213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
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Db      542 CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCTTG 601
QY      233 alThrLeuLeuLeuAspThrLeuProMetLeuGIyAsnValLeuLeuLeuCysPhePheV 253
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Db      602 TCACGTTGCTGCTGATACGCTGCCCATGCTGGGCAACGTCTGCTGCTTCTTCTTG 661
QY      253 alPhePheIlePheGIyIleValGIyValGIuLeuTrpAlaGIyLeuLeuArgAsnArgC 273
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Db      662 TCTTCTTCATCTTCGGCATGCTCGGCGTCCAGCTGTGGGCAAGGCGTCTCGGAACCGAT 721
QY      273 ysPheLeuProGIuAsnPheSerLeuProLeuSerValAspLeuGIuProTyRTrpGIuTr 293
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Db      722 GCTTCTTACTGAGATTTCACTTCCCTCCCTGAGCGTGAACCTGAGCGGCTATTACAGA 781
QY      293 hrGIuAsnGIuAspGIuSerProPheIleCysSerGIuProArgGIuAsnGIyMetArgS 313
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Db      782 CAGAGAACGAGATGAGAGCCCTTCATCTGTCTCCAGCCACGAGAACGCGCATCGGT 841
QY      313 erCysArgSerValProThrLeuArgGIyGIuGIyGIyGIyProProCysSerLeuA 333
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QY      333 spTyRGIuThrTyRAsnSerSerSerAsnThrThrCysValAsnTrpAsnGIuTrpTyRTr 353
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Db      902 ACTATGAGGCTTCAACAAGCTTCAAGCAACACCACTGTGTCACTGGAACAGTACTACA 961
QY      353 hrAsnCysSerAlaGIyGIuHisAsnProPheLySGlyAlaIleAsnPheAspAsnIleG 373
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Db      962 CCAACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGCCATCAACTTGCACAACATTG 1021
QY      373 lyTyRAlaTrpIleAlaIlePheGIuValIleThrLeuGIuGIyTrpValAspIleMetT 393
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Db      1022 GCTATGCTCGATCGCCATCTTCCAGGTCACTACGCTGAGGGCTGGGTGCATCATGT 1081
QY      393 yrPheValMetAspAlaHisSerPheTyRAsnPheIleTyRPhelIleLeuIleIleV 413
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Db      1082 ACTTTGTGATGATGCTCATCTTCTTACAATTTCACTTCACTTCACTTCACTCATCG 1141
QY      413 alGIySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGIuPheSerGIuT 433
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Db      1142 TGGGCTCTTCTTCAATGATCAACCTGTGCTGCTGTGTGATTGCCACGCACTTCTCAGAAGA 1201
QY      433 hrLySGluArgGIuSerGIuLeuMetArgGIuGIuArgValArgPheLeuSerAsnAlaS 453
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Db      1202 CCAAGCAGCGGGAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTTCCTGTCCAAGCCA 1261
QY      453 erThrLeuAlaSerPheSerGIuProGIySerCysTyRGIuGIuLeuLeuLyTyRLeuV 473
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Db      1262 GCACCTGTGCTAGCTTCTCTGAGCCCGGCAAGCTGTATGAGGAGTGTCAAGTACCTGG 1321
QY      473 alTyRleuArgLyAlaAlaArgArgLeuAlaGIuValSerArgAlaIleGIyValA 493
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Db 1322 TGTACATCCTTCGTAAGCAGCCCGCAGCGTGCCTCAGTCTCTCGGGCAGCAGGTGTGC 1381
QY 493 rGAlaGlYleuLeuSerSerProValAlaArgSerGlYGlNGluProGlnProSerGlYs 513
Db 1382 GGGTTGGGCTGCTCAGCAGCCCGCAGCACCCTCGGGGGCCAGAGACCAGCCAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 533
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QY 533 iSHiSHiSHiSTYrHisLeuGlYAsnGlYThrLeuArgValProArgAlaSerProGlui 553
Db 1502 ATCAACCACCTACTACCTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCGAGA 1561
QY 553 leGlnAspArgAspAlaAsnGlYSerArgArgLeuMetLeuProProProSerThrProt 573
Db 1562 TCCAGGACAGGAGTGCATGGGTCCCGCAGGCTCATGTGCACACCACCTCGACGCTTG 1621
QY 573 hrProSerGlYGlYProProArgGlYAlaGluSerValHisSerPheTYrHisAlaAspC 593
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QY 593 ySHiSleuGlYProValArgCysGlnAlaProProProArgCysProSerGlYAlaSerG 613
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QY 613 lYArgThrValGlYSerGlYLYsValTYrProThrValHisThrSerProProProGluI 633
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QY 653 erPheAsnIleProProGlYProPheSerSerMetHisLYsLeuLeuGlYThrGlnSert 673
Db 1862 GCTCAACATCCACCCGCGCCCTACAGCTCATGCACAAGCTGTGAGACACAGAGTA 1921
QY 673 hrGlYAlaCysHisSerSerCysLYsIleSerSerProCysSerLYsAlaAspSerGlYA 693
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Db 2759 TGACCCAGAGAGACTGGAACAAGTCTCTTACAATGTATGGCTCCACGTCGTCTGGG 2818
QY 973 laAlaleuTYrPheIleAlaleuMetThrPheGlYAsnTYrValleuPheAsnleuY 993
Db 2819 CGGCCCTTATTTCATTGCCCTCATGACCTTGCGCAACTACGTGCTCTTCAATTGCTGG 2878
QY 993 alAlaIleleuValGlYlYPheGlnAlaGlu-----GlyAspAlaThrLYsSerg 1003
Db 2879 TCGCCATTCTGTGAGAGGCTTCCAGCGGAGGAATCAGCAACGGGAAGATGCGAGTG 2938
QY 1004 -----GlyAspAlaThrLYsSerg 1010
Db 2939 GACAGTTAAGCTGTATTACGCTGCCTGTGACTCCAGGGGGGAGATGCCAACAGATCCG 2998
QY 1010 lUSerGluProAspPhePheSerProSerValAspGlYAspGlYAspArgLYsArgL 1030
Db 2999 AATCAGAGCCCGATTCTTCTCACCAGCCTGGATGTGTATGGGACAGAGAAGATGCT 3058
QY 1030 euAlaleuValAlaleuGlYlYhISalAGluLeuArgLYsSerLeuLeuProProleuI 1050
Db 3059 TGGCCTTGTTGCTCTGGGAGAGCACCAGAGCTGCGGAAGACCTGTGCGCCTCTCA 3118
QY 1050 leIleHisThrAlaAlaThrProMetSerHisProLYsSerSerSerThrGlYValGlYg 1070
Db 3119 TCATCCACAGCGCCGCACACCCCATGTGCTGCCCAAGAGCACAGACGGGCTGGGCG 3178
QY 1070 luAlaleuGlYSerGlYSerArgArgThrSerSerSerGlYSerAlaGluProGlYAlaA 1090
Db 3179 AGGCGCTGGGCTCGCTGCGCGCCGACCAAGCAGCAGCGGGTGGCAGAGCCTGGGGCGG 3238
QY 1090 laHisIleGlYMetLYsCysProProSerAlaArgSerSerProHisSerProTrpSera 1110
Db 3239 CC---CACGAGATGAAGTCAACCGCCAGCGCCCGCAGCTTCCGACAGCCCCCTGAGCG 3295
QY 1110 laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlYArgAlaProSerL 1130
Db 3296 CTGCAAGCAGCTGGAACCAAGCGGCTTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCC 3355
QY 1130 euLYsArgArgSerProSerGlYluArgArgSerLeuLeuSerGlYGlNGlYGlNGluS 1150
Db 3356 TGAAGCGGAGAACCCCAAGTGAGAGCGGGGTCTCTGTGTGGAGAGGCGCAGAGAGA 3415
QY 1150 erGlnAspGluGluGluSerSerGluGluAspArgAlaSerProAlaGlYSerAspHisA 1170
Db 3416 GCCAGATGAAGAGAGAGCTCAGAAAGAGAGCGGGCCAGCCCTGCGGCAGTGACCATC 3475
QY 1170 rGHisArgGlYSerLeuGluArgGlYAlaLYsSerSerPheAspLeuProAspThrLeuG 1190
Db 3476 GCCACAGGGGGTCCCTGAGCGGGAGGCCAAGATTCTTGAACCTGCGACAGACACTGC 3535

QY	1190	INValProGlyLeuHiSArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC	1210
Db	3536	AGGTGCAGGCGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCAGACT	3595
QY	1210	YbASnglyLySserAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL	1230
Db	3596	GCAATGGCAAGTCGGCTTCAGGGCGCCTGGCCCGGCCCTGGCGCTGATGACCCCCAC	3655
QY	1230	EuASpGlyAspAspAspAsnAspGlyGlyAsnLeuSerLySgLyGluArgLLeGlnAlaT	1250
Db	3656	TGGATGGGATGACCGCGATGACGAGGGCAACCTGACCAAGGGGAACGGGTCCGCCGT	3715
QY	1250	rPValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrlLeP	1270
Db	3716	GGATCCGAGCCCGACTCCCTGCTGCTGCTCGAGCGAGACTCCTGTCAGCCTACATCT	3775
QY	1270	heProProGlnSerArgPheArgLeuLeuCysHisArgLLeLeThrHisLyMetPhea	1290
Db	3776	TCCCTCCTCAGTCCAGGTTCGGCCTCCTGTGTACCGGATCATCACCACAAGATGTTCG	3835
QY	1290	sPHisValValLeuValLLeIlePheLeuAsnCySLeLeThrLLeAlaMetGluArgProL	1310
Db	3836	ACCACGTGGTCTTGTCATCATCTTCTTAAGTCATCACCATCGCCATGAGCGCCCCA	3895
QY	1310	YsILeAspProHisSerAlaGluArgLLePheLeuThrLeuSerAsnTyrlLePheThra	1330
Db	3896	AAATTGACCCCCACAGCGCTGAACGCATCTTCTGACCTCTCCAATTACATCTTCAACG	3955
QY	1330	LaValPheLeuAlaGluMetThrValLySValValAlaLeuGlyTrpCysPheGlyGluG	1350
Db	3956	CAGTCTTTCTGGCTGAATGACAGTGAAGTGTGGCACTGGGCTGTGCTTCGGGGAGC	4015
QY	1350	lnAlaTyrlLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuLLeSerValI	1370
Db	4016	AGCGCTACCTGCGAGCAGTTGGAACGTGCTGACGGGCTGTGCTCATCTTCCTGCA	4075
QY	1370	LeAspLLeLeuValSerMetValSerAspSerGlyThrLySILeLeuGlyMetLeuArgV	1390
Db	4076	TCGACATTCTGTGTCCATGGTCTTGACAGCGGCAACAAGATCCTGGGCATGTCAGGG	4135
QY	1390	alLeuArgLeuLeuArgThrLeuArgProLeuArgValLLeSerArgAlaGlnGlyLeuL	1410
Db	4136	TGCTGCGGCTGTGCGGACCTGCGCCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGA	4195
QY	1410	YsLeuValValGluThrLeuMetSerSerLeuLySProLLeGlyAsnLLeValLLeC	1430
Db	4196	AGCTGGTGTGAGAGACGCTGATGTCTCACTGAAACCATCGGCCAACATTGTAGTCATCT	4255
QY	1430	YbCysAlaPhePheLLeLLePheGlyLLeLeuGlyValGlnLeuPheLySgLyLySPhP	1450
Db	4256	GGCTGTGCTTCTTCATCATTTTCGCATCTTGGGGGTGACGCTTCAAAAGGAATT	4315
QY	1450	heValCysGlnGlyGlyAspThrArgAsnLLeThrAsnLySerAspCysAlaGluAlaS	1470
Db	4316	TCGTGTGCCAGGGCGAGGATCCAGGAACATCACCAATAATCGAAGTGTGCCGAGGCCA	4375
QY	1470	eTrTyrrArgTrpValArgHisLyStryrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL	1490
Db	4376	GTTACCGGTGGGTCCGGCACAACTTGAACAACCTTGGCCAGGCCCTGATGTCC	4435
QY	1490	eupheValLeuAlaSerLySAspGlyTrpValAspLLeMetTyrrAspGlyLeuAspAlaV	1510
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QY	1510	alGlyValAspGlnGlnProLLeMetAsnHisAsnProTrpMetLeuLeuTyrrPheLLeS	1530
Db	4496	TGGGGGTGGACACGACGCCATCATGAACCAACCCCTGATGCTGTACTTCACT	4555
QY	1530	ePheLeuLeuLLeValAlaPhePheValLeuAsnMetPheValGlyValValGluA	1550
Db	4556	CGTTTCTGCTCATTTGTGGCCTTCTTTGCTCTGAACATGTTTGTGGGTGTGTGTGAGACA	4615
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Db	4616	ACTTCCACAAGTGTGGGACAGCACGAGAGAGAGAGCCCGCGCGGAGAGAAAGC	4675
Qy	1570	rgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGlnMetAlaGluAlaGlnC	1590
Db	4676	GCCTACGAAGACTGGAGAAAAAGAGAGAGATAGAGAAGACAGATGGCTGAAGCCAGT	4735
Qy	1590	ysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCyThrS	1610
Db	4736	GCAACCTTACTACTCCGACTACTCCCGCTTCCGGCTCTCGTCCACCACCTTGTCACCA	4795
Qy	1610	erHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValIleHisIleMetAla	1630
Db	4796	GCCACTACCTGAGCCTTTCATCACAGGTGTCAATGGGCTGAACGTGTACCAATGGCCA	4855
Qy	1630	etGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIleP	1650
Db	4856	TGGAGCACTACCAGCAGCCCCAGATTCTGGATGAGGCTCTGAAGATCTGAACATACTCT	4915
Qy	1650	heThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgP	1670
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Qy	1670	hePheGlnAspArgTTPAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyI	1690
Db	4976	TCTTCCAGACAGGTGGAACCACTGACCTGGCCATGTGTCTGTCCATCATGGCCA	5035
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Qy	1710	IeMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetA	1730
Db	5096	TCATGAGGGTGTGCGCATTGCCCGAGTCTGAAGTGGCTGTGGGCATGC	5155
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Db	5156	GGGCGCTGCTGACACGGGTGATGACAGGCCCTGCCAGGTGGGAACCTGGACTTCTCT	5215
Qy	1750	heMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluC	1770
Db	5216	TCATGTGTGTGTTTTCATCTTGACAGCTCTGGCGTGAAGCTCTTGAGACCTGGAGT	5275
Qy	1770	ysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyM	1790
Db	5276	GTCACGAGACACACCCCTGTGAGGGCCTGGGCCGTATGCCACCTTCCGAACCTTGGCA	5335
Qy	1790	etAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTPAsnGlyIleMetLysA	1810
Db	5336	TGGCCTTCCCTAACCCCTTCCGAGTCTCCACAGGTGAACAATTGGAATGCATTATGAAG	5395
Qy	1810	spProSerArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleT	1830
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Qy	1850	euMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaG	1870
Db	5516	TGATGAAGCACCTGAGAGAGACAACAAGAGAGGCCAAGAGAGAGGCCGAGCTAGAGGCTG	5575
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Db	5576	AGCTGAGAGCTGAGATGAAGACCTCAAGCCCAAGCCCACTGCCACTGGCAGCCCTT	5635
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Db 5696 ACCCAGCGGCCACGCGAGATCAGCTCCCACTTTCCCTGGAGCACCACCGATGCAGC 5755
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Qy 1950 lValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAnGlySerThra 1970
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Qy 2010 iSTyrLeuLeuGlnProHisGlyAlaProThrTyrGlyAlaIleProLysLeuProProp 2030
Db 5987 CTCAATCTGCTCCAGCCCAAGCGCCCAACCTGGGGGCAACCATCCCCAACTGCCCCAC 6046
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Qy 2050 erLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGlyPros 2070
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Qy 2070 erCysProLeuThrArgSerSerSerPheTyrGlyGlySerSerIleGlnValGlnGlnA 2090
Db 6167 CCCCCGCTCCGCGCCGCGGCTTCTTCTGGGGCCAGTCAAGTACCAAGGACAGGACAGCAGC 6226
Qy 2090 rGSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGlyL 2110
Db 6227 ACTCCGCAACCCACAGCAAGATCTCCAAACACATGACCCCGCAGCCCTTGGCCAGGCC 6286
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Qy 2169 heTyrLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerg 2189
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Qy 2249 erLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerProSerProLysL 2269
Db 6707 CCAAGGATCCCTTGGCCTGTGGCCCCCTGACAGCATGGCTGCTCGCCCTCCCCAAAGA 6766
Qy 2269 yAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetAspPro 2286
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RESULT 3
US-09-949-016-3859
; Sequence 3859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3859
; LENGTH: 7405
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3859

Alignment Scores:
Pred. No.: 0 Length: 7405
Score: 10739.00 Matches: 2077
Percent Similarity: 92.09% Conservative: 29
Best Local Similarity: 90.82% Mismatches: 95
Query Match: 89.28% Indels: 86
DB: 4 Gaps: 5

US-09-611-257A-24 (1-2287) x US-09-949-016-3859 (1-7405)
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Db 281 CCGCCGGGGCCCCGGGTGCGTGAGGACACTCTCTGAGGGCGCGCTTGCCCTCT 340
Qy 23 SerAspProProGlyProArgLeuAlaArgGlyTyrThrArgArgMetGluArgAla 42
Db 341 CCGGATCGCCCGGGGCCCGGCTGGCCAGAGATGACGAGAGAGAGATGAGCGGCG 400
Qy 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrCysProGlyProGly 62
Db 401 CCGAGAGATCGGACAGCCCCCGAGCTTCATGCGCTCAACGACCTGTGAGGGCGGCG 460
Qy 63 Ala-AlaGlyAla-GlySerThrGlnLysAspProGlySerAlaAspSerGluAlaGln 82
Db 461 GCGGCGCGGGGGGGGTTCAGCAGAAAGAACCCGGGCAAGCGGAGACTCCGAGCGGAGG 520
Qy 82 lYleuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102
Db 521 GAGTCCGTACCCGGCGCTGGCCCCCGGTGTTTCTTCTTACTTGAGCCAGGACAGCCGCC 580
Qy 102 roArgSerTrpCysLeuArgThrValCysAsnPro--TyrPheGluArgValSerMetL 121
Db 581 GCGGAGCTGTGTCTCCGACGGTGTGTAAACCTACCTGTGTTGAGCGCATCAGCATGT 640
Qy 121 euValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaC 141
Db 641 TGGTCATCCTTCAACTGCGTGAACCTGGGCATGTTCGGGCATGCGAGACATCGCCT 700
Qy 141 yAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheA 161
Db 701 GTGACTCCAGCGCTGCGGATCCTGAGGCTTGATGACTTCATCTTGCTTCTTG 760
Qy 161 laValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysEtyrLeuG 181
Db 761 CCGTGAGATGTGTGAAGATGTGTGCTTGGGCATCTTTGGGAAAAAGTGTACTTG 820
Qy 181 lYAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerL 201

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QY 201 euAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeuA 221
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Db 881 TGGACCTGCAGAACGTACGTTCTCAGCTGTCAAGGACAGTCCGTGTGCTGGACCGCTCA 940
QY 221 rgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrLeuP 241
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QY 241 rMeLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValG 261
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Db 1001 CCATGCTGGGCAACGTCCTGCTGCTCTGCTTCTTCTTCATCTTCGTCATCGCTCG 1060
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QY 281 euProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProp 301
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QY 301 heIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuA 321
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Db 1421 AGGTCAATCAGCTGAGGGCTGGGTGCAATCATGTACTTGTGATGATGCTCATTCCT 1480
QY 401 heTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnL 421
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Db 1481 TCTACAATTTCATCTACTTCACTCTCTCATCATCGTGGCTCTTCTCATGATCAACC 1540
QY 421 euCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGlnLeuM 441
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QY 441 eCArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluP 461
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Db 1601 TGGCGGAGCAGCGTGTGCGGTTCCTGCCAACGCGCACACCTGGCTAGCTTCTGAGC 1660
QY 461 roGlySerCysTyrGlnGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaA 481
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QY 481 rgArgLeuAlaGlnValSerArgAlaIleGlyValAlaArgAlaGlyLeuLeuSerSerProV 501
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Db 1721 GCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTGCGGTTGGGCTGCTCAGCAGCCAG 1780
QY 501 aAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgL 521
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Db 1781 CACCCCTCGGGGCCAGAGACCCAGCCACAGCAGCAGCTGCTCTGCCACCGCGCC 1840
QY 521 euSerValHisIleuValHisIleHisIleHisIleHisIleHisIleTyrHisLeuGlyA 541
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Db 1961 CCGCGCGGCTCATGTGCTCCACCAACCTCGACGCTTGCCCTCTCCGGGGCCCCCTGTG 2020
QY 581 lYAlaGluSerValHisSerPheTyrHisAlaAspCysHisIleuGluProValArgCysG 601
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Db 2021 GCGCAGAGTCTGTGACAGCTTCTACCATGCGCACTGCCACTTACAGCCAGTCCGCTGCC 2080
QY 601 lNAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysV 621
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Db 2081 AGCGGCCCCCTCCAGGTCCCATCTGAGGCATCCGGCAGAGACTGTGGGCAAGGAGGAGG 2140
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Db 2201 AGGTGGCTGCCAGCTCTGGGCCCCCAACCCCTCAACCAAGCTCAACATCCACCCGGCCCT 2260
QY 661 heSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysL 681
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QY 721 spSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProH 741
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QY 761 heTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgG 781
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QY 801 roGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaL 821
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QY 841 snIlePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnGlnGlyG 861
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Db 2798 ACATCTTGATGTGTGTCATTGTGTATCATCAGCGTGTGGGAGATCGTGGCCAGAGGGGG 2857
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Db 2858 GCGGCTGTGCTGTGCTGCGGACCTTCCGCTGATGCTGTGCTGAAGCTGTGCGCTTCC 2917
QY 881 euProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrP 901
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Db 2918 TGCCGGGCTGACAGCGGAGCTGTGTGCTCATGAAGACCATGACAAAGTGGCCACCT 2977
QY 901 heCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheG 921
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QY 921 lYcYsLYSPheAlAserGluArgSPGLYAspThrLeuProAspArgLYsAsnpheAsps 941
Db 3038 GCTGCAAGTTTGCTCTGAGCGGGATGGGACACCTGCCAGACCGGAAGAATTTGACT 3097
QY 941 exLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLYsV 961
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QY 1001 lnaIaGluGLYAspAlaThrLYsSerGluSerGluProAspPhePheSerProSerValA 1021
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QY 1081 eTSerGLYSerAlaGluProGlyAlaAlaHisHisGluMetLYsCysProProSerAlaA 1101
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QY 1621 leGlyLeuAsnValValThrMetAlaMetGluHisTYrGlnGlnProGlnIleLeuAspG 1641
Db 5135 TCGGGCTGAACGTGTGTACCATGGCCATGGAGCACTAACAGAGCCCAAGATTCTGATG 5194
QY 1641 lualaleuLYsIleCysAsnTYrIlePheThrValIlePheValPheGluSerValPheL 1661

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Db 5855 CCAGGAGAGGCGCGAGCTAGAGGCTGAGCTGAGCTGAGATGAAGACCCCTCAGCCCCC 5914
Qy 1881 lnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerT 1901
Db 5915 AGCCCCACTCGCCACTGGGCGAGCCCTTCTCTGCGCTGGGTCGAGGGCCCCCGACAGCC 5974
Qy 1901 hrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGlyP 1921
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Qy 1921 heSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyP 1941
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Qy 1981 euProLysAlaGlnSerGlySerlleLeuSerValHisSerGlnProAlaAspThrSerC 2001
Db 6206 TCCCAAAGCTCAGTCAAGCTCCGTCTTGTCCGTCACTCCCAAGCCAGACATACCAAGCT 6265
Qy 2001 ysIleLeuGlnLeuProLysAspValHisTyrrLeuLeuGlnProHisGlyAlaProThrT 2021
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Db 6266 ACATCCTGCAGCTTCCCAAGATGCACCTCATCTGTCTCCAGCCCCACAGCGCCCAACT 6325
Qy 2021 rpglyAlaIleProlyleuProProProGlyArgSerProLeuAlaGlnArgProLeuA 2041
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Qy 2041 rgarGlnAlaIleAlaIleArgThrAspSerLeuAspValGlnGlyleuGlySerArgGluA 2061
Db 6386 GGGCCAGGCAACAATAGGACTGACTCTTGACGTTCAAGGTCGTGGGCAAGCGGGAAG 6445
Qy 2061 sPLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerPheTrpG 2081
Db 6446 ACCTGCTGGCAGAG----- 6459
Qy 2081 lyGlySerSerlleGlnValGlnGlnArgSerGlylleGlnSerLysValSerLysHisI 2101
Db 6459 ----- 6459
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Db 6459 ----- 6459
Qy 2121 hrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuPro 2141
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Qy 2141 exSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrrSerValGluThrg 2161
Db 6460 -----GAGAGCCCCCATCCCAAGGAGCTGGAAGAGTGTACAGCGTGGAGGCC 6511
Qy 2161 lnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerlleAlaV 2181
Db 6512 AGAGCTGCCAGCGCGGCCCACTGCTGGCTGATGATGAGACAGAGACACTTATCGCCG 6571
Qy 2181 alSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyG 2201
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Qy 2201 lyGlnProLeuGlylyGlyProGlySerArgProLysLysLysLeuSerProProSerIle 2221
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Qy 2221 erlleAspProProGluSerGlnGlySerArgProProCysSerProGlyValCysLeuA 2241
Db 6692 CCATAGACCCCGAGAGCAAGGTCTCTCGACCCCGCCAGCCCTGTGATCTGCTCC 6751
Qy 2241 rgarGArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuAspSerT 2261
Db 6752 GGAGGAGGCTCCGTCAGGCACTCCAAGATCCCTTGACCTGCGCCCTGACAGCA 6811
Qy 2261 hrAlaIleSerProSerProLysAspThrLeuSerLeuSerGlyLeuSerSerAspP 2281
Db 6812 TGCTGCTCGCCCTCCCAAGAAAGATGTGCTGAGTCTCTCGGTTTATCTCTGACC 6871
Qy 2281 roThrAspMetAspPro 2286
Db 6872 CAGCAGACTGGAACCC 6888

RESULT 4
US-08-984-709A-49
; Sequence 49, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla

[illegible]

Db	1541	GCCTGGTGTGATTCACGACGAGTTCAGACACCAAGCAGCGGAAGCCAGCTGATGC	1600
QY	442	rgGlInArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGluProG	462
Db	1601	GGAGACAGCGTGTGCGGTCTCTGTCACACGACGACACCCCTGGCTAGCTTCTGAGCCCG	1660
QY	462	lySerCysIYrGluGluLeuLeuLysIYrLeuValTYrIleLeuArgLysAlaAlaArgA	482
Db	1661	GCAGCTGCTATGAGAGAGCTGCTCAAGTACTGTGTATCATCTTCGTAAAGCAGCCCCGA	1720
QY	482	rgLeuAlaGlnValSerArgAlaIleGlyValAlaArgAlaGlyLeuLeuSerSerProValA	502
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QY	502	laArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgArgLeuS	522
Db	1781	CCCTCGGGGGCCAGAGACCAGCCAGCCAGCAGACTGCTCTCGTCCACCGCCGCTTAT	1840
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QY	542	lyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySera	562
Db	1901	GGACGCTCAGGGCCCCCGGGCCAGCCCGGAGATCCAGGACAGGGATGCCAATGGGTCCC	1960
QY	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	1961	GCCGGCTCATGCTGCCACCACTCGACGCTTGCCCTCTCCGGGGCCCCCTTGTTGGCG	2020
QY	582	laGluSerValHisSerPheTYrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
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QY	602	laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2081	CGCCCCCTCCAGGTCCCATCTGAGGCAATCCGACAGACTGTGGGCAAGGGAAGTGT	2140
QY	622	yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2141	ATCCCAACCGTGACACACGACCCCTCCACGGAGACGCTGAAGAGAGAAGGCACTAGTAGAG	2200
QY	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
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QY	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2261	GCTCCATGACAAAGCTGTGAGACACAGATACAGGTGCTGCGCAAGCTTGTGCAAGA	2320
QY	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTYrC	702
Db	2321	TCTCCAGCCCTTGCTTGAAGCAGACAGTGAAGCTGTGTGTCCAGACAGTGCCTACT	2380
QY	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps	722
Db	2381	GTGCCCCGGGGCGGGGACAGGAGGTGAGCTCGCCGACCGTGAATGCTGACTCAGACA	2440
QY	722	erGluAlaValTYrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS	742
Db	2441	GCGAGGCAATTATGAGTTCAACAGATGCCACAGCACAGGACCTCCGGGACCCCCACA	2500
QY	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762
Db	2501	GC--CGGGGCAACGAGCCTGGGGCCAGATGCAGAGCCCAAGCTCTGTGCTGGCCTTCT	2557
QY	762	rPArgLeuIleCysAspThrPheArgLysIleValAspSerLysTYrPheGlyArgGlyI	782
Db	2558	GGAGGCTAATCTGTGACACCTTCCGAAGAATTGTGACAGCAAGTACTTTGGCCGGGGA	2617
QY	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTYrHisGluGlnProG	802

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QY 902 YSMetLeuLeuMetLeuPheilePheilePheSerileuGlyMetHisleuPheGlyC 922
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QY 1022 lYAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA 1042
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Db 3398 GGAAGAGCCTGTGCTGCCCTCTCATATCCACACGGCCGCCACCATGTGCTGCTGCCA 3457
QY 1062 YsSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSerS 1082
Db 3458 AGAGCACCAAGACGGGCTGGGGCGAGGGCTGGGCCCTGCTGCTGCGCCGACACAGCA 3517
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Db 3815 CCTTGACCTGCCAGACACTGCAGAGTGCAGGGCTGCATCGCACCTGCCAGTGGCCGAG 3874
QY 1202 eRserAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT 1222
Db 3875 GGTCTGCTTCTGAGCACCAGAGACTGCAATGGCACTCGGCTTCAGGGCGCTGGCCGCG 3934
QY 1222 hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnLeu 1241
Db 3935 CCTTGGGCTGATGACCCCCCACTGATGGGATGACCGCGATGACGAGGCAACCTG 3993

RESULT 6
US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McIlver, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-404-650-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.74% Conservative: 234
Best Local Similarity: 51.82% Mismatches: 494
Query Match: 45.06% Indels: 413
DB: 3 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-404-650-1 (1-6816)

QY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCCGCCCTCTCATCTGCAGCAAGCCCAAGCGCTGAGCCAGAGTCAACCAAGAGCAG 266
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAlaProArgSer 45
Db 267 CCCGACCCCGG----- 278
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCCCGCCAGGCTGAGAGAGCCTCTGATGAGCT----- 326
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
QY 86 ProAlaLeuAlaProValIlePhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCTATTGCTTCTTCTGCTGCACAGACCAACCAAGCCCGGAAGTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCAATCAAGATGTGTGCAACCCGTGTTGAATGTGTCAAGCATGTGTGATCCTGCTG 464

QY		126	AsnCysValThrLeuGluMetPheArgProCysGluAspIleAlaCysAspSerGlnArg	145
Dd		465	AACTGCCTGACACTTGGCATGTACCAGCCGTGCCAGCACATGGA CTGCTGCCAGCCG	524
QY		146	CysArgIleLeuGlnAlaPheAspSpherIlePheAlaPhePheAlaValGluMetVal	165
Dd		525	TGCAGATCCTGCAGGTCCTTTGATGACTTCATTACTTCTTTGCCATGAGATGGTG	584
QY		166	ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTy rLeuGlyAspThrTrpAsn	185
Dd		585	CTCAAGATGTGGCCCTGGGATTTTTGGCAAGAAGTGCTA CCGGGACACATGGAAC	644
QY		186	ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTy rSerLeuAspLeuGlnAsn	205
Dd		645	CGCTGATTTCTTCATCGTCATGGCAGGAGTGTGAGTA CTCCTGGA CCTTGAGAAC	704
QY		206	ValSerPheSerAlaValArgThrValArgValLeuArgPr oLeuArgAlaIleAsnArg	225
Dd		705	ATCAACCTGTACGCCATCCGACCGTGCCTCTAGGCCCT CAAGCCATCAACGC	764
QY		226	ValProSerMetArgIleLeuValThrLeuLeuAspThrLe uPrometLeuGlyAsn	245
Dd		765	GTCGCCAGTATGCGGATCCTGTGTGAACCTGCTCTGGA CACACTGCCCATGCTGGGAAT	824
QY		246	ValLeuLeuLeuCysPhePheValPhePheIlePheGlyI leValGlyValGlnLeuTrp	265
Dd		825	GTCCTGCTGCTCTGCTCTTTGCTCTTCTTCATCTTTGG CATATAGGTGTGCAGCTCTGG	884
QY		266	AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnP heSerLeuProLeuSerVal	285
Dd		885	GCGGCTGCTGCGTAACGCTGCTCTTGAGAGAACTTCA CCATACAAGGGGATGTG	944
QY		286	AspLeuGluProTy rTy rGlnThrGluAsnGluAspGluSerPro pheIleCysSerGln	305
Dd		945	GCCTTGCCCCCATACTACCAGCCGAGAGAGATGATGATG CCGCTTCATCTGCTCCTG	1004
QY		306	ProArgGluAsnGlyMetArgSerCysArgSerValProThr LeuArgGlyGluGly	325
Dd		1005	TCGGCGCACATGGGATAATGGGCTGCCATGATCCCCCG CTCACAGAGCAG-----	1058
QY		326	GlyGlyProProCysSerLeu-----AspTy rGluThrTy rAsnSer	339
Dd		1059	--GGCGTAGTGTGCTGCTGCCAAGACGACGTCA GACTTTGGGCGGGCGCCAG	1115
QY		340	SerSerAsnThrThr-----CysValAsnTrpAsnGlnTy rTy rThrAsnCysSerAla	357
Dd		1116	GACCTCAATGCCAGCGGCTCTGTGTCACTGGAACCGTT ACTACAATGTGTGCCGACG	1175
QY		358	GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAs nIleGlyTy rAlaTrpIle	377
Dd		1176	GGCAGCGCCAACCCCAACAAGGGTCCATCACTTGACA CAATCGTTATGCTTGGATT	1235
QY		378	AlaIlePheGlnValIleThrLeuGluGlyTrpValaspIle MetTy rPheValMetAsp	397
Dd		1236	GTCATCTTCCAGGTATCACTCTGAAAGCTGGGTGAGATCA GTACTACGTATGGAT	1295
QY		398	AlaHisSerPheTy rAsnPheIleTy rPheIleLeuLeuI leValGlySerPhePhe	417
Dd		1296	GCTCACTCCTTCAACACTTCATCTCACTTCCTGTTATCAT AGTGGGCTCCTTCTTC	1355
QY		418	MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSe rGluThrLysGlnArgGlu	437
Dd		1356	ATGATCAAACCTGTGCTCGTTGTCA TAGCGACCCAGTTCTCGAGACCAAGCAAGCGGAG	1415
QY		438	SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAs nAlaSerThrLeuAlaSer	457
Dd		1416	CACCGGCTGATGTGAGACGACGGCAGCGCTACTCTGTCC-- TCACGACCGGTGGCCAGC	1472
QY		458	PheSerGluProGlySerCysTy rGluGluLeuLeuLysTy rLeuValTy rIleLeuArg	477
Dd		1473	TACGCCGAGCCTGGCAGCTGCTACGAGGAGATCTTCCAG TATGTCTGCCACATCTCTGCC	1532

Qy	478	LysAlaIaIaAArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu	497
Db	1533	AAGGCCAAGCC-----CGGCCCTGGCCTTACCAGGCCCTGCAG	1574
Qy	498	SerSerProValAlaAArgSerGlyGlnIuProGlnProSerGlySerCysThrArgSer	517
Db	1575	AGC-----	1577
Qy	518	HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisIleTyr	537
Db	1578	---CGGCGCCAGGCCCTG-----	1592
Qy	538	HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp	557
Db	1593	-----GGCCCGGAG-----	1601
Qy	558	AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly	577
Db	1602	-----GCCCGCGCCCCCGCCCAACCTGGGCC-----	1628
Qy	578	ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro	597
Db	1629	-----CACGCCAAG-----GAGCCC	1643
Qy	598	ValArgCysGlnAlaProProProArgCysProSerGlyAlaSerGlyArgThrValGly	617
Db	1644	CGGACTACCACTGTGCCCCGCAACATAGCCCCCTGATGCG-----	1685
Qy	618	SerGlyLeuValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys	637
Db	1686	-----ACGCCCCACACC-----	1697
Qy	638	AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro	657
Db	1698	---CTGGTGCA-----CCCATCCCCGCCACGCTGGCTTC-----	1730
Qy	658	ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys---	676
Db	1731	-----GATCCCGCCAGCTGCCCTGTGCTGCCAG	1757
Qy	677	HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro	696
Db	1758	CATGAGGACGGCCGGCGCCCTCGGGCTGGGCAAGCACCAGACTCGGGCCAGGAGGGCTCG	1817
Qy	697	AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal	716
Db	1818	GGCTCC-----GGAGCTCCGCTGTCGCGAGGACGAGCG-----	1853
Qy	717	MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp	736
Db	1854	-----GATGGGGACGGGGCC-----CGGAGCAGCGAGGACGAGCCTCTCCAGAA	1898
Qy	737	LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer	756
Db	1899	CTGGGGAGAGGAGGAGGAGGAGGAGCAG-----GCCGATGGGGCG	1940
Qy	757	SerValLeuAla-----PheTyrArgLeuIleCysAspThrPheArgLysIleValAsp	774
Db	1941	GTCCTGGCTGTCCGGGGATGTGTGGCGGGAGACCGGAGCCAAAGCTCCGGGCATCTGTGAC	2000
Qy	775	SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly	794
Db	2001	AGCAAGTACTTCAACCGGGGCATCATGTGGCCATCTGTCAACACCCGTACGATGGGC	2060
Qy	795	IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal	814
Db	2061	ATCGAGCACCAAGCAGCAGCCGAGAGCTGACCAACATCTTGAGATCTGCAATGTGTCTC	2120
Qy	815	PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGly	834
Db	2121	TTCAACCAAGCATGTTTCCCTGGAGATGATCTTGAAGCTGGCTGCATTTGGGCTCTTCGAC	2180
Qy	835	TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrGlu	854

Db 2181 TACCTGCGTAACCCCTACACACTCTTCGACAGACATATGTGCATCATCAGCATCTGGAG 2240
QY 855 ILeValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCTGGGGGCGAGCGGACGGTGGCTGTCTGGTGTCCGACCTTCCGGCTGTCCGGCTG 2300
QY 875 LeuValLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAACCTGGTGCCTTCATGCTGCCCCCTGCGGCGCACTCTGTGTCTCATGAAGACC 2360
QY 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle 914
Db 2361 ATGCAACGCTGGCCACCTTCGATGCTGCTCATGCTCTTCATCTTCATCTTCAGCATC 2420
QY 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933
Db 2421 CTTCGGATGCATATTTTGGCTGCAAGTTCCAGCTCCGCACGACACTGGAGACACGGTG 2480
QY 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db 2481 CCGGACGAGAAAGAACTTCGACTCTCTGCTGTGGGCCATCTCATCTGTTCAGATCCTC 2540
QY 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973
Db 2541 ACCCAGAGGAACTGGAACGTCGTTCTCTACAATGGCATGGCTCCACTTCTCCCTGGGCC 2600
QY 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
Db 2601 TCCCTCTACTTGTTCGCCCCCTCATGACTTCGCGCAACTATGTCTCTCAACCTGTGCTG 2660
QY 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013
Db 2661 GCCATCTCGTGGAGGCTTCAGCGCGGAGGGTGAGCGCAATCGTCTACTCGAGCAG 2720
QY 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023
Db 2721 GACCAAGCTCATCCACATAGAAGATTGTATAGCTCCAGGAAGCCTGGACAGCAGC 2780
QY 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGlnHisAlaGluLeuArgLys 1043
Db 2781 GGAGATCCCAAG-----CTCTGCCCAATCCCCCATGACCCCCCAATGGGCACCTGACCCC 2834
QY 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer 1059
Db 2835 AGTCTC-----CCACTGGGTGGCACTAGGTCCTGTGGGCTGCGGACCTGGC--- 2885
QY 1060 HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
Db 2886 ---CCCCACTCTCACTGCAGCCGGAACCCCATGCTGTGGCCCTGGGCTCCCGAAAGAC 2942
QY 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099
Db 2943 AGTGCATGTCTTA-----GGAGGATGAGCTATGACCAAGCGCTCCCTGTCCAGC 2993
QY 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119
Db 2994 TCCCGAGCTCTTACTACGGGGCCATGGGCGCGCAAGCGGCTGGGCCAAGCCGTCTCC 3053
QY 1120 SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1139
Db 3054 AGCTGGAAC-----AGCCTCAAGCACAAAGCGCGCTGTGGCGGAGCAT 3095
QY 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu 1158
Db 3096 GAGTCCCTGTCTCTGCGAGCGCGGCGCGCGCGCGCTGTGCGAGGTGCGCGGAC 3155
QY 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3156 GAGGGGCGCGCGGCGCGCACCCCTGCACACCCACACAGCCCAACCATTCATCAGGG 3215
QY 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181

Db 3216 CCCCATCTGGCGCACCGGCCAACCGCACCGCGCGGACGCTGTCCCTCGACAACAGGAC 3275
QY 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201
Db 3276 TCGGTGACCTGGCGGCACTGGTGCCCGGGTGGGGCGCCACCCCGGGCGCGCTGAGG 3335
QY 1202 SerSer-----AlaSerGlnHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db 3336 GCGCGAGCGCGCGCGCGCGCATGAGACTGCAATGGCAGGATGCCACG-----ATC 3389
QY 1220 AlaArgThrLeuArgThrAsp--AspProGlnLeuAspGlyAspAspAspAsnAspGlu 1238
Db 3390 GCCAAAGACGCTTTCACCAAGATGGGCGGACCGCGGGATCGCGGGAGGATGAGAGGAA 3449
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Db 3450 ATGCACTACACCCCTGTGCTCCGCGTCCGCAAGATGATCGACGTCTATTAAGCCGACTGG 3509
QY 1259 CysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgArgLeu 1278
Db 3510 TCGGAGGTCCGCGAAGACTGTGTCTACTCTTCTCTCCGAGAAAGGTTCCGGGTC 3569
QY 1279 LeuCysHisArgIleIleThrHisLysMetPheAspHisValLeuValIleIlePhe 1298
Db 3570 CTGTGTCAACCATATATGTGCCACAACCTCTTCGACTACGTGCTGTGGCTTCATCTTT 3629
QY 1299 LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318
Db 3630 CTCAACTGCATCACCATCGCCCTTGAGCGGCTCAAGATCGAGCGCGGACCAACGAAACGC 3689
QY 1319 IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal 1338
Db 3690 ATCTTTCTACCGTGTGCACTACATCTTCACGGCCATCTTCGTGGCGAGATGACATTG 3749
QY 1339 LysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn 1358
Db 3750 AAGTAGTCTCGCTGGGCTGTACTTCGGCAGCAGGCGTACCTACGCAAGCAGCTGGAAC 3809
QY 1359 ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer 1378
Db 3810 GTGCTGAGTGGCTTCTTGTCTTCGTCTCATGACATCGTGTGCTCCCTGGCCTCA 3869
QY 1379 AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1398
Db 3870 GCCGGGGAAGCAAGATCTGGGGGTCTCCGAGTCTTGCGGCTCCTGCGCACCTTACGC 3929
QY 1399 ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer 1418
Db 3930 CCCCTGGTGTCACTACGCGGCGCGCGGCTGAAGCTGTGTGGAGACACTATCTCC 3989
QY 1419 SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIlePheGly 1438
Db 3990 TCCCTGAAGCCCATCGGCAACATCGTGTCTATCTGTGCTCTTCATCATCTTTGGC 4049
QY 1439 IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg 1458
Db 4050 ATCTGGGAGTGACGCTCTTCAAGGGCAAGTCTTACCACTGTCTGGCGGTGACACCCGC 4109
QY 1459 AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr 1478
Db 4110 AACATCACCAACGCGCTCGACTGCATGGCGCCCAACTACCGCTGGGTCCATCAAAATAC 4169
QY 1479 AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly 1498
Db 4170 AACTTCGAACACTGGCGCAGGCTGTGATGTCCCTTGTCTGTGCATCCAGGATGGT 4229
QY 1499 TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet 1518
Db 4230 TGGGTGAACATCATGTACAATGGACTGGATGTGTGCTGTGACACGACGCTGTGACC 4289
QY 1519 AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe 1538
Db 4290 AACCAACAACCCCTGGATGTGTGTACTTCACTCTCTCTGCTCATGTGTGACTTCTTT 4349

QY 1539 ValLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGln 1558
Db 4350 GTGCTCAACATGTTGTGGGTGTCGTGGTGAAGAACTTCCACAAGTGGCGGACAGCAG 4409
QY 1559 GluGluGluGluValAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArg 1578
Db 4410 GAGGCTGAAGAGGACGCGGCGGTGAGAGAGAGCGGCTCGGCGCTTGAGAGAAAGACCGC 4469
QY 1579 ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer 1598
Db 4470 CGG-----AAGGCCAGCGGCTGCCCTACTATGCCACTATTGT 4508
QY 1599 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1618
Db 4509 CACACCGCGGCTGCTCATCCATGTCAGACCACTACCTGACATCTTCATCACC 4568
QY 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnProGlnIle 1638
Db 4569 TTCATCATCTGCCCTCAACGTCGTCAACCATGTCCCTGGAGCACTACAATCAGCCACGTCC 4628
QY 1639 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer 1658
Db 4629 CTGGAGACAGCCCTCAAGTACTGCCAATAATATGTTCAACACTGTCTTGTGCTGAGGCT 4688
QY 1659 ValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1678
Db 4689 GTGCTGAAGCTGTGGCATTTGGTCTGAGGCGCTTCTTCAAGAACCGATGGAAACCAAGCTG 4748
QY 1679 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1698
Db 4749 GACCTGGCCATTGTGCTACTGTCAGTGAGGCATCACTCGAGGATCGAGATCAAT 4808
QY 1699 LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1718
Db 4809 GCGGCGCTGCCCATCAATCCCACTCATCCGCATCATGAGGTTCTCGGCATTGCCCGA 4868
QY 1719 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738
Db 4869 GTGCTGAAGCTGTTGAAGATGCCACAGGAATGCGGCGCTGTGACACGCTGTGCAA 4928
QY 1739 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1758
Db 4929 GCTTTGCCCCAGGTGGGCAACTGGGCTCTCTTTCATGCTGCTCTTTCATCTATGCT 4988
QY 1759 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1778
Db 4989 GCTCTCGGGGTGAGCTTTTGGGAAGCTGTGTCAAAGAGAGAACCCGTGCGAGGGC 5048
QY 1779 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1798
Db 5049 ATGAGCCGGCATGCCACCTTCAGAACTTCGGCATGCGCTTCCACACTCTTCAGAGTC 5108
QY 1799 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys--AspGln 1817
Db 5109 TCCACGGGTGACAACTGAAACGGGATCATGAAGACACGCTGCGGACTGCACCCACGAC 5168
QY 1818 GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal 1835
Db 5169 GAGCGCAGCTGCTGAGCAGCGCTGCAGTTGTGTGTCGCCCTGTACTTCGTGAGCTTCGTG 5228
QY 1836 LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu 1855
Db 5229 CTACACCGCGCAGTTCTGTCTCATCAACGTGTGTGGTGTGCTGTCTCATGAAGACACTGGAC 5288
QY 1856 GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluGluMet 1875
Db 5289 GACAGCAACAAGAGGCGCAGAGGAGCGCCGAGATGATGCCGAGCTCGAGCTGAGAGATG 5348
QY 1876 ---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly 1894
Db 5349 GCCCATGGCCTGGGCCCTGGGCCGAGGCTGCTTACCGGCTCC----- 5390

QY 1895 ValGluGlyValAsnSerThrAspSerProGlyAlaProHisThrThrAlaHis 1914
Db 5391 ----- 5414
QY 1915 IleGlyAlaAsnSerGlyPheSerLeuGluHisProThrMetValPro----- 1930
Db 5415 ---GGAGGGCGGCGCGG--GGCGACACCGAGGCGGCTTGTGCGGCGCTGTACTC 5470
QY 1931 -----HisProGluGluValProValPro 1938
Db 5471 GCCTGCCAGACTCCTTGAGGGGAGCTGACCATCATGCACAACCTGTGCGGCTCAT 5530
QY 1939 LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958
Db 5531 CTTCCACCACTACTCTCGCCTGCCGCTGCCAAGAAGTCA-----CCA 5575
QY 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly 1978
Db 5576 CGACAA-----GCAAGAGGTGACGCTGGCTGAGACGGA 5608
QY 1979 TrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp 1998
Db 5609 GGCCTTCTCCCTGAACCTCAGACAGTCTCTGTCATCTGTGGGTGACGACCTGAGTCT 5668
QY 1999 ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla 2018
Db 5669 CGAGGA-----CCCCACAGCCTG 5686
QY 2019 ProThrTrpGlyAlaIleProLys----- 2026
Db 5687 CCCACCTG-----CCGCAAGGACAGCAAGGTGAGCTGGAACCACTGAGCCCAT 5737
QY 2027 ---LeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAla 2045
Db 5738 GCGTGTGGAGACTGGGCGGAATGCTTCCCTTGT--CCTCTACGGCGCTCGCCGG 5796
QY 2046 IleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu 2065
Db 5797 ATCCAGAGAACTTCTGT--GTGAGTGAAGAGATCCCAT-----TCAACC 5841
QY 2066 ValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSerIle 2085
Db 5842 CTGTCCGGTCTGCTGAACATGACA----- 5868
QY 2086 GlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla 2105
Db 5869 -----GCAGTCAAGCACCCCAAGTCCCTTCT 5895
QY 2106 ProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeu 2125
Db 5896 CCC-----CGATGCCCTCCAGCC----- 5913
QY 2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGlu 2145
Db 5914 -----CTCTCTGCCCATGCCAGCGGAGTTCTTCCACCTG 5949
QY 2146 ProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSerCys 2163
Db 5950 CAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGCACTGGCACTGGAACCTCCCAAGA 6009
QY 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys 2183
Db 6010 TTGCGCTG-CAGGCTCTCTGGGCATCT-----CTGCGGTCAACCAAGGTCAACTGT 6059
QY 2184 Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu 2199
Db 6060 ACCCTCTCCGGCAGGCCACCGGAGGACACGTGCTGAGCGCCAGCCCAAGCAG--CTC 6118
QY 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSer 2219
Db 6119 CGCGGGCAGCCTGCAAGCACCGCTCGAGGACAGCCTGACCTGAGCGACAGCCCGGCG 6178
QY 2220 IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly 2237

Db 6179 -----TGCCTGGGGCGCGCCCTGCTCCAGACCCCGGGC 6217
QY 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257
Db 6218 CGGCTGTCCCCCGCGCTCGCGCCCTGAGCCTGCGCGCGCGGCTTTCAGCCT 6277
QY 2258 LeuAspSerThrAlaAlaSerProSerProLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6278 GCGGGGCTGCGGGCGCATCAGCGCACACAGCAGCGGGGGCTCCACCAGCCCGGGCTG 6337
RESULT 7
US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGiven, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS, COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5420.00 Matches: 1223
Percent Similarity: 61.74% Conservative: 234
Best Local Similarity: 51.82% Mismatches: 494
Query Match: 45.06% Indels: 413
DB: 4 Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-935-541-1 (1-6816)

QY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCCGCTCTCTCATCTGCAGCAGCCCCCAGCGCTGAGCCAGAGTCAACACGAGCAG 266
QY 26 ProGlyProArgLeuAlaArgGlyTTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCGG----- 278
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCTCCCGCCAGCCTGAGAGCCTCTGATGAGCT----- 326
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
QY 86 ProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAGACCTGGCGCTATTGCTCTTCTGCTGCGACAGACCAACACCGCCGGAAGTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGTTGCAACCCGTTGTAATGTGTCAAGCATGCTGTGATCCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGCGTGAACATTGGCATGTACCAAGCCGTGCGACGACATGACTGCTGTCCGACCGC 524

QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
Db 525 TGCAAGATCCTGCAGGTCTTTGATGACTTCACTTATCTTCTTTGGCATGAGATGTGTG 584
QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
Db 585 CTCAAGATGTGGCCCTGGGGAATTTTGGCAAGAGTGTACTACCTCGGGGACACATGGAAC 644
QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCTGGATTCTTCATCGTCAATGCGAGGATGTCGAGTACTCCCTGACCTTCAGAAC 704
QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 705 ATCAACCTGTACGCCATCCGACCGGTGCGCTGTGAGGCCCTCAAGCCATCAACCGC 764
QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 765 GTGCCAGTATGCGGATCGGTGAACCTGTCTCTGACACACTGCCATGCTGGGAAT 824
QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
Db 825 GTCTGTGCTCTGCTTCTTGTCTTCTTCACTTTGGCATCATAGGTGTGACGCTCTGG 884
QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
Db 885 GCGGGCTGTGCTGCTAACCGCTGCTCTCGAGAGAGAACTTCAACATACAGCGGATGTG 944
QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
Db 945 GCCTTGCCCCATACTACTACCGCGGAGGAGGATGAGATGCCCTTCACTGCTCCCTG 1004
QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
Db 1005 TCGGGGCAATGGATATGCGCTGCCATGAGATCCCCCGCTCAAGGAGCAG----- 1058
QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 ---GGCGGTGAGTGTGCTGCTGTCCCAAGACGACGCTCACTTGGGGCGGGCCGACG 1115
QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1116 GACCTCATGCGCAGCGGCTGTGTCACTGAACCGTTACTACAATGTGTGCCGACG 1175
QY 358 GlyGluHisAsnProPheGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
Db 1176 GGCAGCGGCAACCCCAACAGGGTCCATCACTTTCACAACATCGGTTATGCTTGATTT 1235
QY 378 AlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAsp 397
Db 1236 GTCATCTTCCAGGTGATCACTGTGAAGGCTGGTGAGATCATGTACTACTGATGAT 1295
QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
Db 1296 GCTCACTCTTCTACAACCTTCACTTCACTTCACTTATCATAGTGGGCTCTTCTTC 1355
QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTGTTGTACATAGCAGACCACTTCTCGAGACCAACGAGAG 1415
QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGGCTGATGTGAGCAGCGGAGCGGTACTCTGC---TCCAGCAGGTGGCCAGC 1472
QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TACGCCGAGCTGGCGACTGTCTACGAGGAGATCTTCCAGTATGTCTGCCACATCTGCGC 1532
QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGGCCAAGCGC-----CGCGCCCTGGGGCTCTTACCAGGCGCTGCAG 1574

Qy 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
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Db 1575 AGC----- 1577
Qy 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyr 537
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Db 1578 ---CGGCGCCAGGCCCTG----- 1592
Qy 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
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Db 1593 -----GGCCCGGAG----- 1601
Qy 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577
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Db 1602 -----GCCCGGGCCCGCCAAACCTGGGCC----- 1628
Qy 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
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Db 1629 -----CACGCCAAG-----GAGCCC 1643
Qy 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
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Db 1644 CGGCACTACCAGCTGTGCCCAACATAGCCCCCTGGATGCG----- 1685
Qy 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
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Db 1686 -----ACGCCCAACAC----- 1697
Qy 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
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Db 1698 ---CTGGTCAG-----CCCATCCCCGCCCAAGCTGGCTTCC----- 1730
Qy 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
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Db 1731 -----GATCCCCAGCTGCCCTTGCTGCCAG 1757
Qy 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
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Db 1758 CATGAGACCGCGCGGCTTCGGGCTGGGAGCAACCGACTCGGGCCAGAGGGCTCG 1817
Qy 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
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Db 1818 GGCTCC-----GGGAGCTCCGCTGGTGGCGAGAGAGCG----- 1853
Qy 717 MetProAspSerAspSerGlyAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
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Db 1854 -----GATGGGAGCGGGCC-----CGGAGCAGCGAGGACCGAGCCTCCTCAGAA 1898
Qy 737 LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
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Db 1899 CTGGGGAAGGAGGAGGAGGAGGAGCAG-----GCCGATGGGGCG 1940
Qy 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
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Db 1941 GTCTGGCTGTGCGGGAGTGTGTGGCGGAGAGCGGAGCCAAAGCTGCGGCATCTGTGAC 2000
Qy 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
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Db 2001 AGCAAGTACTTCAACCGGGCATGATGATGGCCATCTGTCAACACCGTCAGCATGGGC 2060
Qy 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
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Db 2061 ATCGAGCACCAAGAGCAGCGGAGAGAGAGCTGACCAACATCTGAGATCTGCAATGTGTC 2120
Qy 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGly 834
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Db 2121 TTCAACCAGCATGTTTGCCCTGAGATGATCTCTGAAGCTGGCTGCATTTGGGCTCTTCGAC 2180
Qy 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGlu 854
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Db 2181 TACCTGCGTAACCCCTACACATCTTCGACAGCAATCTTCATCATCAGCATCTGGGAG 2240
Qy 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874

Db 2241 ATCGTGGGCGAGCGGAGCGGTGGGTCTCGGTCTCGGAGCCTTCCGGCTGCTGCGGTG 2300
Qy 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
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Db 2301 CTGAACCTGTGGCGCTTCATGCTCGCTCGCGGCGCCAGCTGTGGTCTCATGAAGACC 2360
Qy 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIle 914
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Db 2361 ATGGAACAGTGCGCACCTTCTGCATGCTGTCTCATGCTTCATCTTCATCTTCAGATC 2420
Qy 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933
|||||
Db 2421 CTGGGATGCAATTTTGTGGCTGCAAGTTCAAGCTCCGCAAGCACTGGAGACAGGTG 2480
Qy 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
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Db 2481 CCCGACAGGAAGACTTCGACTCCCTGTGTGGCCATCGTCACTGTGTCCAGATCCTC 2540
Qy 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973
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Db 2541 ACCCAGAGGAGCTGGAACGTCGTTCTTCAATGGCATGGCTCCACTTCTCCCTGGGCC 2600
Qy 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
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Db 2601 TCCCTTACTTTGTTCGCCCTCATGACTTTCGGCACTATGTCTCTTCAACCTGCTGTG 2660
Qy 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013
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Db 2661 GCCATCTGTGGAGGGCTTCCAGGGGAGGTGACGCGCAATCGCTCTACTCGGACGAG 2720
Qy 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023
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Db 2721 GACCAGAGCTCATCCAAACATAGAAGATTGTATAGCTCCAGAAAGCCTGACAGACG 2780
Qy 1024 GlyAspArgLysValArgLeuAlaLeuValAlaLeuGlyGlnHisAlaGluLeuArgLys 1043
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Db 2781 GGAGATCCCAAG-----CTGTGCCCAATCCCATGACCCCCCAATGGGCACCTGACCCC 2834
Qy 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer 1059
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Db 2835 AGTCTC-----CCTGGTGGGACCTAAGTCTGTGGGGCTGGGAGCCTGCC--- 2885
Qy 1060 HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
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Db 2886 ---CCCCAGCTTCACTGCAGCCGAGCCCATGCTGTGGGCCCTGGGCTCCCGAAGAGC 2942
Qy 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisIleGluMetLysCysProProSer 1099
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Db 2943 AGTGCATGTCTGTA-----GGGAGATGAGCTATGACCAAGCCTCCTGTGCAGC 2993
Qy 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119
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Db 2994 TCCCGGAGCTCTACTACGCGGCATGGGGCCGACGCGGCTGGGCCAGCCGTGCTCC 3053
Qy 1120 SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1139
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Db 3054 AGCTGGAAC-----AGCCTCAAGCACAGCCGCCGCTCGCGGAGCAT 3095
Qy 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluLysSerGlu 1158
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Db 3096 GAGTCCCTGCTTCTGCGGAGCGCGGGCGGGCGGCCCGGGTCTCGAGGTGCCCGGAC 3155
Qy 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
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Db 3156 GAGGGGCGCGCGGGCGGACCCCTGCACACCCACACGCGCCACACATTATACGGG 3215
Qy 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
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Db 3216 CCCCATCTGGCGCACCGCACCGGCACCGCGGAGCGGTGTCCCTGCACAACAGGGAC 3275
Qy 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201
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QY	1915	ILEGLAAlaAspGlyPheSerLeuGluHisProThrMetValPro-----	1930
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Db	5415	--GGAGGGCGGGCGCGG-GGGCGACACCGAGGGCGGCTGTGCGGGCTGCTACTC	5470
QY	1931	-----HisProGluGluValPro	1938
Db	5471	GCCTGCCAGACTCTTGAGAGGGAGCTGACCATCATCGAACACTGTGGGCTCCAT	5530
QY	1939	LeuGlyProAspLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro	1958
Db	5531	CTTCCACCACCTACTCTCTCGCCTGCGGCTGCAGAAAGTGTCA-----CCA	5575
QY	1959	AsnAspSerTyrMetCysArgAsnGlySerThrIaGluArgSerLeuGlyHisArgGly	1978
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Db	5576	CGACAA-----GCAAGAGGTGCAGCTGGCTGACAGCGA	5608
QY	1979	TrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp	1998
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Db	5609	GGCCTTCTCCCTGAAGCTCAGACAGAGTCTCTGTCATCTCTGGGTGACGACTGAGTCT	5668
QY	1999	ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla	2018
Db	5669	CGAGGA-----CCCAAGACCTG	5686
QY	2019	ProThrTrpGlyAlaIleProLys-----	2026
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Db	5687	CCCACCTGG-----CCGCAAGACAGCAGGGGTGAGCTGAGCCACCTGAGCCCAT	5737
QY	2027	--LeuProProGluArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAla	2045
Db	5738	GGGTGTGGAGAGCCTGGGCGAATGCTTCTTCCCTTGT-CCTTACGGCGCTTCGCCGG	5796
QY	2046	IleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu	2065
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Db	5797	ATCCAGAGAACTTCTGT--GTGAGATGAGAGAGATCCCAT-----TCAACC	5841
QY	2066	ValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSerIle	2085
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Db	5842	CTGTCCGGTCTGCTGAACATGACA-----	5868
QY	2086	GlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla	2105
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Db	5869	-----GCAATCAAGCACCCCAAGTCCCTTCT	5895
QY	2106	ProCysProGlyLeuGluProSerTrpAlaLysAspProGluThrArgSerSerLeu	2125
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Db	5896	CCC-----CGAATGCTCCAGCC-----	5913
QY	2126	GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu	2145
Db	5914	-----CTCTCCTGCCCATGCCAGCGAGTCTTCCACCTG	5949
QY	2146	ProLeuPhePro----ArgAspLeuLysCysTyrSerValGluThrGlnSerCys	2163
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Db	5950	CAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGGCACTGGCACTGGAACCTCCCAAGA	6009
QY	2164	ArgArgArgProGlyPheThrLeuAspGluGlnArgHisSerIleAlaValSerCys	2183
Db	6010	TTCGCTG-CAGGGCTCTGGGCATCT-----CTGGGTCAACCAAGGTCAACTGT	6059
QY	2184	Ieu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu	2199
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Db	6060	ACCCTCTCCGGCAGGCCACCGGAGCGACACAGTCGCTGGAGCCAGCCCCAGCAG-CTC	6118
QY	2200	GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSer	2219
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Db	6119	CGCGGGCAGCCTGCAGACCAAGCTCGAGGACAGACCTTAACCTGAGCGACAGCCCGGGCG	6178
QY	2220	IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly	2237
		:::	
Db	6179	-----TGCCCTGGGGCGCCCGCCCTGCTCCAGGACCCCGGGC	6217
QY	2238	ValCysLeuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro	2257

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Db      6218 CGGCGTGTCCCCCGCGCTCGCCGCCGCTGAGCCTCGCGCGGCGGCGCTTTCAGCCT 6227
QY      2258 LeuaspSerThrAlaIaSerProSerProIysIysAspThrLeuSerLeuSergIyleu 2277
Db      6278 GCGGGGGCTCGCGGCGCATCAGCCGACGACAGCAGCGGGGGCTCCACCAGCCGGGCTG 633

RESULT 8
US-09-404-650-3
; Sequence 3, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGiveern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-404-650-3

Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 61.97% Conservative: 235
Best Local Similarity: 52.01% Mismatches: 500
Query Match: 45.06% Indels: 402
DB: 3 Gaps: 63

US-09-611-257A-24 (1-2287) x US-09-404-650-3 (1-6855)
QY      12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
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Db      207 TCCCCGCCCTCCTCATCTGCAGCAGCCCGCAGCCGCTGAGCCAGAGTCAACCGAGCAG 266
QY      26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
      |||||
Db      267 CCGGAGCCCGG----- 278
QY      46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaIaGly 65
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Db      279 -----AGCCCCCATCCTCCCGCCGACGCGCTGAGAGCCTCTGATGAGCT----- 326
QY      66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
      |||||
Db      327 -----GATCCT-----CATGTCCACAC 344
QY      86 ProAlaLeuAlaProValValPhePheTyrLeuSergIlnAspSerArgProArgSerTrp 105
      |||||::|::|::|::|::|::|::|::|::|::|::|::|
Db      345 CCAGACTGGCGCCTATTGCTTCTTCTGCTGCAGACAGACCACGACCCCGGAACTGG 404
QY      106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeu 125
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Db      405 TGCATCAAGATGTGTGCAACCGGTGTGAATGTGTCAAGCATGTGTGATCTGCTG 464
QY      126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSergIlnArg 145
      |||||::|::|::|::|::|::|::|::|::|::|::|::|
Db      465 AACTGCGTGACACTTGGCATGTATCACGCGGTGCGAGCATGACTGCTGTCCGACCGC 524
QY      146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
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Db      525 TGCAAGATCCTGCAGGTCTTTGATGACTTCATCTTATCTTCTTTGCCATGAGATGTGTG 584
QY      166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185

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QY	895	MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIle	914
Db	2361	ATGACAAACGTGGCCACCTTCTGCATGCTGCTCATGCTCTTCATCTTCATCTTCAGCATC	2420
QY	915	LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp--GlyAspThrLeu	933
Db	2421	CTTGGATGATATTATTTTGGCTGCAGATTCAAGCCTCCGACAGGACACTGGAGACAGGTG	2480
QY	934	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	953
Db	2481	CCCGACAGGAAGAACTTCGACTCCCTGCTGTGGGCCATCGTCACTGTGTTCAGATCCTC	2540
QY	954	ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla	973
Db	2541	ACCCAGGAGGACTGGAACTGCTCTTCTTACAATGGCAATGGCTCCACTTCTCCCTGGGCC	2600
QY	974	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal	993
Db	2601	TCCCTCTACTTGTTCGCTCATGACCTTCGGCACTAATGTGCTCTTCAACCTGCTGTG	2660
QY	994	AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro	1013
Db	2661	GCCATCCTGTGTGAGGGCTTCAGCGGAGGATGACGCCAATCGCTCTACTCGGACGAG	2720
QY	1014	AspPhePheSerProSerVal-----AspGlyAsp	1023
Db	2721	GACCAGAGCTCATCCAACATAGAAGATTGTATAGCTCCAGGAAGCCTGGACAGCAC	2780
QY	1024	GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys	1043
Db	2781	GGAGATCCCAAG-----CTCTGCCCAATCCCATGACCCCAATGGGCACCTGGACCCC	2834
QY	1044	SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer	1059
Db	2835	AGTCTC-----CCACTGGGTGGGCACCTAGTCTGTGGGGCTGGGACCTGCC--	2885
QY	1060	HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr	1079
Db	2886	---CCCCGACTCTCACTGCAGCCGAGCCCATGCTGTGGTGGCTGGGCTCCGGAAGAGC	2942
QY	1080	SerSerSerGlySerAlaGluProGlyAlaAlaHisIleGluMetLysCysProProSer	1099
Db	2943	AGTGTCACTGTCTTA-----GGAGGATGAGCTATGACCAAGCGCTCCCTGTCCAGC	2993
QY	1100	AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer	1119
Db	2994	TCCCGAGCTCTTACTACGGGCTCATGGGGCCGAGCCGCGCTGGGCCAGCCGTGCTTC	3053
QY	1120	SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg	1139
Db	3054	AGCTGGAAC-----AGCCTCAAGACAAGCCGCGCTGGCGGAGCAT	3095
QY	1140	ArgSerLeuLeuSerGlyGlu--GlyGlnGluSerGlnAspGluGluGluSerSerGlu	1158
Db	3096	GAGTCCCTGCTCTTGCAGAGCGCGCGCGCGCGCGGCTTGCAGAGTTGCGCGGAGC	3155
QY	1159	Glu-----AspArgAlaSerProAlaGlySerAspHis-----	1169
Db	3156	GAGGGGGCGCGCGCGCGCACCCCTGCACACACCCACACGCCCCACACATTATCACGGG	3215
QY	1170	-----ArgHisArgGlySerLeuGluArgGluAlaLysSer	1181
Db	3216	CCCCATCTGGCGACCGCCACCGCACCCGCGGACGCTGTCCCTGCACAACAGGAGAC	3275
QY	1182	SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg	1201
Db	3276	TGGGTGACCTGGCGCAAGCTGTGCCCGCGGTGGCGCCACCCCCGGCGCGCTGAGG	3335
QY	1202	SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu	1219
Db	3336	GCGGCAAGCCCGGCCCGCGGCATGAGGACTGCATATGGCAGATGCCAGC-----ATC	3389

OY		1220	AlaArgThrLeuArgThraSp---AspProGlnLeuAspGlyAspAspaAsnAspGlu	1238
Db		3390	GCCAAAGACGTCTTCACCAGAATGGCGCACCGCGGGGATCGCGGAGATGAGAGGA	3449
OY		1239	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys	1258
Db		3450	ATGCATACACCCCTGTGCTTCCGCGTCCGCAAGATGATGACGTTATAAGCCGACTGG	3509
OY		1259	CysArgGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeu	1278
Db		3510	TGCCAGGTCCGCGAAGACTGGTGTCGTCTACCTCTTCTCCGAGAACAGGTTCCGGGTC	3569
OY		1279	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe	1298
Db		3570	CTGTGTCAgACCATATTATGCCCAAACTCTTGACATACGTGCTCGCTTCATCTTT	3629
OY		1299	LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg	1318
Db		3630	CTCAACTGCATCACCATCGCCCTGAGCGGCGCTCAGATCGAGCGCGGACGACCGAACGC	3689
OY		1319	IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal	1338
Db		3690	ATCTTCTCACCGGTGTCCAACATCATCTTCACGGCCATCTTCTGGCGGAGATGACATTG	3749
OY		1339	LysValValAlaLeuGlyTyrCysPheGlyGlyGlnAlaTyrLeuArgSerSerTrpAsn	1358
Db		3750	AAGTAGTCTCGCTGGCGCTGTACTTCGGCAGACGGCTAACCTACGACAGCAGCTGGAAC	3809
OY		1359	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer	1378
Db		3810	GTGCTGATGGCTTCTTGTCTTCGTCCATCATCGACATCGTGTGTCCTCGGCTCA	3869
OY		1379	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
Db		3870	GCCGGGGGAGCCAAAGATCTGGGGCTCTCCGAGTCTGGGCTCCTGCGCACCTACGC	3929
OY		1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1418
Db		3930	CCCCTGCGTGTATCAGCCGGCGCGGGCTGAAGCTGTGTGGAGACACTCATCTCC	3989
OY		1419	SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly	1438
Db		3990	TCCCTCAAGCCCATCGGCACAACATCGTCTCATCTGCTGCTTCTTCATCATCTTTGGC	4049
OY		1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1458
Db		4050	ATCCTGGAGTGCAGCTCTTCAAGGCAAGTTCTACCACTGCTGGCGTGCACACCCGC	4109
OY		1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr	1478
Db		4110	AACATCACCAACCGCTCGAGCTGCATGGCCGCCAACATACCGCTGGGTCCATCAAAATAC	4169
OY		1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
Db		4170	AACTTCGACAACTGGGCCAGGCTGTGATGTCCCTCTTGTCTCGCATCCAAGATGT	4229
OY		1499	TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet	1518
Db		4230	TGGGTGAACATCATGTACAATGACTGGATGCTGTGCTGTGGACCAAGACCTGTGACC	4289
OY		1519	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe	1538
Db		4290	AACCAACACCCCTGGATGCTGCTACTTCATCTCCCTCTGCTCATCGTCAAGTCTTT	4349
OY		1539	ValLeuAsnMetPheValGlyValValAlaGluAsnPheHisLysCysArgGlnHisGln	1558
Db		4350	GTGCTCAACATGTTGTGGGTGTGTGGTGAAGACTTCCACAAGTCCGGGACCAACAG	4409
OY		1559	GluGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArg	1578
Db		4410	GAGGCTGAAGAGGCAACGGCGCGGTGAGGAGAACGGGCTGCGGCGCTGGAGAGAACGCC	4469
OY		1579	ArgSerLysGluLysGlnMetalGluAlaGlnCysLysProTyrTyrSerAspTyrSer	1598

Db 4470 CGG-----AAGCCGCGGCTGCCCTACTATGCCACCTATTGT 4508
QY 1599 ArgPheArgLeuLeuValHisIleuCysThrSerHisTyrLeuAspLeuPheIleThr 1618
Db 4509 CACACCCGGCTGCTCATCCACTCCATGTGCACCGACCACTGACATCTTCATCAACC 4568
QY 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1638
Db 4569 TTCATCATCTGCCTCAACGTGGTCAACCATGTCCCTGGAGCACTACAATCAGCCCCAGCTCC 4628
QY 1639 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer 1658
Db 4629 CTGGAGACAGCCCTCAAGTACTGCACTATATGTTCAACCACTGTCTTGTGTGAGGGCT 4688
QY 1659 ValPheLeuLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1678
Db 4689 GTGCTGAAGCTGTGGCATTTGGTGTGAGCGCTTCTTCAAGACCGATGAACCAAGCTG 4748
QY 1679 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1698
Db 4749 GACCTGGCCATTGTGCTACTGTCAGTCAATGGGCATCACCTGGAGAGATCGAGATCAAT 4808
QY 1699 LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1718
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QY 1719 ValLeuLeuLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738
Db 4869 GTGCTGAAGCTGTGAAGATGGCCACAGAAATGGCGCCCTGCTGACACAGGTGTGCAA 4928
QY 1739 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1758
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QY 1759 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1778
Db 4989 GCTCTCGGGGTGAGCTCTTTGGAGCTGGTCTGCAACGACGAGAACCCGTGCGAGGGC 5048
QY 1779 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1798
Db 5049 ATGAGCCGGCATGCCACCTCGAAGACTTCGGCATGCGCTTCTCACACTCTTCCAGGTC 5108
QY 1799 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys--AspGln 1817
Db 5109 TCCACGGGTGACAACTGGAACGGGATCATGAAGACACGCTGCGGGACTGCACCCACGAC 5168
QY 1818 GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal 1835
Db 5169 GAGCGCAGCTGCTGAGCAGCCTGCAGTTGTGTGCGCGCTGTACTTCGTGAGCTTCGTG 5228
QY 1836 LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu 1855
Db 5229 CTCACCGCGCAGTTCGTGCTCATCAACGTGGTGTGCTGCTCATGAAGACACCTGAC 5288
QY 1856 GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMet 1875
Db 5289 GACAGCAACAAGAGCGCGCAGAGACCCGAGATGATGCCAGCTCGAGCTGAGATG 5348
QY 1876 ---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro--- 1893
Db 5349 GCCCATGGCTGGGCCCTGGCCCGAGGCTGCTTACCGGCTCCCGGGGCC--CCTGGC 5405
QY 1894 -----GlyValGluGlyValAsnSerThrAsp----- 1902
Db 5406 CGAGGCGCGGAGGCGCGGCGCGGCGGCGACACCGAGGCGGCTGTGCGCGGCTGC 5465
QY 1903 ---SerProLysProGlyAlaPro-----HisThrThrAlaHisIleGlyAla 1917
Db 5466 TACTCGCTGC-CCAGAGAACTGTGTGTGACAGCGTCTTTAATCATCAAGGACTC 5524
QY 1918 AlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProVal 1937

Db 5525 CTTGGAGGG---GGAGCTGACCAT-----CATGCAACACTGTGCGGCTC 5566
QY 1938 ProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 1957
Db 5567 CATCTTCCACCACTACTCTCTGCCCTGCCGCGTGCAGAAGTGTCA----- 5611
QY 1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977
Db 5612 CCACGACAA-----GCAAGAGTGCAGCTGGCTGAGAC 5644
QY 1978 GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997
Db 5645 GGAGGCTTCTCCCTGAAGTCAAGACAGTCTCTGTCATCTGTGGTGAAGCACTGAG 5704
QY 1998 AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017
Db 5705 TCTCGAGGA-----CCCCACAGC 5722
QY 2018 AlaProThrTrpGlyAlaIleProLysLeuProPro----- 2029
Db 5723 CTGCCCACTGG-----CCGCAAAAGACAGCAAGGCTGAGCTGACCCCACTGAGCC 5773
QY 2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044
Db 5774 CATGCGTGTGGAGACCTGGCGGAATGCTTCTTCCCTTGT-CCTTACGGCGGCTCTCGC 5832
QY 2045 AlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSer 2064
Db 5833 CGGATCAGAGAACTTCTGT--GTGAGATGAGAGATCCCAT-----TCA 5877
QY 2065 GluValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSer 2084
Db 5878 ACCGTGCCGTCTGCTGTAACATGACA----- 5907
QY 2085 IleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuPro 2104
Db 5908 -----GCAGTCAAGCACCCCAAGTCCCT 5931
QY 2105 AlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSer 2124
Db 5932 TCTCC-----CGAGTCCCTCAGCC----- 5952
QY 2125 LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2144
Db 5953 -----CTCTCGCCCATGCCAGCGGAGTCTTCCACC 5985
QY 2145 GluProLeuPhePro-----ArgAspLeuLysCysTyrSerValGluThrGlnSer 2162
Db 5986 CTGCAGTGTCTGCCAGCAGAAAGCCAGAAAGGCCACTGGCACTGMAACCTCCCA 6045
QY 2163 CysArgArgArgProGlyPheThrLeuAspGluGlnArgArgHisSerIleAlaValSer 2182
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Db 6096 TGTACCTCTCTCCGCGCAGGCCACCGGAGCGACACAGTCCGTGACGCCAGCCAGCAG- 6154
QY 2199 LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro 2218
Db 6155 CTCCGCGGCGAGCTGCAGACCAAGCTGCAGAGACAGCTGACCTGAGCGCAGCCCCCG 6214
QY 2219 SerIleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----Pro 2236
Db 6215 GCG-----TGCCCTGGGCGCGCGCGCTGCTCAAGACCCCG 6253
QY 2237 GlyValCysLeuArgArgArgAlaProAlaSerAspSerLysAspProSerValSerSer 2256
Db 6254 GGCGGCTGTCCCCCGCGCTCGCGCGCTGAGCCTGCGCGCGGCGCTTTCAG 6313
QY 2257 ProLeuAspSerThrAlaIleSerProSerProLysLysAspThrLeuSerLeuSerGly 2276
Db 6314 CTTGCGGGGCTGCGGCGCATCAAGCAGCAAGCAGCGGGGCTCCACAGCCCGG 6373

QY 2277 Leu 2277
Db 6374 CTG 6376

RESULT 9
US-09-935-541-3

/ Sequence 3, Application US/09935541
/ Patent No. 6589787
/ GENERAL INFORMATION:
/ APPLICANT: Dietrich, Paul S.
/ APPLICANT: McGiven, Joseph G.
/ TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
/ TITLE OF INVENTION: AND USES
/ FILE REFERENCE: R0043B-REG sequence listing
/ CURRENT APPLICATION NUMBER: US/09/935,541
/ PRIOR FILING DATE: 2001-08-23
/ PRIOR APPLICATION NUMBER: 09/404,650
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 6855
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (192)..(6755)
US-09-935-541-3

Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 61.97% Conservative: 235
Best Local Similarity: 52.01% Mismatches: 500
Query Match: 45.06% Indels: 402
DB: 4 Gaps: 63

US-09-611-257A-24 (1-2287) x US-09-935-541-3 (1-6855)

QY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 207 TCCCCGCCCTCCTCATCTGCAGCAGCCCGCTGAGCCAGAGTCAACCAAGGAGCAG 266
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 267 CCGGACCCCGG----- 278
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 279 -----AGCCCCCATCTCTCCCGCCAGGCTGAGGAGCCTCTGTGATGGAGCT----- 326
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 327 -----GATCCT-----CATGTCCACAC 344
QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 345 CCAAGACCTGGCGCCTATTGCCTTCTTCTGCTGCAGACAGACCACCAAGCCCGGAACCTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 405 TGCATCAAGATGTTGTGCAACCCGTGTTGATGTGTCAAGCATGCTGTGATCCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 465 AACTGCGTGACACTTGGCATGTACCAAGCCGTGCGAGACATGAGACTGCTGCCAGACCGC 524
QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
Db 525 TGCAGAGATCCTGCAGGTTCTTGATGACTTCATCTTATCTTCTTGCCATGGAGATGTTG 584
QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185

Db 585 CTCAAGATGTTGCCCTTGGGATTTTGGCAAGAGTGTCTACCTCGGGGACACATGTGAAC 644
QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 645 CGCCTGATTTCTTCATGTCATATGGACAGGATGTCGAGTACTCTCGACCTTCAGAAC 704
QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 705 ATCAACCTGTACAGCATCCGCACCGTGCCTGTGAGGCCCTCAAAAGCCATCAACCGC 764
QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
Db 765 GTGCCAGTATGGCGATCCTGTGAACCTGCTCCTGGACACACTGCCATGCTGGGAAT 824
QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyTyrIleValGlyValGlnLeuTrp 265
Db 825 GTCTGTGCTGTGCTTCTTGTCTTCTTCATCTTGGCATCATAGTGTGACGCTCTGG 884
QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
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QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
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QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGlyGly 325
Db 1005 TCGGGCGACAATGGGATATGAGCTGCATGAGATCCCGCGCTCAAGAGCAG----- 1058
QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 ---GGCCGTGAGTGTCTGCTGTCCAAGACGACGTCTACGACTTTGGGCGGGCGCCAG 1115
QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGGCTGTGTGCTCACTGGAACCGCTTACTACAATGTGTGCCGACG 1175
QY 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
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QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
Db 1296 GCTCACTCCTTCAACAATTCACTTCACTCTGCTTATCATAGTGGCTCCTTCTTC 1355
QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTGTTGTATAGCGAACCGATTCTCGAGAACCAAGCAAGGAG 1415
QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGGCTGATGTGAGACAGCGGCGCTACTCTCC---TCCAGCACGTTGGCCAGC 1472
QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TACGCCGAGCCTGGCACTGTCTACGAGAGATCTTCCAGTATGTCTGCCACATCTCTGCC 1532
QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGGCCAAGCGC-----CGCGCCTGGGCTCTTACCAAGGCCCTGCAG 1574
QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC----- 1577
QY 518 HisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyr 537

Db 1578 ---CGGCGCCAGGCCCTG----- 1592
QY 538 HisLeuGluAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 -----GGCCCGGAG----- 1601
QY 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577
Db 1602 -----GCCCGCGGCCCGCCAAACCTGGGCCC----- 1628
QY 578 ProProArgGlyAlaGluSerValHisSerPheTyrrHisAlaAspCysHisLeuGluPro 597
Db 1629 -----CACGCCAAG-----GAGCCC 1643
QY 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
Db 1644 CGGCACTACCAGCTGTGCCCGCAACATAGCCCCCTGGATGCG----- 1685
QY 618 SerGlyLysValTyrrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
Db 1686 -----ACGCCCCACACC----- 1697
QY 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
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QY 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCCGCCAGCTGCCCTTGCTGCCAG 1757
QY 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1758 CATGAGGACGGCGCGGCCCTCGGGCTGGGACACCGACTCGGGCCAGAGGGCTCG 1817
QY 697 AspSerCysProTyrrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGGAGCTCCGCTGGTGGCGAGGACGAGCGC----- 1853
QY 717 MetProAspSerAspSerGluAlaValTyrrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -----GATGGGACGGGGCC-----CGGACGACGAGGACGGAGCCTCTCAGAA 1898
QY 737 LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGGAAAGAGAGAGAGAGAGAGACAG-----GCCGATGGGCG 1940
QY 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
Db 1941 GTCTGGCTGTGCGGGGATGTGTGGCGGGAGACCGGAGCCCAAGCTCGCGGCATCGTGAC 2000
QY 775 SerLysTyrrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGATCATGATGGCCATCTGTCAACACCGTCAGCATGGGC 2060
QY 795 IleGlyTyrrHisGluInProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATCAGACACACGAGCAGCGGAGAGACTGACCAACATCTGAGATCTGCAATGTGTGC 2120
QY 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrrGlyProPheGly 834
Db 2121 TTCAACAGCATGTGTCCCTGAGATGATCTGAAGCTGGCTGATTTGGCTCTTTCGAC 2180
QY 835 TyrrIleLysAsnProTyrrAsnIlePheAspGlyValIleValIleSerValTrpGlu 854
Db 2181 TACCTGGTAACCCCTACAACATCTTCGACAGCATCATTTGCATCATCAGCATCTGGAG 2240
QY 855 IleValGlyGlnGlnGlyGlyLysSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCGTGGGGCAGGGCGGACGGTGGCTGTCTGGTCTGGACCTTCCGGCTGTGCGCGTG 2300
QY 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAACCTGTGTGCGCTTCACTGCTGCCCTGGCGGCCAGCTCGTGTCTCATGAAGACC 2360

QY 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIle 914
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QY 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp--GlyAspThrLeu 933
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QY 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
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Db 2541 ACCCAGGAGACTGGAACGTCGTTCTTAACAATGGCATGGCTCCACTTCTCCCTGGGCC 2600
QY 974 AlaLeuTyrrPheIleAlaLeuMetThrPheGlyAsnTyrrValIleLeuPheAsnLeuVal 993
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QY 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013
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QY 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023
Db 2721 GACCAGAGCTCATCCAACATGAAGAAGTTGTGATAGCTCCAGGAAGCCTGACAGACAG 2780
QY 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGlnHisAlaGluLeuArgLys 1043
Db 2781 GGAGATCCCAAG-----CTTGCCCAATCCCCCATGACCCCAATGGGCACCTGACCCC 2834
QY 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrPrometSer 1059
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Db 2886 ---CCCCGACTGTCACTGCAGCCGCGACCCCATGCTGTGGCCCTGGGCTCCGAAAGAGC 2942
QY 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099
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QY 1120 SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArg 1139
Db 3054 AGCTGGAAC-----AGCTCAAGCAACAAGCCGCTCGGGCGAGCAT 3095
QY 1140 ArgSerLeuLeuSerGlyGlu--GlyGlnGluSerGlnAspGluGluGluSerSerGlu 1158
Db 3096 GAGTCCCTGTCTGTGCGGAGCGCGGCGCGCGCGCGCGGTGCGAGGTTGCGCGGAC 3155
QY 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3156 GAGGGGCGCGCGGGCGGACCCCTGCAACCCACAGCCCAACCATTCATCACGGG 3215
QY 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
Db 3216 CCCCATCTGGCGCACCGCCACCGCCAGCGGAGCGTGTCTCGACAACAGAGGAC 3275
QY 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201
Db 3276 TCGGTGACCTGGGCCGAGCTGTGCCCCGGGTGGGCGGCCACCCCGGGCGCGCTGAGG 3335
QY 1202 SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db 3336 GCGGCAAGCGCGCGCGCGGCGGATGAGAGACTGCAATGGCAGGATGCCAAGC-----ATC 3389

QY		1220	AlaArgThrLeuArgThrAsp--AspProGlnLeuAspGlyAspAspAsnAspGlu	1238
Db		3390	GCCAAAGACGTCTTCAACCAAGATGGCGCACCGCGGGATCGCGGGAGATGACGAGGA	3449
QY		1239	GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys	1258
Db		3450	ATCGACTACACCCTGTGCTTCGCCGCAAGATGCAGCTCTATAAGCCGCACTGG	3509
QY		1259	CysArgGluArgAspSerTrpSerAlaTyrlIlePheProGlnSerArgPheArgLeu	1278
Db		3510	TGCGAGGTCCGGAAGACTGGTCTGTCTACTCTCTCCCGAGAACAAGTTCCGGGTC	3569
QY		1279	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe	1298
Db		3570	CTGTGTCAAGACCATTAATTGCCCAACAACCTCTTGCACTACGTCTCGCTTCATCTT	3629
QY		1299	LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHissSerAlaGluArg	1318
Db		3630	CTCAACTGCATCACCATCGCCCTGGAGCGGCTCAGATCGAGGCGGACACCGAAGCC	3689
QY		1319	IlePheLeuThrLeuSerAsnTyrlIlePheThrAlaValPheLeuAlaGluMetThrVal	1338
Db		3690	ATCTTCTCACCGCTGCCAACATACATCTTCAACGGCCATCTTCTGGCGAGATGACATTG	3749
QY		1339	LysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrlLeuArgSerSerTrpAsn	1358
Db		3750	AAGTAGTCTCGTGGGCTGTACTTGGCGAGCAGCGCTACCTACGACAGCTGGAAC	3809
QY		1359	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer	1378
Db		3810	GTGCTGATGCTTCTTGTCTTCTGTCATCATGCATCATCGTGTCTCCCTGGCCTCA	3869
QY		1379	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
Db		3870	GCCGGGGAGCCAAGATCTTGGGGGCTCTCCGAGTCTTGGGCTCTGGCAACCTTAGC	3929
QY		1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1418
Db		3930	CCCCTCGTGTATCAGCCGGGGCGCGGCTGAAGCTGTGTGGAGACATCTATCTCC	3989
QY		1419	SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly	1438
Db		3990	TCCCTCAAGCCCATCGGCAACATCGTCTCATCTGTGCTTCTTCTTCATCATCTTTGGC	4049
QY		1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyLysAspThrArg	1458
Db		4050	ATCTGGAGTGCAGCTCTTCAAGGGCAAGTTCTACCACTGTCTGGCGTGACACCGCC	4109
QY		1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrrArgTrpValArgHisLysTyr	1478
Db		4110	AACATCACCAACCGCTCGACTGCATGCGCCCACTACCGCTGGTCCATCACAAATAC	4169
QY		1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
Db		4170	AAC TTGCACAACCTGGGCCAGGCTGTATGTCCCTTTTGTCTTGCCATCCAAGATGCT	4229
QY		1499	TrpValAspIleMetTyrrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet	1518
Db		4230	TGGGTGAACATCATGTACATGGACTGGATGCTGTGTGGACCAGACAGCCTGTGACC	4289
QY		1519	AsnHisAsnProTrpMetLeuLeuTyrrPheIleSerPheLeuLeuIleValAlaPhePhe	1538
Db		4290	AACCAACAACCCCTGGATGCTGTACTTCATCTCTTCTGCTCATCGTCAGCTTCTTT	4349
QY		1539	ValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGln	1558
Db		4350	GTGCTCAACATGTTTGTGGGTGTCTGTGTGAGAACTTCCACAAGTCCCGCAGCACAG	4409
QY		1559	GluGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArg	1578
Db		4410	GAGGCTGAAGAGGCA CGGCGCGCTGAGGAGAA GCGGCTGCGGCCCTGGAGAGAAGCGC	4469
QY		1579	ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrrTyrrSerAspTyrrSer	1598

Db	4470	CGG-----	-----AAGGCCAGCGGCTGCCCTACTATGCACTATTGT	4508
Qy	1599	ArgPheArgLeuLeuValHisHisIleu	CysThrSerHisTyrLeuAspPheIleThr	1618
Db	4509	CACACCCGGCTGCTCATCCACTCCATGTCAC	AGCCACTACTGACATCTTCATCACC	4568
Qy	1619	GlyValIleGlyLeuAsnValValThrMet	AlaMetGluHisTyrGlnGlnProGlnIle	1638
Db	4569	TTCATCATCTGCCCTCAACGTGTGCACCATGTC	CCCTGGAGCACTACAATCAGCCACGTCC	4628
Qy	1639	LeuAspGluAlaLeuLysIleCysAsnTyrIle	PheThrValIlePheValPheGluSer	1658
Db	4629	CTGGAGACAGCCCTCAAGTACTGCACACTATATGTT	CAACCACTGTCTTGTGCTGGAGGCT	4688
Qy	1659	ValPheLysLeuValAlaPheAlaPheArgArg	PhePheGlnAspArgTyrPAsnGlnLeu	1678
Db	4689	GTGCTGAAGCTGGGTGGCATTGTGTGAGGCGCTTC	TCAAGGACCGATGGAAACCACTG	4748
Qy	1679	AspLeuAlaIleValIleLeuLeuSerIleMet	GlyIleThrLeuGluGluIleGluValAsn	1698
Db	4749	GACCTGGCCATTGTGCTACTGTCACTATGGGCATC	ACCCTGAGAGATCGATCAAT	4808
Qy	1699	LeuSerLeuProIleAsnProThrIleIleArgIle	MetArgValLeuArgIleAlaArg	1718
Db	4809	GCGGCCCTGCCCATCATCCACCATCATCGCATCAT	GAGGTTCTGCGCATTTGCCGA	4868
Qy	1719	ValLeuLysLeuLeuLysMetAlaValGlyMet	ArgAlaLeuLeuHisThrValMetGln	1738
Db	4869	GTGCTGAAGCTGTGAAGATGGCCACAGGAATGCGG	CCCTGCTGACACGGTGGTGCA	4928
Qy	1739	AlaLeuProGlnValGlyAsnLeuGlyLeuLeu	PheMetLeuLeuPhePheIlePheAla	1758
Db	4929	GCTTGGCCCCAGGTGGGCAACCTGGGCTCTCTTC	TATGCTGCTCTTTCATCTATGCT	4988
Qy	1759	AlaLeuGlyValGluLeuPheGlyAspLeuGlu	CysAspGluThrHisProCysGluGly	1778
Db	4989	GCTCTGGGGTGGAGCTCTTTGGGAAGCTGTCTG	CAACGACGAGAACCCGTGCGAGGGC	5048
Qy	1779	LeuGlyArgHisAlaThrPheArgAsnPheGly	MetAlaPheLeuThrLeuPheArgVal	1798
Db	5049	ATGAGCCGGCATGCCACCTTCGAGAACTTCGCG	CATGCTTCCTCACACTTTCAGGTC	5108
Qy	1799	SerThrGlyAspAsnThrPAsnGlyIleMetLys	AspProSerArgAspCys---AspGln	1817
Db	5109	TCCACGGGTGACAACTGGAACGGGATCATGAAGA	CACGCTGCGGACTGCACCCACGAC	5168
Qy	1818	GluSerThrCysIleTyrAsnThrVal-----	IleSerProIleTyrPheValSerPheVal	1835
Db	5169	GAGCGCAGCTGCTGAGCAGCAGCTGCAGTTGTGT	CGCCGCTGACTTCGTGAGCTTCGTG	5228
Qy	1836	LeuThrAlaGlnPheValLeuValAsnValValIle	AlaValLeuMetLysHisIleGlu	1855
Db	5229	CTCACCGCGCAGTTCGTGCTCATCAACGTTGTGT	GCTGCTCATGAAGCACTTGAC	5288
Qy	1856	GluSerAsnLysGluAlaLysGluGluAlaGlu	LeuGluAlaGluLeuGluMet	1875
Db	5289	GACAGCAACAAGAGGCGCAGAGGACGCCGAGAT	GATGCCGAGCTCGAGTGGAGATG	5348
Qy	1876	---LysThrLeuSerProGlnProHisSerPro	LeuGlySerProPheLeuTyrPro---	1893
Db	5349	GCCCATGGCTGGGCCCTGGCCCCGAGGCTGCTA	CCGGCTCCCGGCGCC---CCTGGC	5405
Qy	1894	-----GlyValGluGlyValAsnSerThrAsp	-----	1902
Db	5406	CGAGGGCGCGGAGGGCGGGCGGGCGCACCCGAG	GGCGGCTTGTGCCGCGGCTGC	5465
Qy	1903	---SerProLysProGlyAlaPro-----	HisThrThrAlaHisIleGlyAla	1917
Db	5466	TACTCGCCTGC-CCAGGAGAACTGTGTGCTG	ACAGCGTCTTTAATCATCAAGAACTC	5524
Qy	1918	AlaSerGlyPheSerLeuGluHisProThrMet	ValProHisProGluGluValProVal	1937

Db 594 GCAAGATCCTGCAGAGTCTTCGATGACTTCACTTTCCTTTGCCATGGAGATGCTGC 653
QY 166 allysmetValAlaleuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsn 186
Db 654 TTAAGATGATGGCCCTGGGCATTTTGGCAAGAGTGTACTCGGAGACACATGGAAACC 713
QY 186 rgleuAspPhePheIleValIlealacIleMetLeuGluTyrSerLeuAspLeuGlnAsnV 206
Db 714 GCCTGGATTCTTCATTGTTCATGGCAGGAGTGGTAGTACTCTCTGGACCTACAGAAACA 773
QY 206 alSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgV 226
Db 774 TCAACCTGTCAAGCCATCCGCACTGTGCTGTCTGAGGCTCTCAAAAGCCATCAACCGTGG 833
QY 226 alProSerMetArgIleLeuValThrLeuLeuAspThrLeuProMetLeuGlyAsnV 246
Db 834 TACCAGCATGCGGATCCTGTGAACTGTCTGACACAGCTGCCCATGTGGGGAACG 893
QY 246 alLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpA 266
Db 894 TGCTCCTGCTCTGTTCTTCTGCTTCTTCATCTTCGACATCATTTGGCGTGCAGCTCGGG 953
QY 266 lAgIlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerValA 286
Db 954 CAGGCTGTCTACGGAACCGCTGCTTCCTGGAAGAGAATTCAACATCAACAAGGGATGTGG 1013
QY 286 splLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnP 306
Db 1014 CCCTGCCCCCTTAATTAACAACAGAGAGATGACGAGATGCCCTTATCTGCTCCCTGA 1073
QY 306 roArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGlyGlyG 326
Db 1074 CTGGGGACAATGGCATCATGGGCTGCCAGAGATCCCCCACTGAAGAGACAG----- 1126
QY 326 lYgIlyProProCysSerLeu-----AspTyrGluThrTyrAsnSerS 340
Db 1127 --GGCCGGGAATGCTGCTGTCCAAAGATGATGTATGACTTCGGGGCGGGCGCCAGG 1184
QY 340 erSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrAsnCysSerAlag 358
Db 1185 ACCTCAACGCGCAGCGGTCTGTGCGTCAACTGGAAACCGCTACTACAACGTCGTGCCGCA 1244
QY 358 lYgIluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleA 378
Db 1245 GCAACGCCAACCCCTCAACAAGGGCGCCATCACTTGACAACAATTGGCTATGCCGGATTG 1304
QY 378 laIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspA 398
Db 1305 TGATTTTCCAGGTGATCACTCTGGAAGGCTGGGTGGAGATCATGTACTATGTGATGGACG 1364
QY 398 laHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheM 418
Db 1365 CACATTCTTTCTACAACCTTCATCTACTTCATTCTGCTCATCATAGTGGCTCCTTCTTCA 1424
QY 418 ecIleAsnLeuCysLeuValValIlealathrGlnPheSerGluThrLysGlnArgGluS 438
Db 1425 TGATCAACTTGTGCTCGTGTGCATAGCAACCAAGTTCTTGAGACCAAGCAACGGGAGC 1484
QY 438 erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerP 458
Db 1485 ACCGGCTGATGCTGAGCAACGCGCAGCTGTCC--TCCAGACAGGTTGCCAGATT 1541
QY 458 heSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgL 478
Db 1542 ACGCTGAGCCCGGTGATGTCTATGAGAGATCTTCCAATATGTCTGTACATCCTTCGCA 1601
QY 478 ySAAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuS 498
Db 1602 AAGCCAAAGCGC-----CGTGCCCTAGGCGCTTACACAGGCCCTG----- 1639
QY 498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518
Db 1640 -----CAGA 1643

QY 518 iSAArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisTyrH 538
Db 1644 ACCGGCGCCAGGCC----- 1657
QY 538 iSLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspA 558
Db 1658 --ATGGGCCCGGGACA----- 1672
QY 558 laAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP 578
Db 1673 -----CCAGCCCTGCCCAAGCCTGGGCC----- 1696
QY 578 roProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProV 598
Db 1697 -----CATGCCAAG-----GAGCCCA 1712
QY 598 alArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlyS 618
Db 1713 GCCACTGCAAGCTGTGCCCAAGACAGACAGCCCCCTGGAC----- 1750
QY 618 erGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysA 638
Db 1751 -----CCACTCCCAACACA----- 1765
QY 638 laLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProP 658
Db 1766 --CTGTGCAG----- 1774
QY 658 roGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisS 678
Db 1775 -----CCCATCTCTGCCATTCTG----- 1792
QY 678 erSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspS 698
Db 1793 -----GCCCTGACCCCAAGCA 1808
QY 698 erCysProTyrCysAlaArg-----ThrGlyAlaGlyGluProGluS 712
Db 1809 GGTGCCCTCACTGCCAGCAGAGGCAAGCAGCGGCCCTCTGGCTGGGCGACACTGACT 1868
QY 712 erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA 732
Db 1869 CAGGCCAGGAAGGCTCAGGTTCTGGTCTGTGCAGAGGCCGAAGCCAAATGGGATGGAC 1928
QY 732 laGlnHisSerAsp-LeuArgAspProHisSer-----ArgArgArgGlnArgSerLeu 749
Db 1929 TCCAGAGCAGTGAAGATGGGCTCTCTCGACCTGGGGGAAGAGAGAACAGAGAGACG 1988
QY 750 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 769
Db 1989 GGG-----CAGCCCGACTGTGTGGG-GATGTGTGGCGCGAGACAGCAAAAGCTG 2038
QY 770 ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 789
Db 2039 CGGGGCATCGTGACAGCAAGTACTTCAACAGAGGTATCATGATGCTATCTGTGTAAC 2098
QY 790 ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 809
Db 2099 ACAGTCAAGATGGGCATCGAGCAACAGAACAGCCGAGAGACTGACCAACATCCTGGAG 2158
QY 810 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuVal 829
Db 2159 ATCTGCAATGTGTCTTACCAAGATATGTTGCCCTCGAGATGATCCTGAACATGGCCGCC 2218
QY 830 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 849
Db 2219 TTGGGCTCTTGACTACTCGGAACCTTACAACATCTTTGACAGCATCATGCTCATC 2278
QY 850 IleSerValTrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPhe 869
Db 2279 ATCAGCACTCGGAATCGTGGGGCAGCGGACGCTGCTGTGTGTGGCACCTTTC 2338

QY	870	ArgLeuMetArgValleuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuVal	889
Db	2339	CGGTGTCTGCGGGTGCTGAAGCTGTGCGCTTATGCCGGCGCTGCGCGCACTCGTG	2398
QY	890	ValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIle	909
Db	2399	GTGCTCATGAAGACCATGGACAACAGTGGCCACCTTCTGCATGTCTACTCATGTCTTCATC	2458
QY	910	PheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp	929
Db	2459	TTCATCTTACGATTCCTTGGATGATATCTTTGGCTGCAAATTTCAGCCTCCGCACGGAC	2518
QY	930	---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThr	948
Db	2519	ACGGAGACACCGCTTCTGACAGGAAGAACTTCGATTCTTACTGTGGGCCATTGTCACA	2578
QY	949	ValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSer	968
Db	2579	GTGTTCCAGATCTCTACTCAGAGGACTGGAACGTTGCTCTGTAACATGGCATGGCTCC	2638
QY	969	ThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeu	988
Db	2639	ACCACCCCTGGGCTCCCTCTATTGTTGGTCCCTCATGACCTTTGGCAACTACGTTCTC	2698
QY	989	PheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLys	1008
Db	2699	TTCATCTCTCGTGGCTATCTCTGTAGAGGCTTCCAGCTGAGGCTGATGTTAATCGT	2758
QY	1009	SerGluSerGluProAspPhePheSerProSerValAspGly-----	1022
Db	2759	TCCTGCTCTGATGAGGACCAAGACTCATCCAAATTGGAGGAGTTTGACAAGCTCCACAG	2818
QY	1023	-----AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGlu	1040
Db	2819	GGCTTGACACACAGTAGAGATCTCAAGCTCTGCCCAATACCATGACACCCCAATGGACAC	2878
QY	1041	LeuArgLysSerLeuLeuProProLeuIleIleHis-----ThrAlaAlaThrProMet	1058
Db	2879	CTGACCCCTAGCCTC-----CCTCTGGGTGCGCATGTGGGTCCTGCTGTACCAATGGGT	2932
QY	1059	SerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArg	1078
Db	2933	ACTGCCCCCGCCTCTCACTGCAGCCAGACCCGGTACTGGTGGCCCTAGACTCTCGGAAA	2992
QY	1079	ThrSerSerSerGlySerAlaGluProGlyAlaAlaHisIleGluMetLysCysProPro	1098
Db	2993	AGCAGTGTATGTCCCTG-----GGCAGATGAGCTATGATCAGCGATCCTTGTCC	3043
QY	1099	SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg	1118
Db	3044	AGCTCCCGGAGCTCTTACTACGGGCCCTGTGGCGCGACGTGGGACTAGCCGCGCC	3103
QY	1119	SerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGlu	1138
Db	3104	TCCAGCTGGAAC-----AGCCTGAACAACAAGCCGCCCTCAGCTGAG	3145
QY	1139	ArgArgSerLeuLeuSerGlyGlyGlnGluSer-----GlnAspGluGluGluSer	1156
Db	3146	CATGAGTCTTACTGTCTTGGGAGGGGTGAGGTAGCTGCGTCAAGGGCCTGTGAAGCGCC	3205
QY	1157	SerGluGlu-----AspArgAlaSerProAlaGlySerAspHis-----	1169
Db	3206	CGGAGGAGGCGCAACTGCACCGCACCCCTGCATGCTCCACACGCGCACCGCGCAC	3265
QY	1170	-----ArgHisArgGlySerLeuGluArgGluAla	1179
Db	3266	CATGACCCCACTGGCACACCGTCAACCGACACCAACCGCGGACTGTCTCTGATACC	3325
QY	1180	LysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer	1199
Db	3326	AGGAACTCTGTTGACCTGGGAGAGCTGGTGCCCGTGGGTGCCCACTACGCGGCGCT	3385
QY	1200	-----GlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGly	1217

Db	3386	TGAGAGGGGGGGGT	CAGGCCCTGGG	GCAGAGACTGCAATG	CAGAAATGCCAAC	---	3442						
QY	1218	ArgLeu	AlaArg	ThrLeu	ArgThr	AspProGlnLeu	AspGlyAspAspAsn	1236					
Db	3443	---	ATAGCCAA	GAGATGTCTT	CACCAAGATG	ATGACCGCGC	GGGAGAGAG	3499					
QY	1237	AspGlu	GlyAsn	LeuSer	LeysGly	GluArg	IleGlnAla	TrpValArgSer	ArgLeuPro	1256			
Db	3500	GAGAGATG	CACTATAC	CCCTGTGTTT	CCGGGTCC	CAAGATGATG	ATGTGT	ACAAGCCG	3559				
QY	1257	AlaCys	CysArg	GluArg	AspSer	TrpSer	AlaTyr	IlePhe	ProProGln	SerArgPhe	1276		
Db	3560	GACTGTG	CGAAGTCC	CGAGAGACTG	GTGGTCTAC	CTTCTTCC	CCCCGAG	ACAAGTTC	3619				
QY	1277	ArgLeu	Leu	CysHis	ArgIle	IleThr	His	MetPhe	AspHis	ValValLeu	ValIle	1296	
Db	3620	CGATCCTG	TGTCA	GACCATCATG	CTCACA	AGCTTTTG	ACTACGTG	GTCTTG	CCCTT	3679			
QY	1297	IlePhe	Leu	AsnCys	IleThr	IleAla	MetGlu	ArgPro	LysIle	AspPro	HisSer	Ala	1316
Db	3680	ATCTTCT	CACTGAT	CAACCATG	CTCTGGA	GAGACCCAG	ATTGAAG	CTGTG	ACACT	3739			
QY	1317	GluArg	IlePhe	LeuThr	LeuSer	AsnTyr	IlePhe	ThrAla	ValPhe	LeuAla	GluMet	1336	
Db	3740	GAGCGCAT	TTCTCT	CACGGTGT	CTAACA	CTTCA	CAGCCATCTT	CGTGG	CGAGATG	3799			
QY	1337	ThrVal	LysVal	ValAla	LeuGly	TyrCys	Phe	GlyGlu	GlnAla	TyrLeu	ArgSer	1356	
Db	3800	ACACTGA	AGTGTTCT	CTGGGCTG	TACTTGG	TGAGCAG	CGGTAC	CTCGT	AGCAGC	3859			
QY	1357	TrpAsn	ValLeu	AspGly	LeuLeu	ValLeu	IleSer	ValIle	AspIle	LeuVal	SerMet	1376	
Db	3860	TGGAATG	TACTGATG	GTTCCTG	TGCTTGTG	TCCATCAT	CGATAT	CGTAGT	GTCCGTG	3919			
QY	1377	ValSer	AspSer	GlyThr	LysIle	LeuGly	MetLeu	ArgVal	LeuArg	LeuLeu	ArgThr	1396	
Db	3920	GCCTCTG	CTGGGGAG	CCAAAGATT	CTGGGGGT	CTCCGGGT	CTCGGCT	CTCGGT	AC	3979			
QY	1397	LeuArg	ProLeu	ArgVal	IleSer	ArgAla	GlnGly	LeuLys	LeuVal	ValGlu	ThrLeu	1416	
Db	3980	TTACGT	CTTTGAG	GGTTAT	CAGCCGG	CCCTGGG	CTGAAG	CTGTG	TAGAG	CGCTC	4039		
QY	1417	MetSer	SerLeu	LysPro	IleGly	AsnIle	ValVal	IleCys	CysAla	PhePhe	IleIle	1436	
Db	4040	ATCTC	CTCCCTCA	AGCCCAT	TGGGA	CATCGT	CTCATCTG	CTGCTT	CTTCAT	CAATC	4099		
QY	1437	PheGly	IleLeu	GlyVal	GlnLeu	PheLys	GlyLys	PheVal	CysGln	GlyGlu	Asp	1456	
Db	4100	TTGCGAT	CTCGGGGTG	CAGCTTTT	CAAGGCA	AGTTCTA	CCATTGTT	TGGAG	TGGAC	4155			
QY	1457	ThrArg	AsnIle	ThrAsn	LysSer	AspCys	AlaGlu	AlaSer	TyrArg	TrpVal	ArgHis	1476	
Db	4160	ACCCGAA	CATCACC	CAACCGAT	CTGACTG	CGTGG	CGCCAACTA	CCGCTG	GGTGCAT	CAAC	4219		
QY	1477	LysTyr	AsnPhe	AspAsn	LeuGly	GlnAla	LeuMet	SerLeu	PheVal	LeuAla	SerLys	1496	
Db	4220	AAATACA	ACTTTGA	CAACCTG	GGCCAG	GCAATG	ATGCCCTT	TTGCTT	TGGCT	CCAAG	4279		
QY	1497	AspGly	TrpVal	AspIle	MetTyr	AspGly	LeuAsp	AlaVal	GlyVal	AspGln	Pro	1516	
Db	4280	GACGGCT	GGGTGA	CATCATG	TATTA	TGATTAG	ATGCTG	TGTG	TGAC	CAGCAG	CCA	4339	
QY	1517	IleMet	AsnHis	AsnPro	TrpMet	LeuLeu	TyrPhe	IleSer	PheLeu	LeuIle	ValAla	1536	
Db	4340	GTGAC	GAACCA	CAACCCCTG	GATGCTA	CTGACTT	CTTCATT	TCGTT	CTGCT	CAATC	GTCA	4399	
QY	1537	PhePhe	ValLeu	AsnMet	PheVal	GlyVal	ValVal	GluAsn	PheHis	LysCys	ArgGln	1556	
Db	4400	TTCTTTG	TGCTCA	ATGTTT	TGTGG	CGGTG	TGTGAG	AACTT	CCACA	AGTCC	CGG	4459	
QY	1557	HisGln	GluGlu	GluAla	ArgArg	ArgGlu	GluLys	ArgLeu	ArgArg	LeuGlu	Lys	1576	

D	b		4460	CACCAGGAGGCTGAGGAGCGCCGGAGCGGTGAGGAGAAACGGCTGC GGCGCCTGGAAAAG	4519
O	y		1577	LysArgSerLysGlusGlmMetAlaGluAlaGlnCysLysProTyrTyrSerAsp	1596
D	b		4520	AAGCCCGT-----AAGCTCAGAGGCTGCCCTACTATGCTACC	4558
O	y		1597	TyrSerArgPheArgLeuValHisIleLeuCysThrSerHisTyrLeuAspLeuPhe	1616
D	b		4559	TACTGTCCCACAAGGCTGTCATCCACTCCATGTGCACAGCACTACTGACATCTTC	4618
O	y		1617	IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro	1636
D	b		4619	ATTACCTTCATCATCTGCCTCAATGTTGTCAACCATGTCCCTGAAGCACTAACAGCCT	4678
O	y		1637	GlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPhe	1656
D	b		4679	ACATCCCTAGAGACAGCCCTTAAGTACTGCACACTACATGTTCAACCACTGCTTTGTCTG	4738
O	y		1657	GluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsn	1676
D	b		4739	GAGGCTGTGCTGAAGCTGTGGCATTTGGCCTGAGCGCTTCTTCAAGACCGATGAAC	4798
O	y		1677	GlnLeuAspLeuAlaIleValleuLeuSerIleMetGlyIleThrLeuGluIleGln	1696
D	b		4799	CAGCTGACCTGGCCATTTGTCTGCTGTCGTCATGGGCATCACACTGAGAGAATGAG	4858
O	y		1697	ValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle	1716
D	b		4859	ATCATATGCCGCCCTTCCCATCAACCCCAACCATCATCCGATCATGCGTGTCGCGTATC	4918
O	y		1717	AlaArgValleuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrVal	1736
D	b		4919	GCCCCGGGTGTGAAGCTATTGAAGATGGCCACAGGAATCGGGCCCTGCTGCACACAGTG	4978
O	y		1737	MetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIle	1756
D	b		4979	GTAACGGCTCTGCCCCAGGTGGCAAACCTGGGCTGCTTTCATGCTCTTCTTCATC	5038
O	y		1757	PheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGlnCysAspGluThrHisProCys	1776
D	b		5039	TATGCTGCTCTGGAGTGAAGCTTTCGAAAGCTGTCGCAATGACAGAAACCCGTGT	5098
O	y		1777	GluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPhe	1796
D	b		5099	GAGGGCATGAGCCGACGCCACCTTTGAAACTTCGGCATGGCCTTCCTCACGCTCTTC	5158
O	y		1797	ArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---	1815
D	b		5159	CAGTCTCCACAGCGCATTACTGGAATGGAATTATGAAGACACCCCTCGAGACTGTACC	5218
O	y		1816	AspGlnGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSer	1833
D	b		5219	CATGATGAGCGCACGTCCTTAAGACAGCCTGCAGTTGTGTCAACGCTTACTTTGTAGC	5278
O	y		1834	PheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHis	1853
D	b		5279	TTCGTGCTCACAGCTCAGTTGCTGCTCATCAACGTGTGTGGCCGTGCTGATGAACAT	5338
O	y		1854	LeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeu	1873
D	b		5339	CTGGATGACAGCAACAAGAGGCCCAAGAGATGACAGATGATGATGATGATGATGATG	5398
O	y		1874	GluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro	1893
D	b		5399	GAGATG-----	5404
O	y		1894	GlyValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAla	1913
D	b		5405	---GCCCATGGCCTGGGCCCTGCTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5443
O	y		1914	HisIleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGln	1933
D	b		5444	-----CCCTGCCCTGCTGC	5455

QY	1934	GLuValProValPro---LeuGlyProAspLeuLeuThrVal-----	1946
Db	5456	CCCTGCCCTGCCCTGTGCTGTGCGCCGAGGCTGCCCACTAGTTCACTGGGGCTCCGGGG	5515
QY	1947	ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsn	1966
Db	5516	CGAGGATCGGAGGGGGCAGGTGCTGAGGC---GACACCGAGAGTCACTGTGCCGGCAC	5572
QY	1967	---GlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGln	1985
Db	5573	TGCTATTCTCCAGCCCAAGAGACCCTG-----TGG-----CTGGAC	5608
QY	1986	SerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeu	2005
Db	5609	AGCGTCTTTAATCATCAAGACTCTCTTGAGGGGGAGCTGACCATCATTCACAACCTG	5668
QY	2006	ProLysAspVal---HisTyrLeuLeuGlnProHisGlyAla-----	2018
Db	5669	TCTGGTCCGTTCTCCACCACCTACGCTGACGGCTGTGCAAGTGTCAACCATGAC	5728
QY	2019	-----ProThrTyrGlyAlaIleProLysLeuProProPro	2030
Db	5729	AAGCAAGACAGCTCTTCATCCATCCCTGCTGGGGATGACCTGAGTCTTGAGAACCCCA	5788
QY	2031	GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer	2050
Db	5789	CGGCTGCCACAGGGGCCCAAGAGAGCAAGGGTGACTAGAGCCTCCGAGCCCATGC	5848
QY	2051	LeuAspValGlnGlyLeuGlySerArgGlnAspLeuLeuSerGlu-----ValSerGly	2068
Db	5849	AGGTGAGACCTGATGATGATGCTTTGGCCCTTTGCCAAGCAGACGAGTGTCCACAGGC	5908
QY	2069	ProSerCysProLeuThrArgSerSerSerPheTrpGlyIleSerSerIleGlnValGln	2088
Db	5909	CCAGAGAG-CTGTGTGTGCAGAT-----GGGGCCATTCATTCAAACC-CTG	5954
QY	2089	GlnArgSerGlyIleGlnSerIleValSerIleHisIleArg-----	2102
Db	5955	TCCAGTCCCTGGCTCAACAACGAGACGACCAACCCACAGACCCTTCTCCCCGGATG	6014
QY	2103	-----LeuProAla	2105
Db	6015	GCTCCAGCCCTCTCTGTAGATGCTGTGAGTTCTTCCACCCTGTGTGTGCAAGCC	6074
QY	2106	-----ProCysProGly-----LeuGluPro	2112
Db	6075	AGAAGGGCAGGAACGGGCATGAGTGCAAGAACCTGCCCAAG-ATTGCACTTCAAGGG	6133
QY	2113	SerTrpAlaLys---AspProProGluThrArgSerSerLeuGluLeuAspThrGluLeu	2131
Db	6134	TCCTGGGCATCGCTGAGGTCACCGAGTGTCACTGCACCCTTTGCCGCAAGCTACTGTG	6193
QY	2132	SerTrpIleSerGlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAsp	2151
Db	6194	AGTGACACGTCCTTGGAATGCCAGTCTTAGCAGCTCA-----	6229
QY	2152	LeuLysLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeu	2171
Db	6229	-----	6229
QY	2172	AspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProArg	2191
Db	6230	-----GCGGGCAGCCTACAGACCACTGAAGACAGTGTGACT-----	6268
QY	2192	LeuCysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgPro	2211
Db	6269	CTGAGTGACAGTCCCGGGCTGCCCTGGGGCCCGGTCCAGGTGCTGGG-----CCA	6322
QY	2212	LysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArg	2231
Db	6323	CGGGCTAGCCTGTCAACCGGCCACCCCGGGCG-----CGGCTCAGCCTGCGGGGCCGTGG	6376


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Oy      2232 ProProCySerPro-GlyValCysLeuArgAlaProAlaSer----- 2247
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Db      6377 CCTGTTAGTCTGCGTGGGCTGCGGCCCATCAGCGTAGCCACAGACAGTGGCGCTCCAC 6436

Oy      2248 -----AspSerLysAspProSer 2253
      ||| ||| ||| ||| ||| ||| |||
Db      6437 CAGCCCTGCTGCACCTCACACGACTCCATGAGACCCCTCT 6476

RESULT 11
; US-09-935-541-12
; Sequence 12, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
; US-09-935-541-12

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Alignment Scores:	
Pred. No.:	0
Score:	5407.00
Percent Similarity:	61.05%
Best Local Similarity:	51.08%
Query Match:	44.95%
DB:	4
	Gaps: 60
	Length: 6503
	Matches: 1234
	Conservative: 241
	Mismatches: 502
	Indels: 444
	Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-935-541-12 (1-6503)

Oy		3	ProHisArgValProArgCysValArgThrProProLeuAlaArgGlySerAlaArgProSer	22
Db		64	CCCCCGGGCCCGGCCCTGCATGCGCGTRCCCCCTCGCCCCGGGGCGCA-----	114
Oy		23	SerAspPro-----ProGlyProArgLeuAlaArgGlyTrpThrArgArg	38
Db		115	GCTGATCCCGGAATCCGAGCGGTGGGGCCGGCGGG-GGCGGGGTCCCTTCACAGCCGG	173
Oy		39	Met-----Glu-ArgAlaProArg-----SerArgAspSerProValAla-----	51
Db		174	CTTCCGGGACACCGCGTCAACCCCGCGTCTCTGCCCGGGACGACCCCGTGCCCGCCACG	233
Oy		52	-----SerArgSerSerThrTh	57
Db		234	TCCATGCCAAGGGCTCCCTGCTCACGCTGACATGGCTGACAGCAACTTACC GCCCTCAT	293
Oy		57	rCySProGlyProGly-----AlaAlaGlyAla-GlySerThrg	70
Db		294	CTGCAGACGCCCCGGCCCTGAGCCGGGAATCACTGAGACGCGGGCCCGGAGTCCC	353
Oy		70	IuLyAspProGlySerAlaAspSerGluAlaGly-----LeuProTyP	86
Db		354	CTCCATCCCTCCAGGCTGAGAGACCATTTGAAGAACAACCTGACGTCCACATC	413
Oy		86	roAlaLeuAlaProValValPhePheTyrlleuSerGlnAspSerArgProArgSerTryc	106
Db		414	CAGACCTGGCTCTGTGCTTCTTCTGCTCGCCGACGACCAAGCCACGGAAC TGST	473
Oy		106	ySeUeArGthrValCysAsnProTrpPheGluArgValSerMetLeuVallleuleuA	126
Db		474	GCATCAAGATGTTGTAAACCCGTTGAGTGTGTGACATGCTGTTATTCTCTGA	533
Oy		126	sncYsValThrleuGlyMetPheaArgProCySGluAspIleAlaCysAspSerGlnArgC	146

Db	534	ACTGTGTGACCCCTGGGCGATGTACCAGCCATGTGATGACATGAGATGCGCTGTCGGACCGTT	593
Qy	146	ysArgIleLeuGlnAlaPheAspSppheIlePheAlaPhePheAlaValGluMetVal	166
Db	594	GCAAGATCCCTGACGGTCTTCGATGACTTCATCTTCATCTTCTTGCCATGGAATGTGC	653
Qy	166	allysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn	186
Db	654	TTAAGATGTGGCCCTGGGCATTTTGGCAAGAAGTGCTACCTCGGACACATGGAACC	713
Qy	186	rgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn	206
Db	714	GCCTGATTTCTTCATGTTCATGGCAGGAGTGTGAGTACTCTCTGACCTACAGACA	773
Qy	206	alserPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg	226
Db	774	TCAACCTGTACGCCATCCGACCTGCGTGTCTGAGGCTCTCAAGCCATCAACCGTG	833
Qy	226	alProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn	246
Db	834	TACCAGCATGCGGATCCGTGGTGAACCTGCTGCGACACGCTGCCCATGCTGGGAAACG	893
Qy	246	alleuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp	266
Db	894	TGCTCTGCTCTGTTCCTTCCTTCCTTCATCTTCGCATCATTTGGCGTGCAGCTGTGG	953
Qy	266	IaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal	286
Db	954	CAGGCTGTACCGAACCGCTGCTTCTTGAAGAGAACTTACCACATACAGGGGATGTGG	1013
Qy	286	spleuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln	306
Db	1014	CCCTGCCCTTATTACCAACAGAGAGATGAGATGCCCTTATCTGCTCCCTGA	1073
Qy	306	roArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGlyGlyG	326
Db	1074	CTGGGACAAATGCGATCATGGGCTGCCACGAGATCCCCCACTGAGAGAGCAG-----	1126
Qy	326	IyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSers	340
Db	1127	--GGCGGGAAATGCTGCTGTCCAAAGATGATGTATGACTTCGGGGCGGGCGCCAGG	1184
Qy	340	erSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla	358
Db	1185	ACCTCAACGCCAGCGGTCTGTGGCGTCAACTGGAACCGCTACTCAACAGTCTGCCGACGG	1244
Qy	358	IyGluHisAsnProPheIleGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle	378
Db	1245	GCAACGCCAACCTCTACAAAGGCGCCATCACTTGAACAACATTGGCTATGCCGGATTG	1304
Qy	378	IaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAsp	398
Db	1305	TGATTTTCCAGGTGATCATCTTGAAAGGCTGGGTGAGATCATGTACTATGTGATGACG	1364
Qy	398	IaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe	418
Db	1365	CACATTCCTTCTACAACTTCACTTCACTTCTGCTCATCATAGTGGGCTCTTCTTCA	1424
Qy	418	etIleAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrIleGlnArgGlu	438
Db	1425	TGATCAACTTGTGCTCTGTTCATAGCAACCCAGTTCTTGAGACCAAGCAACGGGAGC	1484
Qy	438	erGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer	458
Db	1485	ACCGGCTGATCTGAGCAACGCCAGCGCTACCTGTCC--TCCAGCACGGTGGCCAGTT	1541
Qy	458	heSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg	478
Db	1542	ACGCTGAGCCCGGTGATGTCTATGAGAGATCTTCCAATATGTCTGTACATCTTGC	1601
Qy	478	ysAlaIaIaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu	498

Db 1602 AAGCCAAGCC-----CGTGCCCTAGGCTCTACAGGCCCTG----- 1639
QY 498 erSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerH 518
Db 1640 -----CAGA 1643
QY 518 isARgArGLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyH 538
Db 1644 ACCGGCCGCGAGGCC----- 1657
QY 538 isLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspA 558
Db 1658 --ATGGGCCCCGGGACA----- 1672
QY 558 laAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyP 578
Db 1673 -----CCAGCCCCCTGCCAAGCCTGGGCC----- 1696
QY 578 roProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProV 598
Db 1697 -----CATGCCAAG-----GAGCCCA 1712
QY 598 alArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlys 618
Db 1713 GCCCACTGCAGCTGTGCCACGACACAGACCCCTTGAC----- 1750
QY 618 erGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysA 638
Db 1751 -----CCCACTCCCAACACA----- 1765
QY 638 laLeuValGluValAlaProSerProGlyProProThrLeuHisSerPheAsnIleProP 658
Db 1766 --CTGTGCAG----- 1774
QY 658 roGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisS 678
Db 1775 -----CCCATCTCTGCCATTCTG----- 1792
QY 678 erSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAsps 698
Db 1793 -----GCCTCTGACCCCAAGCA 1808
QY 698 erCysProTyrCysAlaArg-----ThrGlyAlaGlyGluProGlnS 712
Db 1809 GCTGCCCTCACTGCCACGACGAGGCAAGCGCCCTCTGGCCTGGGCGACACTGACT 1868
QY 712 erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA 732
Db 1869 CAGGCCAGGAAGGCTCAGGTTCTGTGGCTCTGCAGAGGCCGAAGCCAATGGGATGAC 1928
QY 732 laGlnHisSerAsp-LeuArgAspProHisSer-----ArgArgArgGlnArgSerLeu 749
Db 1929 TCCAGAGCAGTAGAGATGGGGTCTCTCGGACCTGGGAAGAGAGAAACAGAGACG 1988
QY 750 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 769
Db 1989 GCG-----CAGCCCGACTGTGTGGG-GATGTGTGGCGCGAGACACGAAAAAGCTG 2038
QY 770 ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 789
Db 2039 CGGGGCATCGTGACAGCAAGTACTTCAACAGAGGTATCATGATGGCTATCCTGTGAAC 2098
QY 790 ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 809
Db 2099 ACAGTCAGCATGGGCTCGAGCACACGACAGACCCCGAGGAGCTGACCAACATCCTGAG 2158
QY 810 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuVal 829
Db 2159 ATCTGCAATGTGGTCTTCAACAGTATGTTGCCCTGAGATGATCTGAAAACTGGCCGCC 2218
QY 830 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 849
Db 2219 TTGGGCTCTTGACTAACCTGCGGAACCTTAAACAACATCTTTGACAGCATCATCGTATC 2278

QY 850 IleSerValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPhe 869
Db 2279 ATCAGCATCTGGAAATCTGGGGCAGGCGGAGCGGTGGCTGTCTGTGCTGCCACCTTC 2338
QY 870 ArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuVal 889
Db 2339 CGGTGCTGCGGGTGTCTGAAGCTGTGCGCTTCATGCGGCGCTGCGGCGCACTCGTG 2398
QY 890 ValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIle 909
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QY 910 PheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp 929
Db 2459 TTCATCTTACGATCTCTGGGATGCATATCTTTGGCTGCAATTCAGCCTCCGCAAGGAC 2518
QY 930 ---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThr 948
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Db 2579 GTGTTCAGATCTCTCACTCAGAGGACTGGAACGTTGTCTGTACAATGGCATGGCCTCC 2638
QY 969 ThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeu 988
Db 2639 ACCACCCCTGGGCTCCCTCTTAATTTGTGTGCCCTCAAGACCTTTGGCAACTACGTTCTC 2698
QY 989 PheAsnLeuLeuValAlaIleLeuValGlyGlyPheGlnAlaGlyLysAspAlaThrLys 1008
Db 2699 TTCAATCTCTGTGGTATCTGTGATAGAGGTTTCCAGGCTGAGGATGATGTAATCGT 2758
QY 1009 SerGluSerGluProAspPhePheSerProSerValAspGly----- 1022
Db 2759 TCCTGCTGTGATGAGGACCAAGCTCATCCAATTGGAGGAGTTGACAAAGCTCCAGAG 2818
QY 1023 -----AspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGlnHisAlaGlu 1040
Db 2819 GGCCTGACAAACAGTAGATCTCAAGCTCTGCCCAATACCCATGACACCCCAATGAGAC 2878
QY 1041 LeuArgLysSerLeuLeuProLeuIleIleHis-----ThrAlaAlaThrProMet 1058
Db 2879 CTGACCCCTAGCCTC-----CCTCTGGGTGCGCATGGGTCCTGTGTTACATGGGT 2932
QY 1059 SerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArg 1078
Db 2933 ACTGCCCCCGCCTCTCACTGCAGCCAGCACCCGGTACTGTGGTGGCCCTAGACTCTCGGAAA 2992
QY 1079 ThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProPro 1098
Db 2993 AGCAGTGTCAATGTCCTG-----GGCAGAGTAGAGTATGATCAGCGATCCTTGTCC 3043
QY 1099 SerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArg 1118
Db 3044 AGCTCCCGGAGCTCTACTACGGGCCCTGGGGCCGCACTGGGGAACCTGGGCTAGCCGCCG 3103
QY 1119 SerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGlu 1138
Db 3104 TCCAGCTGGAAC-----AGCCTGAACAACAAGCCGCTCAGCTGAG 3145
QY 1139 ArgArgSerLeuLeuSerGlyGlyGlyGlnGlnSer-----GlnAspGluGlnGlnSer 1156
Db 3146 CATGAGTCTTACTGTCTGGGAGGTGAGGTAGCTGCTCAGGGCTGTGAAGCGGCC 3205
QY 1157 SerGluGlu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3206 CGGAGGAGGCGCCAACCTGCACCGCACCCCTGCATGCTCCACACGCGCACCGCGCAC 3265
QY 1170 -----ArgHisArgGlySerLeuGluArgGluAla 1179
Db 3266 CATGACCCCACTTGACACACCGTACACCGACACCGCGGAGACTGTGTCCCTTGATACC 3325

Qy	1180	LYS	SerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer	1199
Db	3326	AGG	ACTCTGTGGACCTGGGAGAGCTGTGCGCCGTGGTGGTGCCCACTCAGCGGCCGT	3385
Qy	1200	-----G	lyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGly	1217
Db	3386	TGG	AGGGGGGGCGGGTCAGGCCCTGGGCACAGAGACTGCATGGCAGAATGCCCAAC---	3442
Qy	1218	ArgLeuAlaArgThrLeuArgThrAsp--	AspProGlnLeuAspGlyAspAspAsn	1236
Db	3443	--	ATAGCCCAAGAGATGTCCTTCAACCAAGATGATGATGACCGCCGACCGGGGAGACGAG	3499
Qy	1237	AspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuPro	1256	
Db	3500	GAG	AGATCGACTATACCTGTGTTCGGGTCCGCAAGATGATTGATGTACAAAGCCG	3559
Qy	1257	AlaCysCysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPhe	1276	
Db	3560	GAC	TGTGGCAGAGTCCGCGAGAGACTGTGCGGTACTCTTCCCCCGAACAAGTTC	3619
Qy	1277	ArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValLeuValIle	1296	
Db	3620	CGG	ATCTCTGTGTACAGACCATCATTTGCTCACAAAGCTTTTGACTACGTGTCCTTGCCCTTT	3679
Qy	1297	IlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAla	1316	
Db	3680	ATCTTCCTCAACTGTATACCATTTGCTCTGAGAGACCCAGATTGAAGCTGTAGCACT	3739	
Qy	1317	GluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMet	1336	
Db	3740	GAG	CGCATCTTCCTCAGCGGTGTCTAATACTATCATCTTCACAGCCATCTTCGTGGCGAGATG	3799
Qy	1337	ThrValLysValValAlaLeuGlyTrpCysPheGlyGlnAlaTyrLeuArgSerSer	1356	
Db	3800	ACACTGAAGGTGTTCTCTGGGCCCTGTA	CTTGGTAGACAGCGCGTACCTGCGTAGCAGC	3859
Qy	1357	TrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMet	1376	
Db	3860	TGA	ATGTACTGATGGTTCCTGTGCTTGTGTCCATCATGATATCGTAGTGTCCGTG	3919
Qy	1377	ValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThr	1396	
Db	3920	GCTCTGCTGGGGGAGCCAGATTTCTGGGGTCTCCGGGTCTGCGGCTCCTGCGTACC	3979	
Qy	1397	LeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeu	1416	
Db	3980	TTACGTCCTTTGAGGGTTATCAGCCGGGCCCTGGGCTGAAGCTGTGTAGACGCTC	4039	
Qy	1417	MetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIle	1436	
Db	4040	ATCTCCTCCCTCAAGCCCATTTGGGAACATCGTCTCATCTGTGCTTCTTCATCATC	4099	
Qy	1437	PheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAsp	1456	
Db	4100	TTCCGCATCCTGGGGGTGCA	GCTTTTCAAGGCAAGTCTTACCATTTGTTGGAGTGGAC	4159
Qy	1457	ThrArgAsnIleThrAsnLysSerAspCysAlaGlnAlaSerTyrArgTrpValArgHis	1476	
Db	4160	ACCCGAAACATCACCAACCATCTGACTGCGTGGCGGCCCACTAACCGCTGGGTGCATCAC	4219	
Qy	1477	LysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLys	1496	
Db	4220	AAATACAACCTTGCACAACCTGGGCCAGGCATTGATGTCCCTTGTCTTGCCCTCAAG	4279	
Qy	1497	AspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnPro	1516	
Db	4280	GACGGCTGGGTGAACATCATGTATATGATTGATGTCTGTGCTGTGACACAGACCA	4339	
Qy	1517	IleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAla	1536	
Db	4340	GTCAGCAACCAACCCCTGGATGCTACTGTACTTCAATTTCGTTCTCTGCTCATCGTCAGC	4399	
Qy	1537	PhePheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGln	1556	

Db	4400	TTCTTGTGCTCAACATGTTTGTGGCGTGGTGTGAGAACTTCCACAGTGC	CGGAG	4459
Qy	1557	HisGlnGluGluGluAlaArgArgGluGluLysArgLeuArgLeuGluLys		1576
Db	4460	CACCAAGAGCGCTGAGGAGCGCGGAGCGTGAGGAGAAACGGCTGCGCGCTG	GA	4519
Qy	1577	LysArgArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSer	Asp	1596
Db	4520	AAGCGCGCT-----AAGGCTCAGAGGCTGCCCTTACTATGCTACC		4558
Qy	1597	TyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPhe		1616
Db	4559	TACTGTCCCAAGAGCTGCTCATCCACTCATGTCACAGCCACTACTGACATCTTC		4618
Qy	1617	IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro		1636
Db	4619	ATTACCTTCATCATCTGCTGCTCATGTTGTTCACCATGTCTCCCTGAGACATCAAC	CA	4678
Qy	1637	GlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPhe		1656
Db	4679	ACATCCCTAGACAGACGCCCTTAAGTACTGCACACTACATGTTCCACCACCTGTCTT	GTGCTG	4738
Qy	1657	GluSerValPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTyrAsn		1676
Db	4739	GAGCTGTGCTGAAGCTGTGTGCATTGGCCCTGAGGCGTTTCTTCAAGACGATGGAAC		4798
Qy	1677	GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlu		1696
Db	4799	CAGCTGACCTGGCCATGTGTGCTGTCCGTCACTGGGCATCACACTGGAGAGATCGAG		4858
Qy	1697	ValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle		1716
Db	4859	ATCAATGCCGCCCTTCCCATCAACCCACCATCATCCGTATCATGCGTGTTCGGTATC		4918
Qy	1717	AlaArgValLeuLysLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrVal		1736
Db	4919	GCCCGGCTTGAAGCTATTGAAGATGGCCACAGGAATGCCGGCCCTGTGTGACACAGTG		4978
Qy	1737	MetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIle		1756
Db	4979	GTACAGGCTCTGCCCCAGGTGGGCAACTGGCGCTGCTTCATGCTGCTCTTCTCATC		5038
Qy	1757	PheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCys		1776
Db	5039	TATGCTGCTTGGAGTGGAGCTTTCGGAAGCTGGTCTGCAATGACGAGAACCCGTGT		5098
Qy	1777	GluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPhe		1796
Db	5099	GAGGCGATGAGCCGCGCACGCCACTTGAACACTTGGCATGGCCTTCCTCAGCTCTTC		5158
Qy	1797	ArgValSerThrGlyAspAsnTyrAsnGlyIleMetLysAspProSerArgAspCys---		1815
Db	5159	CAGGTCTCCACAGCGCATTACTGAGATGAATATGAAGGACACCCTGCGAGACTGTACC		5218
Qy	1816	AspGlnGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSer		1833
Db	5219	CATGATGAGCGCACGTGCCCTAAGCACCTGCAGTTGTGTACACCGCTCTACTTGTGAGC		5278
Qy	1834	PheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHis		1853
Db	5279	TTCGTGCTCAAGCTCAGTTGCTGTCTCATCAACGTTGGTGGCCGTGTGATGAACAAT		5338
Qy	1854	LeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeu		1873
Db	5339	CTGATGACACGACAAGAGGCCACAGAGATGACAGATGATGCTGAGATCGAGCTG		5398
Qy	1874	GluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTyrPro		1893
Db	5399	GAGATG-----		5404
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Db 5444 -----CCCTGCCCTGC 5455
QY 1934 GluValProValPro---LeuGlyProAspLeuLeuThrVal----- 1946
Db 5456 CCCTGCCCCCTGCTGTGCTGCGCCGAGCTGCCCACTAGTTCACTGGGGCTCCGGGG 5515
QY 1947 ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsn 1966
Db 5516 CGAGGATCGGGAGGGGAGGTGCTGAGGC--GACACCGAGACTCACTGTGCCGGGAC 5572
QY 1967 ---GlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGln 1985
Db 5573 TGCTATTCTCCAGCCCAAGAGACCCCTG-----TGG-----CTGGAC 5608
QY 1986 SerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeu 2005
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QY 2006 ProlysAspVal---HisTyrLeuLeuGlnProHisGlyAla----- 2018
Db 5669 TCTGGGTCCGTCTTCCACCACTACGCCCTCACCTGACGGCTGTGGAAGTGCACCATGAC 5728
QY 2019 -----ProThrTyrGlyAlaIleProlysLeuProProPro 2030
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QY 2031 GlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaIleArgThrAspSer 2050
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QY 2069 ProSerCysProLeuThrArgSerSerSerPheTyrGlyGlySerSerIleGlnValGln 2088
Db 5909 CCAGAGAG-CCTGCTGTGCAGAT-----GGGGCCATTCCATTCAACC-CTG 5954
QY 2089 GlnArgSerGlyIleGlnSerLysValSerLysHisIleArg----- 2102
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QY 2103 -----LeuProAla 2105
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QY 2192 LeuCysProSerProSerSerLeuGlyGlnProLeuGlyGlyProGlySerArgPro 2211
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QY 2212 LysLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnGlySerArg 2231
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QY 2232 ProProCysSerPro-GlyValCysLeuArgArgAlaProAlaSer----- 2247
Db 6377 CCGTTTACTCTGCGTGGGCTGGGGCCCATCAGCGGTAGCCACAGACAGTGGCGGCTCCAC 6436
QY 2248 -----AspSerLysAspProSer 2253
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RESULT 12
US-09-949-016-15601
; Sequence 15601, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15601
; LENGTH: 70308
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15601
Alignment Scores:
Pred. No.: 9.78e-114 Length: 70308
Score: 2055.00 Matches: 697
Percent Similarity: 21.05% Conservative: 35
Best Local Similarity: 20.04% Mismatches: 108
Query Match: 17.09% Indels: 2640
DB: 4 Gaps: 21
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QY 18 SerAlaArgProSerSerAspProProGlyProArgLeuAlaArg-----GlyTyrThr 35
Db 9539 TTGTTCTTCTTTACAGATGAGGAAGCTGGGTCAGAGAGGTGAGATGACCAAGGTG--- 9595
QY 36 ArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArgSer--- 54
Db 9596 -----GACTCCCTTCTCTGATGAGGAGTCTG 9622
QY 55 -----SerThrThrCysProGlyProGlyAlaIaIaGlySerThr 69
Db 9623 GGGCTGGGGCTGCTGCGTGTATGTCAAGGCCCTGGCACCAACCTGCT---TAGCCT 9679
QY 70 GluLysAspProGly-----SerAlaAspSerGluAla 80
Db 9680 CAGATGAGACCAAGAGGTAAACGAGAGAGAGGTGTTAGGGGGGGCTCGGGGGCGGCTT 9739
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Db 12802 CACAGGCATGCGCATCTTGTTCACGTTGTCTGTGATACGCTGCCCATGCTGGGCAACGT 12861
QY 246 1LeuLeuLeuCysPhePheValPhePhe11ePheGly11eValGlyValGlnLeuTrpAl 266
Db 12862 CCTGCTGCTCTGCTTCTTCTTCTTCTTCTTCCATCTTCGGCATCGTCGGCGTCCAGCTGTGGC 12921
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QY 412 ----- 412

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Db 14481 GTTACAGAGTCTGTCTTTTTTTGTAAAGACAAGGGAGTCAATTGGCAATTTGTTACTG 14540
QY 412 ----- 412
Db 14541 GGGAGGGGAGAGAAAGCTAAACATCCTGAATGCTTGCAATTAAGAATTAATTCTACCA 14600
QY 412 ----- 412
Db 14601 AAATTCGATCAGTGAATGGTGTAAATGCTGCTGATCTTATTCCTGCGCAGTT 14660
QY 412 ----- 412
Db 14661 CAGAAATTGCCAGACTTTAAGAGCAGAAGCGAGCAAAAGCACAATATTAAATAG 14720
QY 412 ----- 412
Db 14721 TTTTAATCACTACCATTCATAGTTAATACTTCATCGCCACCACTTTGAGTAATAATTA 14780
QY 412 ----- 412
Db 14781 TTGAGCACTTACTATGCGCCAGCCCTGATCTAAGCACTTCAATGTGCTGCAATTA 14840
QY 412 ----- 412
Db 14841 ATCCTCACCCTGATCCTCTCAATTTTACAGATGAGAACTGACATTTCTCATTTATCT 14900
QY 412 ----- 412
Db 14901 GACCTTACGAGCGCTTGGCTATGCTGTATTAATCTCCAAGAGTGGGGCATCACTGC 14960
QY 412 ----- 412
Db 14961 TGACGTATGCTTAACATCTGCTGCTGTTAATCCTGCTGCTCCCTGTGAGGTCCAG 15020
QY 412 ----- 412
Db 15021 GGCAGGATTGTGTCCTCCCATCTCTTAAATGAGAAATTCAGCGCCCCAGAGGGTGGGTAC 15080
QY 412 ----- 412
Db 15081 TGGGCAAGATCACACAGAAAGTAAGCGGCTGGGCTGAGAAATTCAGTCCAGGCTAAAG 15140
QY 412 ----- 412
Db 15141 ACTCCATTCAGCCTTTCTTCATGTCAACCAAGAGGCCAAGCAGAGCCAGAGAGG 15200
QY 412 ----- 412

Db 15201 GACAGACATTGAGAGAAAGAGATTTAAGAAAGATTAAGATCTACTCAGGACCTAGAGTAG 15260
QY 412 ----- 412
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QY 412 ----- 412
Db 15321 TGAGAAAGACAAGTCCCCAAGGCCACTCTATTCTGCTGCTAACTTCCCCGTGTGCGG 15380
QY 412 ----- 412
Db 15381 AAGAGTGGCAGGCTTGGGGCGAAGCCTGACTGAGGCTGTTCATCCCTGCGCACCA 15440
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Db 15441 CCTCAAGGGGTGAGGCCAGTCTTCAAGGAAGTGGGCTCTTCTCAACATGTGCCCCCCC 15500
QY 412 ----- 412
Db 15501 ACCCCCACTCCCTTTCCCTCCTGGGCTTGGGAGAGGGGGAAGAGACAGAGAGATA 15560
QY 412 ----- 412
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QY 412 ----- 412
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QY 412 ----- 412
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QY 412 ----- 412
Db 15981 AGCAGAGTCTGTAAATGATGTTTTGTCAAGATCTCAAGGCTCAATATAATTGAAAA 16040
QY 412 ----- 412
Db 16041 CCCCATGTCCCTAATATTCGTTCAATTTCCACAGCATTCGCTACTCTTAATGAAATTGC 16100
QY 412 ----- 412
Db 16101 GGAAGGGTGTGCTGCTCTGCAAGTGTGCGTTTAAAGGACAGGAAATTTGAGAGATTG 16160
QY 412 ----- 412
Db 16161 CAGATAACCATGTTCAATAGCAATATCTTGAAATTTATAGAGCTTGGTTCAGTCT 16220
QY 412 ----- 412
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QY 412 ----- 412
Db 16281 GTTCTTAACCTGTCTGATGAGATTACAATAGCATCACCTCTGAGGCTGTCTTAATAAA 16340

QY 412 ----- 412
Db 16341 TAAATGAGATAATGCTTGAAAATACTGAGCGGTGGCTCATAGGAATGCTC 16400
QY 412 ----- 412
Db 16401 CGTATGTGTGGTGGCACTGTGATTCACCTTTCTTCAGGACATTCTCTTCGTCC 16460
QY 413 -----ValGlySerPhePheMetIleasnLeuCysLeuValIleAlaThrG 429
Db 16461 CACCCCTACAGGTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGGTGATGCCACGC 16520
QY 429 InPheSerGluThrLysGlnArgGluSerGlnLeuMetArgGlnArgValArgPheL 449
Db 16521 AGTTCTCAGAGACCAAGCAGCGGAAAGCAGCTGATGCGGAGCAGCGTGTGCGGTCC 16580
QY 449 euserAsnAlaserThrLeuAlaserPheSerGluProGlySerCysTyrGlnGluLeuL 469
Db 16581 TGTCCAACGCCAGCACCTGGCTAGCTTCTTGAGCCCCGGCAGCTGCTATGAGGAGCTGC 16640
QY 469 eulYsTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgA 489
Db 16641 TCAAGTACCTGGTGTACATCCTTCGTAGCGAGCCCCGACAGCTGTGCTCATGGTCTCTCGG 16700
QY 489 IaIleGlyValArgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProG 509
Db 16701 CAGCAGGTGTGCGGTGGCTGTGCTCAGACGCCAGACCCCTCGGGGGCCAGGAGACC 16760
QY 509 InProSerGlySerCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisH 529
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QY 529 iSHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgA 549
Db 16821 ACCACCAACCAACCATCAACCACTACCACTGGGCAATGGGACGTCAAGGCCCCCCGGG 16880
QY 549 laseRProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProp 569
Db 16881 CCAGCCCGGAGATCCAGAGACAGGAGTGGGTCCCCGCCGCTCATGTGCCACCAAC 16940
QY 569 roSerThrProThrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheT 589
Db 16941 CCTCGACGCTGCTCTCTCGGGGCCCTGCTGTGGCGCAGAGTCTGTGCACAGCTTCT 17000
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Db 17001 ACCATGCCGACTGCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCAT 17060
QY 609 erGluAlaserGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerP 629
Db 17061 CTGAGGCATCCGGCAGACGTGTGGCAGCGGGAAGTGTATCCCAACGTGCACACCAAGCC 17120
QY 629 roProProGluIleLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProp 649
Db 17121 CTCCACCGGAGACGCTGAAGAGAGAGACACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCC 17180
QY 649 roThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuG 669
Db 17181 CAACCTCAACGCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAAGCTGCTGG 17240
QY 669 luThrGlnSerThr----- 673
Db 17241 AGACACAGAGTACAGGTGAAGAACTGTGGTGAGGCATGTGGTGCCCTCGTGTGGGAC 17300
QY 673 ----- 673
Db 17301 TGGGTGCGTCCCAAGGGGGACTAGGGGCTGTGAGTCAGAGGGAACGAGGCTTATATTC 17360
QY 673 ----- 673
Db 17361 TCATGCTGCCTCTCATGGCTTAGGACCTTCAACAGTCACATCCCTGCTATGAGCTCGA 17420

QY 673 ----- 673
Db 17421 ATTTTCATCTGCTAAAGTGAACCTCATTAATTCCTACATTTGTAATAGCAGTAATATCA 17480
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Db 17541 ATGCTGTGCTGTACATGCTTTGCCGGCAAAATTCATTGGATCCTCTACCCAT 17600
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Db 17601 TAAGTATAGCCTTCTTAGCATCCCATTTGTGTGATGAGAACAGAGGCTTGAGGGG 17660
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Db 17721 GGACTCCTGTGTGAGGCTCAGAGAGAAATGTTGTGACTGTGCCAGCTTCATGCC 17780
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QY 673 ----- 673
Db 17901 CTCTCCCAAGACAGACAGTTCACTGTAGCTGCAGCCACGGCCTGTGTTCAGGAAGAT 17960
QY 673 ----- 673
Db 17961 GTGGACGTGGGGAGCAGCGGATATTCTGTGGGATGTTAAGTGGAAATGSGGCTGGGA 18020
QY 673 ----- 673
Db 18021 CCAGAGGTGCTATCACAGAACCCAGACGAAAGTTTCTATGCCAGTCTCTCCACTACC 18080
QY 673 ----- 673
Db 18081 CTGCCACGGGACGTGGGCCAGTGCATGCACCCACGTTTTTATTCTCCTGTGTAAAG 18140
QY 673 ----- 673
Db 18141 GCAAGGCTGGGCCATTAATTACTCTCAGTGGGTGCTTACTGACTCCCTCTGTGTCCAGA 18200
QY 673 ----- 673
Db 18201 TGCAGTCAAGGGAAGAAATGTCGCTGAGAGCCCACTGGGGCCAGGCCCTGACGGGGGGC 18260
QY 673 ----- 673
Db 18261 TTCCACATCATGCTTTACTGTGTACTCTCTGAGGTTCTCATATTCTGTGATCAAAAGCTG 18320
QY 673 ----- 673
Db 18321 GATTAAAGGACATTGATGTCTTGGGCTAGGTCCCTGAGTGTGTGCCACGAGTGATC 18380
QY 673 ----- 673
Db 18381 TAGTATCGGTATGCGTCTATGTCCATGAAGGGGTCCAGTGTGTGTGTGCGTGTG 18440
QY 673 ----- 673
Db 18441 CATGACGTGTCTGTGTTCATATGCAATATGTGTGCACATGTGCTTGATGTGTAGGTG 18500
QY 673 ----- 673

Db 2 TGCGGCTCCGAGCGCTGCAACATCCTGGAGGCTTTGACGCTTCATTTTCGCTTTT 61
QY 161 AlValGluMetValValIlysMetValAlaleuGlyIlePheGlyIysCysTyrLeu 180
Db 62 GCGGTGAGATGATCATCAAGATGGTGGCTTGGGGCTGTTCGGGCAGAGTGTTCCTG 121
QY 181 GLYAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer 200
Db 122 GGTGACACGTGGAAcAGGCTGGATTTCCTTCATCGTCGTGGCGGCATGATGAGTACTCG 181
QY 201 LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgProLeu 220
Db 182 TTGGACGGACACACGTAGCCTCTCGGCTATCAGACCGTGGGGTGTCTGGCGCCCTC 241
QY 221 ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrLeu 240
Db 242 CGCGCCATCAACCGCGTGCCTAGCATGGGATCCTGTCACTCTGCTGTGATACGCTG 301
QY 241 PrometLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVal 260
Db 302 CCCATGCTCGGAAcGTCTTCTGTGCTGTCTTCTGCTTCCTTCATTTTCGCATCGTT 361
QY 261 GLYValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer 280
Db 362 GCGGTCCAGCTGTGGCTGGCTCCTGCGGAACCGTGCTTCTGGAACAGTGCCCTTGTG 421
QY 281 LeuProLeuSerValasp--LeuGluProTyrTyrGlnThrGluAsnGluAspGluSer 299
Db 422 AGGAACAACAACCTGACCTTCCTGCGGCGGTACTACCAAGACGAGAGGGCGAGAGAAC 481
QY 300 ProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThr 319
Db 482 CCGTTCATCTGCTCTCAcCGCGAGACAGGCATGACAGAGTGTCTGCACATCCCC--- 538
QY 320 LeuArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsn--- 338
Db 539 -----GGCCGCCGAGAGCTGCGCATGCCCTGGACCCCTGGGCTGGAGGCCCTACACGAG 592
QY 339 -----SerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 352
Db 593 CCGCAGGCCGAGGGGTGGGCGCTGCACGCAAGCCTGCATCACTGGAACcAGTACTAC 652
QY 353 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 372
Db 653 AACGTGTGCCGCTGGGTGACTCCAAcCCCAACAAGGTGCCATCACTTCGACAACATC 712
QY 373 GLYTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 392
Db 713 GGCTACGCTGTGATGGCATCTTCAGGTGATCAcGCTGGAGGCTGGGTGACATCATG 772
QY 393 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 412
Db 773 TACTACGTATGAGCGCCACTCATTCACACTTCATCTATTTCATCTGCTCATCATC 832
QY 413 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 432
Db 833 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGGTGTGATGGCAGCAGTTCTCGGAG 892
QY 433 ThrLysGlnArgGluSerGlnLeuMetArgGluArgValArgPheLeuSerAsnAla 452
Db 893 ACGAAGCAGCGGAGAGTCAcGTGATGCGGAGCAGCGGCACCGCACTGTCCAACGAC 952
QY 453 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 472
Db 953 AGCAGCGCTGGCAGCTTCTCCGAGCCTGGCAGCTGTACGAAGAGCTG----- 1000
QY 473 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVal 492
Db 1000 ----- 1000
QY 493 ArgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGly 512
Db 1000 ----- 1000

QY 513 SerCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 532
Db 1000 ----- 1000
QY 533 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGlu 552
Db 1000 ----- 1000
QY 553 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 572
Db 1000 ----- 1000
QY 573 ThrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAsp 592
Db 1000 ----- 1000
QY 593 CysHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSer 612
Db 1000 ----- 1000
QY 613 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 632
Db 1001 -----CCCGTACTGCAC----- 1012
QY 633 IleLeuLysAspLysAlaLeuValGluValAlaProSerProGly-ProProThrLeuTh 652
Db 1013 -----CCGTGCCCTGGAAGACCGG----- 1031
QY 652 rSerPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSe 672
Db 1031 ----- 1031
QY 672 rThrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerTyrAlaAspSerG 692
Db 1032 -----GAGGTGAGCTCAGCGGCTCGGAAGTGG 1060
QY 692 yAlaCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSe 712
Db 1061 A----- 1061
QY 712 rAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAl 732
Db 1062 -----GACTCAGATGGCCGTGGCGCTTATGAATTCAcGACGAGACGT 1102
QY 732 aglnHisSerAspLeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAs 752
Db 1103 CCGGACCGGTGACCGCTGGGACCC-----ACGCGACCAcCCCG 1141
QY 752 pAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysI 772
Db 1142 -GGCAGCGCAGGCTGATGGCGCGCTGTGGTTACTTCAGCGGCAAGCTGCGCGCAT 1200
QY 772 eValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSe 792
Db 1201 CGTGACAGCAAGTACTTCAGCGGTGGCATCATGATGGCCATCCTGTCAACAGCCTGAG 1260
QY 792 rMetGlyIleGluTyrHisGlnGlnProGluGluLeuThrAsnAlaLeuGluIleSerAs 812
Db 1261 CATGGCGGTGAGTACCATGAGCAGcCCGAGGAGCTGACTAATGCTCTGAGATCAcCAA 1320
QY 812 nIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPr 832
Db 1321 CATGTGTTCACcAGCATGTGTGCTTGAGATGCTGTAAGCTGTGGCTCGCGGCC 1380
QY 832 oPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerVa 852
Db 1381 TCTGGGTATCATCCGAACCCGTAAcATCTTCAGCGGCATCATCGTGTATCAcCGGT 1440
QY 852 lTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMe 872
Db 1441 CTGGGAGATCGTGGGGCAGGCGGACGGTGGCTTGTGTGTGCTGCGCACCTTCGGGCTGCT 1500

Db 707 GCCA-----ACACTGAGGCGCTGTGCGTGTGAGGCCCTGAAGCTGGT 751
QY 223 eAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrLeuProMetIe 243
Db 752 GTCTGGGATTCAGATTGGCAGGTGGTGTCAAGTCCATCATGAGAAGCCATGGTCCACT 811
QY 243 uGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGl 263
Db 812 CCTGCAGATTGGCGTGTCTTCTCTTGGCCATCTCATGTGTTGCCATCATGTGGCCCTGGA 871
QY 263 nLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProIe 283
Db 872 GTTCTACATGGGCAAGTTCACACAAGCGCTGTTTC-----CCCAA 910
QY 283 uSerValAspLeuGluProTyrTrpGlnThrGluAsnGluAspGluSerProPheIleCy 303
Db 911 CAGCACAGATGCGGAGCCCGTG----- 932
QY 303 sSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGl 323
Db 932 ----- 932
QY 323 uGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerAsnTh 343
Db 933 -----GGTGACTTCCCTGTGGCAGAGAGCCCGGCTGTGCGAGGCGCACAC 985
QY 343 rThrCysValAsnTrpAsnGlnTyrTrpThrAsnCysSerAlaGlyGluHisAsnProPh 363
Db 986 TGAAGTGC-----CGGAGTACTGGCCA-----GGACCCAA 1015
QY 363 eLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIl 383
Db 1016 CTTTGGCATCACCACCTTGGACAATATCTGTTGGCCATCTTGACGGGTGTTCCAGTGCA 1075
QY 383 eThrLeuGluGlyTrpValAspIleMetTyrPheValMetAsp---AlaHisSerPheTy 402
Db 1076 CACCATGAGGCGTGGACTGACATCCTCTTAATAACAACGATGCGGCGGCAACACCTG 1135
QY 402 rAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuCy 422
Db 1136 GAAGTGGCTTACTTCATCCCTCTCATCATCATCGGCTCTTCTTCATGCTCAACCTGGT 1195
QY 422 sLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSer----- 438
Db 1196 GCTGGGCGTCTCTCGGGGAGATTGGCCAAGAGAGAGAGGGTGGAGAACC GCCGCGC 1255
QY 439 -----GlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAl 456
Db 1256 CTTCTGAAGCTGCGCGGCGCAGCAGCAGATCGAG----- 1289
QY 456 aSerPheSerGluProGlySerCysTyrGlnGluLeuLeuLysTyrLeuValTyrIleIe 476
Db 1290 -----CGAGAGCTCAACGGGTACTGAGTGGATCTT 1321
QY 476 uArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLe 496
Db 1322 CAAGGCGAGAGAGTATGCTGGCCGAGAGGAC----- 1355
QY 496 uLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrAr 516
Db 1356 -----AGGAATGCAGAGAGAAGTCCCTTTGGACGTGCTGAAGAG 1396
QY 516 gSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHis 536
Db 1397 AGCGGCCACCAAGAGAGACAATAATGACCTGATCCAC----- 1433
QY 536 sTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspAr 556
Db 1434 -----GCAGAGAGGAGAGAGACC 1453
QY 556 gAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProThrProSerG 576
Db 1454 GTTTGCAGAT----- 1463

QY 576 yGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGl 596
Db 1463 ----- 1463
QY 596 uProValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrVa 616
Db 1463 ----- 1463
QY 616 lGlySerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAs 636
Db 1463 ----- 1463
QY 636 pLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIl 656
Db 1463 ----- 1463
QY 656 eProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCy 676
Db 1463 ----- 1463
QY 676 sHisSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPr 696
Db 1464 -----CTGTGTGCTGTGGATCCCTTCGCGCCGCCACG----- 1499
QY 696 oAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVa 716
Db 1500 -----CTCAGAGCGGGAGAAGACAGAGAGCTGTCATACTT 1534
QY 716 lMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAs 736
Db 1535 C----- 1535
QY 736 pLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSe 756
Db 1536 -----CGAGGAAAGAGAG----- 1550
QY 756 rSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLy 776
Db 1551 ----ATGTTCCGGTTTTT-----ATCCGGCGCATGGTGAAGCTCA 1588
QY 776 sTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetCylIleGl 796
Db 1589 GAGCTTCTACTGGGTGGTGTGCTGCTGCGTGGTGGCCCGCAACACTGTGTGTGCCATGGT 1648
QY 796 uTyrHisGlnGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheTh 816
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QY 816 rSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIl 836
Db 1709 GGGTCTCTTCTCACAGAGATGTCCTGAAGATGTATGCGCTGGGCCACAGAACTACTT 1768
QY 836 eLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleVa 856
Db 1769 CCGTCTCTCTTCAACTGCTTGACTTTGGGTCATCGTGGGAGCGTCTTGAAGTGGT 1828
QY 856 lGlyGln-----GlnGlyGlyGlyLeuSerValLeuArgThrPheArgLe 871
Db 1829 CTGGGCGGCCATCAAGCCGGGAAGCTCTTTGGGATCAGTGTGCTGCGGCGCTCCGCCCT 1888
QY 871 uMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLe 891
Db 1889 GCTGAGGATCTTCAAAAGTACAGAACTACTGGAAGTCCCTGCGGAACCTGGTGTGCTCCT 1948
QY 891 uMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIl 911
Db 1949 GCTGAAGTCAAGTCAATGATCAAGCCTGCTTCTTGTGCTCTTCCGTGTCAATTGTGCT 2008
QY 911 ePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAs 931
Db 2009 CTTGCGCCTGTGGGATGACAGCTGTTGGGGAGACAGTTCAACTTCCAGAGATGAGACTCC 2068

QY	931	pThrLeuProaspArgLysAsnPheaspSerLeuThrPalaIleValThrValPheG1	951
Db	2069	CACA-----ACCAACTTCGACACCTTCCCTGCCGCATCTCACTGTCTTCCA	2116
QY	951	nIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMet-----	966
Db	2117	GATCCTGACGGGAGAGAGACTGGAATGCAGTGATGTATCACGGGATCGAATCCGAAGCGG	2176
QY	967	-AlaSerThrSerSerTrpAlaIleuTyrPheIleAlaLeuMetThrPheGlyAsnTy	986
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Db	2177	CGTCAGCAAGGAGATGTTCTCGTCTTTACTTTCATTTGTCCTGACACTGTTTCGAAACTA	2236
QY	986	rValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGlyAspAl	1006
		:::::	
Db	2237	CACCTGCTGTAATGTCTTCTTGCGCATCGCTGTGGACAACCTGGCCAAAGCCCAAGAGCT	2296
QY	1006	aThrLysSerGluSerGluProAsp-----	1014
		:::	
Db	2297	GACCAAGGATGAAGAGAGATGGAAGAAGCAGCCCAATCAGAAGCTTGCTCTGCAAAAGGC	2356
QY	1015	-----Phe-PheSerProSerValAspGlyA	1023
Db	2357	CAAGAAGTGCTGAAGTCAGCCCATGTCTGCGCGGAACATCTCCATCGCCGCAAGCA	2416
QY	1023	sPGLysPArgLysLysArg-LeuAlaLeuValAlaLeuGlyGluHisAla-----	1039
		:::::	
Db	2417	GCAGAACTCGGCCAAGCGCGCTCGTGTGGAGACAGCGGCCAGCAAGCTAAGGCTGCA	2476
QY	1040	-----GluLeuArgLysSerLeu-----ProProLeu	1049
		:::::	
Db	2477	GAACTGCGGGCCAGCTGCGAGCGCTGTACAGCGAGATGGAACCCGAGAGCGGCTGCG	2536
QY	1050	IleIleHisThrAlaAlaThrPrometSerHisProLysSerSerSerThrGlyValGly	1069
		::: :::::	
Db	2537	CTTCGCACTACGCGCCACCTGCGGCCGACATGAAGACGCACTGACCGCGCGCTGCT	2596
QY	1070	GluAla-LeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAl	1089
Db	2597	GGTGAGCTGGCGCGCAGCG	2656
QY	1089	ala-----HisHis-----GluMe	1094
		:::	
Db	2657	TGCGGAGGCCCCGAGGCGTCGACCTCCGCGCAGGACCAACCGGCACCGCAACAAGA	2716
QY	1094	CLysCysPro-----	1097
Db	2717	CAAGACCCCGCGCGGGGACCAAGACCGAGCAGAGCCCCGAAGGCGGAGACGGGGA	2776
QY	1098	-ProSerAlaArgSerSer-----ProHisSerProTrpSerAlaIleSerSerTr	1114
Db	2777	GCCCGGTGCCGAGAGAGCG	2834
QY	1114	pThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSe	1134
		:: ::	
Db	2835	-----GGGGCCCCGAGGCGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	2875
QY	1134	rProSerGlyLysArgArgSerLeuLeuSerGlyGluGlnGluSerGlnAspGluG1	1154
Db	2876	CCCCGAGGCG	2935
QY	1154	u-----GluSerSerGluGluAspArgAlaSerPr	1164
		:: ::	
Db	2936	GCCCCGAGCGCACCGCGCGACCGGACCAAGATCCGAGCAAGAGTGCGCGCGCGCGCAA	2995
QY	1164	calagLysSerAspHisArgHisArgGlySerLeuGlu-----ArgGluAlaLysSe	1181
Db	2996	GGGCGAGCGAG	3055
QY	1181	rSerPheAspLeuProAspThrLeuGlnValProGly----LeuHisArgThrAlaSerG1	1200
		::	
Db	3056	CGGG-----GAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA	3094
QY	1200	YArgSerSerAlaSerGlu-----HisGlnAspCysAsnGlyLysSerAlaSerGlyAr	1218

Db	3095	GGCGGAGCTTGCTCACGAGGCTGTGAGAAAGAGACCACGAGAAAGAGGCCACGAGAA	3154
Qy	1218	gLeuAla-----ArgThrLeuArgThrAspProGlnLe	1230
Db	3155	GGAGGCTGAGATAGTGAAGCCGACAGAAAGAGAGCTCCGGAACCAAGCCCGCGGA	3214
Qy	1230	uAspGlyAspAspAspAspGluGlyAsnLeuSerLysGlyGluArgIleGlnAlaTr	1250
Db	3215	GCCACACTGTGACCTGGAGACCAGTGGACTGTGACTGTGGTCCC-----	3260
Qy	1250	pValArgSerArgLeuProAlaCysCysArgGluArg-----	1262
Db	3261	---ATGCACACACTGCCCGCACCTGTCTCCAGAGGTGAGAAACAGCCAGAGATGC	3316
Qy	1263	-AspSerTrp-----	1265
Db	3317	AGACATCAAGCGGACGCTCACTCCGATGGCAGTCAGCCCCAGACCCGAACACTATTGT	3376
Qy	1265	-----	1265
Db	3377	ACATATCCCACTGATGCTGACGGGCCCTCTTGGGGAAGCCACGGTCGTTCCAGTGTA	3436
Qy	1265	-----	1265
Db	3437	CGTGAAGCTGAAAGCCAAAGCAGAGGGAAGAGAGGTGAAAGCGATGACGTGATGAG	3496
Qy	1266	-----SerAlaTyrIlePheProGlnSerAr	1275
Db	3497	GAGCGGCCCCGGCCTATCGTCCCATACAGCTCCAGTGTCTGTTAAGCCCCACCAACCT	3556
Qy	1275	gpPheArgLeuLeuCySHisArgIleIleThrHisLysMetPheAspHisValLeuVa	1295
Db	3557	GCTCCGCGCTTGTGCCACTACATCGTGACCATGAGTAATTCCAGGTGGTCACTTCGT	3616
Qy	1295	IleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSe	1315
Db	3617	GGTCATCGCCTTGAGCAGCATGCCCTGGCTGCTGAGAACCCA--GTGCCACAGACTC	3673
Qy	1315	rAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGl	1335
Db	3674	GCCAGGACACAGCCTCTGAATATACCTGATTAATCACTTCACTGTGCTTTAACCCTTGA	3733
Qy	1335	uMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSe	1355
Db	3734	GATGTGATTAAGATGATGACTTGCGGACTGCTGCTTCAACCTGAGGCTTATTTCCGGGA	3793
Qy	1355	rSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSe	1375
Db	3794	CTTGTGAAACATTTCTGGAC-----TTCAATGTGGTCAATGGCGCCTGTGGTGGC	3841
Qy	1375	rMetVal---SerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLe	1394
Db	3842	GTTTGCTTTCTCAGGATCCAAAGGAAAGACATCAATACCATCAAGTCTCTGAGAGTCT	3901
Qy	1394	uArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValGlnI	1414
Db	3902	TCTGTCTCTGGCGGCCCTCAAGACCATCAACGGCTGCCCAAGCTCAAGGCTGTGTTGA	3961
Qy	1414	uThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePh	1434
Db	3962	CTGTGTGTGAACCTCCCTGAAGATGTCTCAACATCTGATTGTCTACATGCTCTTCAT	4021
Qy	1434	eIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGl	1454
Db	4022	GTTCATATTTGCCGTCATTTGCGGTGACGCTCTTCAAGGGAAGTTTCTTCACTGACAGA	4081
Qy	1454	YGLU-----AspThrArgAsn-----IleThrAsnLysSerAspCy	1466
Db	4082	TGAATCCAAGAGACTGAGAGGACTGCAGGGGTCAAGTATTGATTATGAGAAAGAGGA	4141
Qy	1466	sAlaGluAlaSerTyrArg--TrpValArgHisLysTyrAsnPheAspAsnLeuGlyGl	1485

Db 4142 AGTGAAGCTCAGCCAGCAGTGAAGAATACGACTTTCACTACGACAATGTGCTCTG 4201
QY 1485 nAlaleuMetSerleuPheValleuAlaSerlysAspGlyTrrValAspIleMetTyrAs 1505
Db 4202 GGCTCTGCTGACGCTGTTCACAGTGTCCACGGAGAGGCTGCCCATGTGCTGAACA 4261
QY 1505 pGlyleuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrrMetIe 1525
Db 4262 CTCGGTGATGACCCTATGAGGAGCAGGCTCCAAAGCCCTGGGTACCCGATGAGCTGTC 4321
QY 1525 uLeuTrrPheIleSerPheleuLeuIleValAlaPhePheValleuAsnMetPheValG 1545
Db 4322 CATCTTCTACGTGCTCTACTTGTGGTCTTCCCTTCTTCTTCGTCACATCTTTGTGC 4381
QY 1545 yValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgAr 1565
Db 4382 TTTGATCATCATCACTTC-----CAGGACAGGGGACAAAGGTGAT 4423
QY 1565 gArgGluGluLysArgleuArgArgleuGluLysLysArgArgSerLysGluLysGlnMe 1585
Db 4424 GTCTGAA-----TGCAGCCTGGAGAAGAAGAGGGCTTGCAATGACTTCGC 4471
QY 1585 tAlaGluAlaGlnCysLysProTrrTrrSerAspTrrSerArg-----PheArgleu 1603
Db 4472 CATCAGCGCCAAACCCCTGACACGGGTACATGCCCAAACCGGCAGTCGTTCCAGTATA 4531
QY 1603 uValHisHisleuCysThrSerHisTrrleuAspLeuPheIleThrGlyValIleGly 1623
Db 4532 GACGTGACATTTGTTGGTCTCCCGCCCTTTGAATACCTTCATCATGGCCATGATAGCCCT 4591
QY 1623 uAsnValValThrMetAlaMetGluHisTrrGlnGlnProGlnIleleuAspGluAla 1643
Db 4592 CAACACTGTGGTGTGATGATGAAAGTTCTATGATGACCCCTATGAGTACGAGCTGATGCT 4651
QY 1643 uLysIleCysAsnTrrIlePheThrValIlePheValPheGluSerValPheLysleuVa 1663
Db 4652 GAAATGCCCTGAACATCGTGTTCACATCCATGTTCTCCATGGAATGCGTGAAGATCAT 4711
QY 1663 lAlaPheAlaPheArgArgPhePheGlnAspArgTrrAsnGlnleuAspLeuAlaIleVa 1683
Db 4712 CGCCTTTGGGTGCTGAACATATTTCAAGATGCCGTGAATGTCTTGACTTTGTCACTGT 4771
QY 1683 lLeuLeuSerIleMetGlyIleThrleuGluGluIleGlu-----ValAs 1698
Db 4772 GTTGGAGATATTACTGATATTTTAGTAAACAGAGATTGCCGAACGAACAATTTCATCA 4831
QY 1698 nLeuSerleuProIleAsnProThrIleIleArgIleMetArgValleuArgIleAlaAr 1718
Db 4832 CCTCAGC-----TTCCTCCGCTCTTTGAGCTGCGG 4864
QY 1718 gValleuLysleuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetG 1738
Db 4865 GCTGATCAAGCTGCTCCGACAGGCTACACCATCCGATCCTGCTGTGACCCTTTGTCCA 4924
QY 1738 nAlaLeuProGlnValGlyAsnleuGlyleuLeuPheMetLeuLeuPhePheIlePheAl 1758
Db 4925 GTCTTCAAGGCCCTGCCCTACGTGTGTGCTCATTTGCCATGCTGTCTTCATCTACGC 4984
QY 1758 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG 1778
Db 4985 CATCATCGGCATGCAGGTGTTGGGAATATTGCCCTGGATGATGAC-----ACCAG 5035
QY 1778 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrleuPheArgVa 1798
Db 5036 CATCAACCGCCACAACAACCTTCGGACGTTTTCGAAGCCCTGATGCTGTTCAGAG 5095
QY 1798 lSerThrGlyAspAsnTrrAsnGlyIleMetLysAsp-----ProSerArgAspCysAs 1816
Db 5096 CGCCACGGGGAGGCTGGCAGAGATCATGCTGCTGCTGAGCAACAGGCGCTGTGA 5155
QY 1816 pGlnGlu-----SerThrCysTrrAsnThrValIleSerProIleTrrPheValSerPh 1834
Db 5156 TGAGCAGGCCAATGCCACCGAGTGTGAAGTGACTTTGCCCTACTTCTACTTCGTCCTT 5215

QY 1834 eValleuThrAlaGlnPheValleuValAsnValValIleAlaValleuMet----- 1851
Db 5216 CATCTTCTGTGCTCTTCTGTATGTGAACCTTTTGTGGCTGTGATCATGACAATT 5275
QY 1852 -----LysHisleuGluGlu-SerAsnL 1859
Db 5276 TGAGTACCTCAGCGGACTCTTCATCTAGTCTTCACCACCTTGATGATTCATCCG 5335
QY 1859 ySgluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeu- 1878
Db 5336 GGTCTGGCTGAATACGACCGGCTGCGTGTGGCCGATCAGTTACAATGACATGTTGA 5395
QY 1879 SerProGlnProHisSerProleuGlySerProPheleuTrrProGlyValGluGlyVal 1898
Db 5396 GATGCTGAACACATGTCCCGCCTCTGG-----GCTGGGAGAAATGCC 5443
QY 1899 AsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAla 1918
Db 5444 TGCTCGAGTTGCTTACAGCGCCTGTTG--CATGAACATGCCCATCTCCAACGAGGA 5500
QY 1919 SerGlyPheSerleuGluHisProThrMetValProHisProGluGluValProValPro 1938
Db 5501 CATGACTGTTCACTTCACGCTCCACGCTGATGGCCCTCATCCGACGGCACCTGAGATCAA 5560
QY 1939 LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerleuPro 1958
Db 5561 GCTGGCCCAAGCTG-----GACAAAGCAGCATCAGTGTGACCGGAGTTGAG 5608
QY 1959 AsnAspSerTrrMetCysArgAsnGlySerThrAlaGluArgSerleuGly----- 1975
Db 5609 GAAGAGATTTCCGTTGT---GTGGCCAATCTGCCCAAGAAGACTTTGGACTTGCTGTGT 5665
QY 1976 -----HisArgGlyTrrGlyLeuProLysAlaGlnSerGly 1987
Db 5666 ACCACCCCAATAAGCCTGATGATGACAGATGGGGAAGTTTATGACGCTGATGATATT 5725
QY 1988 SerIleuSerVal-----HisSerGlnPro----- 1996
Db 5726 TGACTTCTTCAAGCAGAACAAACCAACAGAGACCATGACAGAGGCTCTGAGGCCT 5785
QY 1997 ---AlaAspThrSerCysIleleuGlnleuProLysAspValHisTrrleuLeuGlnPro 2015
Db 5786 CTCCAGATGGGTCTGTGTCTGCTTCCACCCCTGGAAGGCCAC----- 5830
QY 2016 HisGlyAlaProThrTrrGlyAlaIleProLysleuPro----- 2028
Db 5831 CCTGAGACAGACAGCCGCTGTGCTCCGAGAGCCGGGTTTCTTCGACAGAAAGAG 5890
QY 2028 ----- 2028
Db 5891 TTCACCTCCCTCAGCAATGGCGGGCCATACAAACCAAGAGATGGCATCAAGAGTC 5950
QY 2029 -----ProProGly 2031
Db 5951 TGTCTCTGGGGCACTCAAAGAACCCAGATGCACCCATGAGGCCAGCCACCCCTGGA 6010
QY 2032 ArgSerProleu-AlaGlnArgProleuArgArgGlnAlaAlaIleArgThrAsp----- 2049
Db 6011 GCGTGCCACTCCACAGAGATCCTGTGGGGCGGTACAGACCACTGGCTGTGACGTTCA 6070
QY 2050 -----SerleuAspValG 2054
Db 6071 GATGACAGCATTAACCCGAGGGCCCTGATGGGAGGCCCAAGCTGGGTGAGAGCCA 6130
QY 2054 nGlyleuGlySerArgGluAspLeuSerGluValSerGlyPro-----SerCy 2071
Db 6131 GGTGAGCGGCTCCATGCCCCGCTTGCGGCGGAGACTCAGCCGTCACAGATGCCAG 6190
QY 2071 sProleuThrArgSerSerPheThrGlyGlySerSerIleGlnValGlnGlnArgSe 2091
Db 6191 CCCCATGAAGCGCTCATCTCC-----ACGCTGGCCCAAGCGGCC 6229

QY 2091 rGlytIleGlnSerIyValSerIyShisIleArgLeuProAlaProCysProGlyLeu-- 2110
Db 6230 CCGTGG-GACTCATCTTTGCAGCACCACCCCGGACCCCGCTAGCCAGCGTGGT 6288
QY 2111 ----GluProSerTrpAlaIyAspProProGlu-ThrArgSerSerLeuGluLeuAspT 2129
Db 6289 CGCACCAACCACCAACCGCTGCACCGCCGCGGAGACAGAAAGCAGAGTCCCTGAGA 6348
QY 2129 hrGluLeuSerTrpIleSerGlyAspLeu-----LeuProSerSerGlnGluProL 2147
Db 6349 AGGGGGCCAGC---CTGTCTGCCGATATGATGGCGCACCAAGCAGTGTGTGGGCGCG 6405
QY 2147 euphePro-----ArgAspLeuIyIyS CysTyrSerV 2158
Db 6406 GGCTGCCCGCGGAGAGGGCCCTACAGGCTGCCGCGGGAACGAGAGCGCGGACAGAGC 6465
QY 2158 aIGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHis 2178
Db 6466 GGGGCGCGTCCAGAGCGGAGGAGCGCCCTCATCTCTCTCGGAGAGCAGCGCTTC- 6524
QY 2178 erIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSer- 2197
Db 6525 -----TACTCTCGACCGCTTTGGGGCGGTGAGCCCCCGAAGCCCAAGCCCTCC 6576
QY 2197 ----- 2197
Db 6577 TCAGCAGCCACCAACGTGCGCCAACAGCTGGCGCAGAGCCGGAGCCCAACCAAGGCA 6636
QY 2198 -----SerLeuGlyGlyGlnProLeu-----G 2205
Db 6637 GTGGTTCCTGATGGAGGCCCTTGCTGTCAACATCTGTGTAGCACCCCGCGCGCG 6696
QY 2205 IyGlyProGlySerArgProIySlySlyLeuSerPro---ProSerIleSerIleAsp 2224
Db 6697 GTGGGCGGAGGAGGAGCTCCCGCAGAGCGCCCTGACTCCCGCCCAAGCATCACTACAAGA 6756
QY 2224 roProGluSer-----GlnGlySerArgProProCysSerP 2236
Db 6757 CGGCCCACTCTCACCACCATCACTTCGCGGGGCTCAGACCAGCCTTCCTGCTTCTCC 6816
QY 2236 roGly-----ValCysLeuArgArgAlaProAla 2247
Db 6817 CAGCGCGGCTCAGCGGTGGCTTTCGACACAAAGCCCTGTGACAGAGACCCCTCA 6876
QY 2247 erAsp-----SerIyAspProSerValSerSerProLeuA 2259
Db 6877 GCCAGCCCTGGCCCTGGCTCTCGAATTGGCTGTGACCTTACCTGGGGGAGCGTCTGG 6936
QY 2259 spSerThrAlaIaIaSerProSerProIySlyAspThrLeuSerLeu----- 2274
Db 6937 ACAGTGAGGCTCTGTCTCAGCGCCCTGCTGAGGACACGCTCACTTTCGAGAGGCTGTGG 6996
QY 2275 -----SerGlyLeuSerSer 2279
Db 6997 CCACCAACTCGGCGGCTCTCC 7019

RESULT 15
US-08-193-078B-7
; Sequence 7, Application US/08193078B
; Patent No. 5846757
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Ellis, Steven
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: McCue, Ann
; APPLICANT: Brenner, Robert
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWN, MARTIN, HALLER & MCCLAIN
; STREET: 1660 UNION STREET

; CITY: SAN DIEGO
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,078B
; FILING DATE: 07-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/868,354
; FILING DATE: 10-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,206
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-53607
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7362 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 144..7163
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..143
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 7161..7362
; US-08-193-078B-7

Alignment Scores:
Pred. No.: 2.92e-96 Length: 7362
Score: 1745.50 Matches: 662
Percent Similarity: 37.80% Conservative: 356
Best Local Similarity: 24.58% Mismatches: 879
Query Match: 14.51% Indels: 798
Gaps: 84
DB: 2

US-09-611-257A-24 (1-2287) x US-08-193-078B-7 (1-7362)
QY 14 ProLeuArgGlySerAlaArgProSerSerAspProProGlyProArgLeuAlaArgly 33
Db 66 CCGCTCTGAGCGCGCTGGCGCGCCCGCCCTCTCCCTGCGGGGCGG---CTGGGCGGGGA 122
QY 34 TrpThrArg-ArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerAr 53
Db 123 TGCACGCGGGGCGCGGAGCCATGTCTCGGGGAGCAGAGCTGGGCGCGCTATGGA 182
QY 53 gSerSerThrTrpCysProGlyProGlyAlaIaIaGly---AlaGlySerThrGluIySAs 72
Db 183 GGGCGCGCGCGGAGAGCGGGCGCGGGCGGGCGGGCGGGCGGGCGGGCGGGGT 242
QY 72 pProGlySerAlaAspSerGluAlaGluGlyLeu----- 83
Db 243 CCGGGGGGGGTGC---AGCCCGGACAGGGGTCTTACAAGCAATGATCGCGAGCGC 299
QY 84 -----ProTyrProAlaLeuAlaProVal----- 91
Db 300 GCGCGGACCATGCGCTGTACAAC-CCCATCCCGGTCAAGCAGAACTGCTTACCGTCAA 358

QY	92	----	ValPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrVa	110
Db	359	CCGCTCGCTCTTCGCTTCACGAGGACAACGTCGTCGCAAAATACGCGAAGCCGATCAC		418
QY	110	1CysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLe	130	
Db	419	CGAGTGGCCTCCATTCGAGAATATGATCCTGGCCACCACATCATGCCAACTGCATCGTCT	478	
QY	130	uGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGl	150	
Db	479	GGCCCTG-----GAGCAGCACCTCCCTGATGGGGACAACAAAGCCCATGTCGGA	526	
QY	150	nAlaPheAspAsp-----PheIlePheAlaPhePheAlaValGluMetValVally	167	
Db	527	GCGGCTGGACGACACGAGACCCCTATTTCATCGGATCTTTTGCTTCGAGCAGAGATCAA	586	
QY	167	smetValAlaLeuGly---IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnAr	186	
Db	587	AATCATCGCTCTGGGCTTGCTCTTCACACAAGGGCTCTTACCTCGGGAACGGCTGAACGT	646	
QY	186	gleuAspPhePheIleValIleAlaGlyMetLeuGluTyrSer-----LeuAspLe	203	
Db	647	CATGCACTTCGTGGTCGTCCTCACAGGATCCTTGCCACGGCTGGAACGTACTTCGACCT	706	
QY	203	uGlnAsnValSerPheSerAlaValArgThrValArgValleuArgProLeuArgAlaI	223	
Db	707	GCGA-----ACACTGAGGGCTGTGCTGCTGAGGCCCTGAAGCTGCT	751	
QY	223	eAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLe	243	
Db	752	GTCCTGGATTCCAAGTTTGACAGTGTGCTCAAGTCCATCATGAAGCCATGTTCCACT	811	
QY	243	uGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGl	263	
Db	812	CCTGCAGATTGGGCTGCTCTCTTCTTGCCATCCTCATGTTGCCATCATGGCCCTGA	871	
QY	263	nLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLe	283	
Db	872	GTTCTACATGGGCAAGTTCACAAAGCCTGTTTC-----CCCAA	910	
QY	283	uSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCy	303	
Db	911	CAGCACAGATGCGAGCCCGTC-----	932	
QY	303	sSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGl	323	
Db	932	-----	932	
QY	323	uGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSerSerAsnTh	343	
Db	933	-----GGTGACTTCCCTGTGGCAAGAGAGGCCCCAGCCGGCTGTGCGAGGGCGACAC	985	
QY	343	rThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPh	363	
Db	986	TGAGTGC-----CGGAGTACTGGCCA-----GGACC	1015	
QY	363	eLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValI	383	
Db	1016	CTTTGGCATCACCAACTTTGACAATATCCTGTTTGCCATCTTGACGCTGTTCCAGTGCA	1075	
QY	383	eThrLeuGluGlyTyrTrpValAspIleMetTyrPheValMetAsp--AlaHisSerPheTy	402	
Db	1076	CACCATGGAGGGCTGCACTGACATCCTCTATATACAACAGATGCGGCCGCAACACCTG	1135	
QY	402	rAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuCy	422	
Db	1136	GAACGTGGCTTACTTCATCCCTCTCATCATCATCGGCTCTTCTTCATGCTCAACCTGCT	1195	
QY	422	sLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSer-----	438	
Db	1196	GCTGGGCGTGTCTCTCGGGGAGTTTGCCAAGAGCGAGAGAGGTTGAGAACCGCCGCGC	1255	

Oy		439	-----GlnLeuMetArgGlulnArgValAlaArgPheLeuSerAsnAlaSerThrLeuAl	456
Db		1256	CTTCCTGAAGCTGCCCGGCAGACAGATCGAG-----	1289
Oy		456	aserPheSerGluproGlySerCysTyrGluleuLeuLysTyrLeuValTyrIleLe	476
Db		1290	-----CGAGAGCTCAACGGGTACTGTGAGTGATCTTT	1321
Oy		476	uArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLe	496
Db		1322	CAAAGCCGAGAAGTCAATCATGCTGCCCCAGAGAAC-----	1355
Oy		496	uLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrAr	516
Db		1356	-----AGGAATGCAGAGAGAGAGATGCCCTTGGACGTGCTGAAGAG	1396
Oy		516	gSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHi	536
Db		1397	AGCGGCCAACAAGAGAGACAGAAATGACCTGATCCAC-----	1433
Oy		536	sTyrrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspAr	556
Db		1434	-----GCAGAGAGGAGAGAGACC	1453
Oy		556	gAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerG	576
Db		1454	GTTTGCAGAT-----	1463
Oy		576	yGlyProProArgGlyAlaGluSerValHisSerPheTyrrHisAlaAspCysHisLeuG	596
Db		1463	-----	1463
Oy		596	uProValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrVa	616
Db		1463	-----	1463
Oy		616	IglySerGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAs	636
Db		1463	-----	1463
Oy		636	pLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIl	656
Db		1463	-----	1463
Oy		656	eProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCy	676
Db		1463	-----	1463
Oy		676	sHisSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPr	696
Db		1464	-----CTCTGTGCTGTGGATCCCTTCGCCCGCCAGC-----	1499
Oy		696	cAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVa	716
Db		1500	-----CTCAAGAGCCGGGAAGACAGAGAGCTCGTCACTATT	1534
Oy		716	lmetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAs	736
Db		1535	C-----	1535
Oy		736	pLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSe	756
Db		1536	-----CCGAGGAGAGAGAG-----	1550
Oy		756	rSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLy	776
Db		1551	-----ATGTTCCGGTTTTT-----ATCCGGCGCATGTGAAGCTCA	1588
Oy		776	sTyrrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGl	796
Db		1589	GAGCTTCTACTGGGTGGTGTGCTGTGCGTGGCCCTGAACACACTGTGTGTGGCCATGCT	1648
Oy		796	uTyrrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheTh	816

Db 1649 GCATTACACACCGCGCGGCTTACCACGACCTGTATTTTGACAGATTGTTTCCCT 1708
QY 816 rSerleuPheAlaleuGluMetleuLeuValTyrGlyProPheGlyTyr11 836
Db 1709 GGGTCTCTTCTCACAAGATGTCCCTGAAGATGATGCGCTGGGGCCAGAACTACTT 1768
QY 836 eLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrGluIleVa 856
Db 1769 CCGGTCTCTTCTCAACTGCTTTCACCTTGGGGTCATCGTGGGAGCGTCTTGAAGTGT 1828
QY 856 IGlyGln-----GlnGlyGlyLeuSerValLeuArgThrPheArgLe 871
Db 1829 CTGGGCGGCATCAAGCCGGGAAGCTCTTGGGATCAGTGTGCTGCGGCGCTCCGCT 1888
QY 871 uMetArgValleuLysLeuValArgPheLeuProAlaleuGlnArgGlnleuValle 891
Db 1889 GCTGAGGATCTTCAAAGTCAAGAACTACTGAGCTCCCTCGGAACCTGTGTCTCCCT 1948
QY 891 uMetLysThrMetAspAsnValAlaThrPheCysMetleuLeuMetleuPheIle 911
Db 1949 GCTGAACCTCCATGAAGTCCATCATCAGCCTGCTCTTGTCTCTTCCATTTGTGT 2008
QY 911 ePheSerIleleuGlyMetHisleuPheGlyCysLysPheAlaSerGluArgAspGlyAs 931
Db 2009 CTTCGCCCTGCTGGGATGCACGTGTTGGGGACACTTCAACTCCAGATGAGACTCC 2068
QY 931 pThrLeuProAspArgLysAsnPheAspSerleuLeuTyrAlaIleValThrValPheG 951
Db 2069 CACA-----ACCACTTCGACACCTTCCTGCCGCATCTCATCTGTCTTCCA 2116
QY 951 nIleLeuThrGlnGluAspTyrAsnLysValleuTyrAsnGlyMet----- 966
Db 2117 GATCTGACGGAGAGAGATGCAATGATGATGATGATGATGATGATGATGATGATGATG 2176
QY 967 -AlaSerThrSerSerTyrAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTy 986
Db 2177 CGTCAGCAAGGCATGTCTCGCTCTTTACTTCTCATGTCTGACACTGTTCGGAACA 2236
QY 986 rValleuPheAsnleuLeuValAlaIleleuValGlnGlyPheGlnAlaGlnGlyAspAl 1006
Db 2237 CACTCTGCTGAATGTCTTCTTGCCATCGCTGTGACAACTGGCCACGCCAAGAGCT 2296
QY 1006 aThrLysSerGluSerGluProasp----- 1014
Db 2297 GACCAAGATGAAGAGAGATGAAGAAGCAAGCAATCAGAACTTGCTCTGCAAAAGGC 2356
QY 1015 -----Phe-PheSerProSerValaspGlyA 1023
Db 2357 CAAGAAGTGGCTGAAGTCAAGCCCCATGTCTGCCGGAACATCTCCATCGCCGCAAGCA 2416
QY 1023 spGlyAspArgLysLysArg-LeuAlaleuValAlaLeuGlyGluHisAla----- 1039
Db 2417 GCAGAAGTCCGCAAGCGCGCTGGTGTGGAGCAGCGGGCCAGCAGCTACGGCTGCA 2476
QY 1040 -----GluLeuArgLysSerleuLeu-----ProProleu 1049
Db 2477 GAACCTGGGGCCAGCTGCGAGCGCTGTACAGCGAGATGACCCCGAGAGCGGCTGCG 2536
QY 1050 IleIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGly 1069
Db 2537 CTTCGCCACTACGCGCCACCTGCGGCCGACATGAAGACCACTTGACCGGCGCTGCT 2596
QY 1070 GluAla-LeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAl 1089
Db 2597 GGTGAGCTGGCGCGCAGCGCGCGGGGGCCCGTGGAGGCAAAAGCCGACCTGAGGC 2656
QY 1089 aAla-----HisHis-----GluMe 1094
Db 2657 TGGGAGGCGCGCGAGGCGGTGACCTTCGCGCAGGACACCGGACCGGCAAGGA 2716
QY 1094 cLysCysPro----- 1097

Db 2717 CAAGACCCCGCGCGGGGACCAAGACCGAGAGGCCCCGGAAGCGGAGCGGGA 2776
QY 1098 -ProSerAlaArgSerSer-----ProHisSerProTyrSerAlaAlaSerSerTr 1114
Db 2777 GCGCGGTGCCCGGAGAGCGCGCGCGCCGACCGCAGCAGCAAGAGAGCGCGC-- 2834
QY 1114 pThrSerArgArgSerSerArgAsnSerleuGlyArgAlaProSerleuLysArgArgSe 1134
Db 2835 ----GGGCCCCCGAGCGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2875
QY 1134 rProSerGlyGluArgArgSerleuLeuSerGlyGlnGlnGlnSerGlnAspGlnG 1154
Db 2876 CCGCGAGGCG 2935
QY 1154 u-----GluSerSerGluLysAspArgAlaSerPr 1164
Db 2936 GCGCGGAGCGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 2995
QY 1164 oAlaGlySerAspHisArgHisArgGlySerleuGlu-----ArgGluAlaLysSe 1181
Db 2996 GCGCGAGCG 3055
QY 1181 rSerPheAspLeuProAspThrleuGlnValProGly--LeuHisArgThrAlaSerG 1200
Db 3056 CGGG-----GAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 3094
QY 1200 yArgSerSerAlaSerGlu-----HisGlnAspCysAsnGlyLysSerAlaSerGlyAr 1218
Db 3095 GCGCGAGCGCTGTCTCAGAGCGCTGTGAGAGAGAGACCAAGAGAGAGCGGAGGCA 3154
QY 1218 gLeuAla-----ArgThrleuArgThrAspAspProGlnLe 1230
Db 3155 GGAGGCTGAGATAGTGAAGCCGACAAAGAAAGAGCTCCCGAAACCAAGCGCGGGA 3214
QY 1230 uAspGlyAspAspAsnAspGlnGlyAsnleuSerLysGlyGluArgIleGlnAlaTr 1250
Db 3215 GCCACACTGTGACCTGGAGACCAAGTGGAGTGTGAGTGTCC----- 3260
QY 1250 pValArgSerArgleuProAlaCysCysArgGluArg----- 1262
Db 3261 ----ATGCACACACTGCCAGCACTGTCTCCAGAAAGGTGAGAGAACCCAGAGATGC 3316
QY 1263 -AspSerTrp----- 1265
Db 3317 AGACAATCAGCGGAAGCTCACTCGCATGGGAGTCAAGCCCCAGACCGGAACATAATTGT 3376
QY 1265 ----- 1265
Db 3377 ACATATCCAGTATGTGACGGGCGCTTGGGGAAGCCACGGTGTTCCTCCAGTGTTAA 3436
QY 1265 ----- 1265
Db 3437 CGTGACCTGGAAGCCAGACAGAGGGAAGAGAGTGGAAGCGGATGACGTGATGAG 3496
QY 1266 -----SerAlaTyrIlePheProGlnSerAr 1275
Db 3497 GAGCGGCGCGCGCGCTATGCTCCCATACAGCTTCATGTCTGTTAAGCCCAACCACT 3556
QY 1275 gPheArgleuLeuCysHisArgIleIleThrHisLysMetPheAspHisValleuVa 1295
Db 3557 GCTCGCGCGCTTCTGCGCACTACATCGTGAACCATGAGGTACTTCGAGGTGTCTCTCGT 3616
QY 1295 IleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSe 1315
Db 3617 GGTCAATCGCTTGAGCAGCATCGCCCTGCTGTGAGGACCA--GTGCGCACAGACTC 3673
QY 1315 rAlaGluArgIlePheLeuThrleuSerAsnTyrIlePheThrAlaValPheleuAlaG 1335
Db 3674 GCCCAGGAACAACGCTGAATAATCCTGATATACATTTTCACTGTGTCTTACCTTTGA 3733
QY 1335 uMetThrValLysValAlaIleleuGlyTyrCysPheGlyGlnGlnAlaTyrleuArgSe 1355
Db 3734 GATGTGATTAAGATGATGACTTGGGACTGTGCTTACCCCTGAGAGCTATTTCGCGGA 3793

QY 1355 rSerTrpAsnValIleuAspGlyLeuLeuValIleuIleSerValIleAspIleLeuValSe 1375
Db 3794 CTTGTGAACATTTCTGGAC-----TTCAATTGTGTCAGTGGCGCCCTGTGGC 3841
QY 1375 rMetVal---SerAspSerGlyThrIysIleLeuGlyMetLeuArgValLeuArgLeuLe 1394
Db 3842 GTTGTCTTTCTCAGGATCCAAAGGAAAGACATCAATACCATCAAGTCTCTGAGAGTCCT 3901
QY 1394 uArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValG1 1414
Db 3902 TCGTGTCTCGCGGCCCTCAAGACCATCAACGGCTGCCAAGCTCAAGCTGTGTGA 3961
QY 1414 uThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePh 1434
Db 3962 CTGTGTGTGAACCTCCCTGAAGAATGTCTCAACATCTTGATTGTCTACATGCTCTTCAT 4021
QY 1434 eIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnG1 1454
Db 4022 GTTCATATTGTCCGTCAATTGCGGTGCAGCTCTTCAAGGGAAGTTTCTACTGCACAGA 4081
QY 1454 YGlu-----AspThrArgAsn-----IleThrAsnLysSerAspCys 1466
Db 4082 TGAATCCAAGAGCTGAGAGGAGCTGCAAGGCTCAGTATTGTGATTATGAGAAGGAGA 4141
QY 1466 sAlaGluAlaSerTyrrArg---TrpValArgHisLysTyrrAsnPheAspAsnLeuGlyG1 1485
Db 4142 AGTGAAGCTCAGCCAGCGAGAGTGAAGAATAACGACTTTCACACGACAATGTGCTCTG 4201
QY 1485 nAlaLeuMetSerLeuPheValIleuAlaSerLysAspGlyTrpValAspIleMetTyrrAs 1505
Db 4202 GGCTCTGTGACGCTGTTCACAGTGTCCACGGGAGAAGGCTGGCCATGTGCTGAACA 4261
QY 1505 pGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetIle 1525
Db 4262 CTCCTGTGATGCCACCTATGAGAGCAGGCTCCAAGCCCTGGGTACCCGATGAGCTGTC 4321
QY 1525 uLeuTyrrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValG1 1545
Db 4322 CATCTTCTACGTGTCTACTTGTGTGCTTTCCTTCTTCTTCTGTCACACATCTTTGTGC 4381
QY 1545 yValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgAr 1565
Db 4382 TTTGATCATCATCACTTC-----CAGAGCAGGGGAGCAAGGTGAT 4423
QY 1565 gArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGlnMe 1585
Db 4424 GTCTGAA-----TGCAGCCTGGAGAAGAAGAGGCTTGCACTTGCTGC 4471
QY 1585 tAlaGluAlaGlnCysLysProTyrrTyrrSerAspTyrrSerArg-----PheArgLeuLe 1603
Db 4472 CATCAGCGCCAAACCCCTGACACGGTACATGCCCCCAAACCGGCACTCGTTCAGTATA 4531
QY 1603 uValHisHisLeuCysThrSerHisTyrrLeuAspLeuPheIleThrGlyValIleGlyLe 1623
Db 4532 GACGTGACATTTGTGTGCTCTCCCGCCCTTTGAATACTTCATCATGCGCATGATAGCCCT 4591
QY 1623 uAsnValValThrMetAlaMetGluHisTyrrGlnGlnProGlnIleLeuAspGluAlaLe 1643
Db 4592 CAACACTGTGTGTGATGATGAAGTTCTATGATGACCCCTATGAGTACGAGCTGATGCT 4651
QY 1643 uLysIleCysAsnTyrrIlePheThrValIlePheValPheGluSerValPheLysLeuVa 1663
Db 4652 GAAATGCCTGAACATCGCTTTCACATCCATGTTCTCCATGAAATGCGTCTGAAGATCAT 4711
QY 1663 lAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleVa 1683
Db 4712 CGCCTTTGGGCTGCTGAACATATTTCAGAGATGCCCTGAATGTCTTGACTTGTCACTGT 4771
QY 1683 lLeuLeuSerIleMetGlyIleThrLeuGluGluIleGlu-----ValAs 1698
Db 4772 GTTGGGAAGTATTACTGATATTTTAGTAAACAGAGATTGCGGAACGAAACAATTTCATCAA 4831

QY 1698 nLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1718
Db 4832 CCTCAGC-----TTCTCCGCGCTCTTTGAGCTGCGCG 4864
QY 1718 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetG1 1738
Db 4865 GCTGATCAAGCTGTCTCCGCGCAGGCTACACCATCCGCATCCGTGTGAGCTTGTCCA 4924
QY 1738 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl 1758
Db 4925 GTCTTCAAGGCCCTGCGCTACGTGTGTCTGTCTCATTTGCCATGTCTGTTCATCTACGC 4984
QY 1758 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG1 1778
Db 4985 CATCATGCGCATGCAAGTGITTTGGGAATATTGCCCTGGATGATGAC-----ACCAG 5035
QY 1778 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1798
Db 5036 CATCAACGCCACACAACACTTCCGACGTTTGTGCAAGCCCTGATGCTGTCTGTCAAGAG 5095
QY 1798 lSerThrGlyAspAsnTrpAsnGlyIleMetLysAsp-----ProSerArgAspCysAs 1816
Db 5096 CGCCACGGGGGAGGCGCTGCGACGAGATCATGCTGTCTGCTGAGCAACCAAGCCTGTGA 5155
QY 1816 pGlnGlu-----SerThrCysTyrrAsnThrValIleSerProIleTyrrPheValSerPh 1834
Db 5156 TGAGCAGGCCAATGCCACCCGAGTGGGAAGTGACTTTGCCCTACTTCTACTGCTCCTT 5215
QY 1834 eValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet----- 1851
Db 5216 CATCTTCTGTGCTCTCTTCTGTGATGTGAACCTCTTGTGGCTGTGATCATGACAATTT 5275
QY 1852 -----LysHisLeuGluGln-SerAsnL 1859
Db 5276 TGAGTACCTCAGCGGACTTTCATCTCCTAGGTCCTCACCACTTGATGATTCATCCG 5335
QY 1859 ySGluAlaLysGluGluAlaGlnLeuGluAlaGlnLeuGluLeuMetLysThrLeu- 1878
Db 5336 GGCTGGGCTGAATACGACCCGCGTGCGTGGCGCATCAGTTACAATGACATGTTTGA 5395
QY 1879 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyVal 1898
Db 5396 GATGCTGAACAACATGTCCCGCCTCTGG-----GCTGGGAAGAAATGCC 5443
QY 1899 AsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAla 1918
Db 5444 TGCTCGAGTTCTTACAAGCCGCTGTTGC---CATGAACATGCCCATCTCCAAAGAGA 5500
QY 1919 SerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProValPro 1938
Db 5501 CATGACTGTTCACCTTCAAGTCCAGCGTGATGGCCCTCATCCGAGCGGACCTGGAGATCAA 5560
QY 1939 LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958
Db 5561 GCTGGCCCGCAGCTGG-----GACAAAGCAGCATCAGTGTAGCGCGGAGTTGAG 5608
QY 1959 AsnAspSerTyrrMetCysArgAsnGlySerThrAlaGluArgSerLeuGly----- 1975
Db 5609 GAAGGAGATTCCGTTGT---GTGGGCCAATCTGCCCAAGAAGACTTTGACTTGTGCTGT 5665
QY 1976 -----HisArgGlyTrpGlyLeuProLysAlaGlnSerGly 1987
Db 5666 ACCACCCCAATAAGCCTGATGATGACAGTGGGGAAGGTTATGACGCTGTGATGATATT 5725
QY 1988 SerIleLeuSerVal-----HisSerGlnPro----- 1996
Db 5726 TGACTTCTACAAGCAGAAACAACCAACAGAGACCAAGATGCCAGAGGCTCTGAGGCGCT 5785
QY 1997 ---AlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrrLeuLeuGlnPro 2015
Db 5786 CTCCCAAGATGGGTCTGTGTCTGTTCACCCCTTGAAAGGCCAC----- 5830
QY 2016 HisGlyAlaProThrTrpGlyAlaIleProLysLeuPro----- 2028


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Db 5831 C|T|G|A|G|C|A|G|A|C|A|G|C|C|G|G|T|G|T|C|C|G|A|G|A|G|C|C|G|G|T|T|T|C|T|T|G|A|C|A|G|A|G|A|G| 5890
QY 2028 -----
Db 5891 T|T|C|C|A|C|T|C|C|T|C|A|G|C|A|T|G|G|G|G|G|G|C|C|A|T|A|C|A|A|A|C|C|A|G|A|G|A|G|T|G|G|C|A|T|C|A|A|G|A|G|T|C| 5950
QY 2029 -----ProGly 2031
Db 5951 T|G|T|C|T|C|T|G|G|G|G|C|A|C|T|C|A|A|A|G|A|C|C|C|A|G|A|T|G|C|A|C|C|C|C|A|T|G|A|G|G|C|C|A|G|G|C|C|C|T|G|A| 6010
QY 2032 A|r|g|S|e|r|P|r|o|l|e|u|-|A|a|G|l|n|a|P|r|o|l|e|u|A|r|g|A|l|a|I|a|l|e|A|r|T|H|r|A|s|P|----- 2049
Db 6011 G|C|G|T|G|C|C|A|C|T|C|C|A|C|A|G|A|T|C|C|T|G|T|G|G|G|C|G|G|T|C|A|G|A|G|C|A|C|T|G|G|C|T|G|G|A|C|G|T|T|C|A| 6070
QY 2050 -----SerLeuAspValG1 2054
Db 6071 G|A|T|G|C|A|G|A|G|C|A|T|A|A|C|C|C|G|A|G|G|G|C|C|T|G|A|T|G|G|G|A|G|C|C|C|C|A|G|C|C|T|G|G|C|T|G|A|G|A|G|C|C|A| 6130
QY 2054 n|g|l|y|e|u|S|e|r|A|r|g|l|u|A|s|p|l|e|u|S|e|r|G|l|u|V|a|l|S|e|r|G|l|P|r|o|-----SerCy 2071
Db 6131 G|G|G|T|G|A|G|C|G|G|C|C|T|C|C|A|T|G|C|C|C|C|C|C|T|T|G|C|G|G|C|C|G|A|G|A|C|T|C|A|G|C|C|C|G|T|C|A|G|A|T|G|C|C|A|G| 6190
QY 2071 s|P|r|o|l|e|u|T|H|r|A|r|g|S|e|r|S|e|r|P|H|e|T|r|G|l|y|S|e|r|S|e|r|l|e|g|l|n|a|l|G|l|n|A|r|g|S|e| 2091
Db 6191 C|C|C|C|A|T|G|A|G|C|G|C|T|C|C|A|T|C|T|C|-----ACGCTGGCCAGCGGCC 6229
QY 2091 r|G|l|y|l|e|g|l|n|S|e|r|L|y|S|v|a|l|S|e|r|L|y|H|s|l|e|A|r|g|l|e|u|P|r|o|l|a|P|r|o|C|y|S|P|r|o|G|l|y|l|e|u|-- 2110
Db 6230 C|C|G|T|G|G|-|G|A|C|T|C|A|T|C|T|T|T|G|C|A|G|A|C|C|A|C|C|C|G|A|C|C|G|C|C|C|C|A|C|C|C|C|T|A|G|C|C|A|G|G|C|G|T|C|G|T| 6288
QY 2111 ---G|l|u|P|r|o|S|e|r|T|T|p|a|l|a|L|y|S|A|s|P|P|r|o|G|l|u|-|T|H|A|r|g|S|e|r|S|e|r|L|e|u|G|l|u|L|e|u|A|s|P|T| 2129
Db 6289 C|G|C|A|C|C|A|C|C|A|C|C|A|C|C|C|G|T|G|C|C|A|C|C|G|C|G|A|G|G|A|G|A|G|A|G|A|G|A|G|A|G|T|C|C|T|G|A|G|A| 6348
QY 2129 h|r|G|l|u|e|u|S|e|r|T|T|p|l|e|S|e|r|G|l|y|A|s|p|l|e|u|-----LeuProSerSerGlnGluProL 2147
Db 6349 A|G|G|G|C|C|C|A|G|C|-----C|T|G|T|C|T|G|C|G|A|T|A|T|G|A|T|G|G|C|G|C|A|C|C|A|G|C|A|G|T|G|T|G|G|G|C|C|G|G| 6405
QY 2147 e|u|P|H|e|P|r|o|-----A|r|g|A|s|p|l|e|u|L|y|S|L|y|S|C|y|T|y|S|e|r|V| 2158
Db 6406 G|G|C|T|G|C|C|C|C|C|G|G|G|A|G|G|G|G|C|C|T|A|C|A|G|G|C|T|G|C|C|G|G|G|G|A|A|C|G|A|G|C|G|C|G|C|A|G|A|G|C| 6465
QY 2158 a|l|G|l|u|T|H|r|G|l|n|S|e|r|C|y|S|A|r|g|A|r|g|A|r|P|r|o|G|l|y|P|H|e|T|T|p|l|e|u|A|s|P|G|l|u|G|l|n|A|r|g|A|H|s|S| 2178
Db 6466 G|G|G|G|C|C|G|T|C|C|C|A|G|A|G|C|G|G|A|G|C|C|C|T|C|A|T|C|T|C|T|C|T|C|G|G|A|G|A|G|A|G|C|G|C|T|T|C|- 6524
QY 2178 e|r|l|e|a|l|a|V|a|l|S|e|r|C|y|S|L|e|u|A|s|P|S|e|r|G|l|y|S|e|r|G|l|n|P|r|o|A|r|g|l|e|u|C|y|S|P|r|o|S|e|r|P|r|o|S|e|r|- 2197
Db 6525 -----T|A|C|T|C|T|G|C|G|A|C|C|G|C|T|T|T|G|G|G|G|C|C|G|T|G|A|G|C|C|C|C|G|A|G|C|C|C|A|G|C|C|T|C|C| 6576
QY 2197 ----- 2197
Db 6577 T|C|A|G|C|A|G|C|C|A|C|C|C|A|C|G|T|C|G|C|C|A|C|A|G|C|T|G|C|C|A|G|A|G|C|C|G|G|G|A|C|C|C|A|C|C|C|A|G|G|G|C|A| 6636
QY 2198 ---S|e|r|L|e|u|G|l|y|G|l|n|P|r|o|l|e|u|-----G 2205
Db 6637 G|T|G|G|T|C|C|G|T|G|A|T|G|G|A|G|C|C|C|C|T|T|G|C|T|G|T|C|A|C|A|C|A|T|G|T|G|T|C|T|A|G|C|A|C|C|C|C|G|C|G|C|G| 6696
QY 2205 l|y|G|l|y|P|r|o|G|l|y|S|e|r|A|r|g|P|r|o|L|y|S|L|y|S|L|e|u|S|e|r|P|r|o|---P|r|o|S|e|r|l|e|S|e|r|l|e|A|s|P| 2224
Db 6697 G|T|G|G|G|C|G|A|G|G|C|A|G|C|T|C|C|C|C|A|G|A|G|C|C|C|C|T|G|A|C|T|C|C|C|C|G|C|C|C|C|A|G|C|A|T|C|A|C|T|A|C|A|G|A| 6756
QY 2224 r|o|P|r|o|G|l|u|S|e|r|-----G|l|n|G|l|y|S|e|r|A|r|g|P|r|o|P|r|o|C|y|S|e|r|P| 2236
Db 6757 C|G|G|C|C|A|C|T|C|T|C|A|C|C|C|A|T|C|C|A|C|T|T|C|G|C|C|G|G|G|G|C|T|C|A|G|A|C|A|G|C|C|T|C|C|T|G|C|T|T|C|T|C|C| 6816
QY 2236 r|o|G|l|y|-----V|a|l|C|y|S|L|e|u|A|r|g|A|r|g|A|l|a|P|r|o|l|a|S| 2247
Db 6817 C|A|G|G|C|C|G|G|C|T|C|A|G|C|C|G|T|G|G|C|T|T|C|G|A|A|C|A|C|A|C|G|C|C|T|G|T|G|C|A|G|A|G|A|G|A|C|C|C|C|T|C|A| 6876
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Job time : 1483.31 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2005, 18:24:02 ; Search time 2796.34 Seconds
(without alignments)
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Searched: 7389322 seqs, 333128559 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	11829	98.3	7285	10 US-09-383-894-3	Sequence 3, Appli
3	11673	97.0	7129	10 US-09-383-894-1	Sequence 1, Appli
4	10963.5	91.1	7825	22 US-10-756-149-31	Sequence 31, Appli
5	10963.5	91.1	7825	22 US-10-786-148-120	Sequence 120, App
6	10845.5	90.2	7648	19 US-10-377-139-10	Sequence 10, Appl
7	10845.5	90.2	7648	19 US-10-757-262-15	Sequence 15, Appl
8	10707	89.0	8116	17 US-10-062-674-2011	Sequence 2011, Ap
9	6242	51.9	7898	22 US-10-483-467-3	Sequence 3, Appli
10	6103	50.7	3993	21 US-10-930-301-51	Sequence 51, Appli
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16	5407	45.0	6503	9 US-09-935-541-12	Sequence 12, Appl
17	5407	45.0	6503	16 US-10-425-800-12	Sequence 18, Appl
18	3950	32.8	5562	9 US-09-030-482B-18	Sequence 11, Appl
19	3861.5	32.1	6073	19 US-10-377-139-11	Sequence 11, Appl
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21	1745.5	14.5	7362	17 US-10-375-253-11	Sequence 11, Appl
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23	1739.5	14.5	7364	9 US-09-954-456-1179	Sequence 1179, Ap
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39	1717.5	14.3	6083	22 US-10-726-216-21	Sequence 41, Appl
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ALIGNMENTS

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; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7
; LENGTH: 6942
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-377-139-7

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Db	376	TGCTGTCAATTCTTCACTGTGTGACTCTGGGTATGTTCAAGCCGTGTAGACATTG	435
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QY	160	heAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysCysTyrL	180
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QY 1140 rgSerLeuLeuSerGlyGlyGlyGlnGluSerGlnAspGluGluGluSerSerGluGluA 1160
Db 3436 GTCCCTGCTGTGTGGAAGAGGCCAGAGAGTCAAGATGAGAGGAAAGTTCAGAAAGAG 3495
QY 1160 sPArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaL 1180
Db 3496 ACCGGGCCAGCCCGACAGGCAAGTGAACCATGCCACAGGGGTTCTTGGAACGTGAGGCCA 3555
QY 1180 ySSeuSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerG 1200
Db 3556 AGAGTTCCTTGACTGCTGACACTCTGCAAGGTGCCGGGGCTGCACCGCACAGCCAGCG 3615
QY 1200 lYArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA 1220
Db 3616 GCCGAGCTCTGCTCTGAGCACCAAGACTGTAAATGGCAAGTCCGCTTCAGGGCGTTTGG 3675
QY 1220 lAArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAspGluGlyA 1240
Db 3676 CCCGACCCCTGAGGACTGATGACCCCACTGGATGGGATGATGAACAATGATGAGGAA 3735
QY 1240 snLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysA 1260
Db 3736 ATCTGACCAAGGGGAACGCATACAAAGCCTGGGTCAAGTCCCGGCTTCCTGCTTGC 3795
QY 1260 rgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuC 1280
Db 3796 GAGAGCGAGATTCCTGGTGGCCTATATCTTCTCCTCAAGTCAAGTTTCTCTCCTGT 3855
QY 1280 ySHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuA 1300
Db 3856 GTCAACCGATCATCAACCAAGATGTTGACCATGTGTCCTGTCATCATCTTCTCTCA 3915
QY 1300 snCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIleP 1320
Db 3916 ACTGTATCACCATCGCTATGAGCGCCCCAAATTGACCCCCACAGCGCTGAGCGCATCT 3975
QY 1320 heLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysV 1340
Db 3976 TCCTGACCCCTCTCCAATAATCATCTTCAAGGAGTCTTTCTAGCTGAATGACAGTAAGG 4035
QY 1340 aValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValL 1360
Db 4036 TGGTGGCACTGGGCTGTGCTTTGGGAGAGCGCCTACCTGCGCAGACTGGAATGTGC 4095
QY 1360 euAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAsps 1380
Db 4096 TGAACGGCTTGCTGTGCTCATCTCCGTATGCACATCCTGTGTCTCATGTCTCCGACA 4155

QY 1380 erGLyThrLysrIleuGLyMetIleuArgValIleuArgIleuLeuArgThrIleuArgProL 1400
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Db 4156 GCGGACCAAGATCTTGGCATGCTGAGGGTGTGGGCTGCTGGGACCTGCGTCCAC 4215
QY 1400 euArgValIleSerArgAlaGlnGlyLeuLysIleuValValGluThrIleuMetSerL 1420
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Db 4216 TCAGGGTCATCAGCCGGGCCAGGAGCTGGAAGCTGGTGTAGAGACTGTGATGTCAATCC 4275
QY 1420 euLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleL 1440
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Db 4276 TCAAAACCATTTGGCAACATTGTGTCAATTTGCTGTGCTCTTTCATCATTTTGGAAATTC 4335
QY 1440 euGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnI 1460
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Db 4336 TCGGGGTGACGCTCTTCAAAAGGAAGTTCTTGTGTGAGGGTGAGGACACACAGGAACA 4395
QY 1460 IeThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnP 1480
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Db 4396 TCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGATGGGTCCGGACAAGTACAAC 4455
QY 1480 heAspAsnLeuGlyGlnAlaLeuMetSerIleuPheValIleuAlaSerLysAspGlyTrpY 1500
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Db 4456 TTGACAAACCTGGGCCAGGCTCTGATGTCTCTGTGTGTGCTGGCTCCAAAGATGTTGGG 4515
QY 1500 aLAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnH 1520
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Db 4516 TTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTGATCAGCAGCCCATCATGAACC 4575
QY 1520 iSAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValL 1540
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Db 4576 ACAACCCCTGGATGCTGTATACTTCACTTCCTCTCTCATGTGGCTTCTTTGTTC 4635
QY 1540 euAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluG 1560
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Db 4636 TGAACATGTTTGGGCGTGTGTGTGAGAACTTCATAAGTGACAGACAGCACCAGGAGG 4695
QY 1560 IuGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgS 1580
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Db 4696 AGGAGAGGCGAGGCGCGGTGAGAGAAAGCACTACGAGGCTGGAGAAAGAGAGAGGA 4755
QY 1580 erLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgP 1600
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Db 4756 GTAAGAGAGAGCAGATGCGCCGAGAGCCAGTGCAGACCTACTACTGACTACTCGAGAT 4815
QY 1600 heArgLeuLeuValHisHisIleuCysThrSerHisTyrLeuAspLeuPheIleThrGlyY 1620
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Db 4816 TCCGGCTCCTTGTCCACCACTGTGTATCCAGCCACTACCTGGACCTTTCATCACTGGTG 4875
QY 1620 aIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuA 1640
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Db 4876 TCATCGGGCTGAACGTGTCTCATATGGCCATGGAACATTACCAGAGCCCCAGATCCTGG 4935
QY 1640 spGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValP 1660
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Db 4936 ACGAGGCTCTGAAGATCTGCAATTACATCTTAAACGTCATCTTGTCTTGGAGTCAGTTT 4995
QY 1660 heLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeuAspL 1680
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Db 4996 TCAAACTTGTGGCCTTGGCTTCCGCCGTTCTTCCAGGACAGGTGGAACAGCTGAGCC 5055
QY 1680 euAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuS 1700
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Db 5056 TGGCTATTGTGCTTGTCTTCATCATGGGCATCACTGGAGGAGATTGAGGTCAATCTGT 5115
QY 1700 erLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValL 1720
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Db 5116 CGCTGCCCATCAACCCCAACCATCATCCGATCATGAGGGTGTCCGCAATTGCTCGAGTTC 5175
QY 1720 euLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaL 1740
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Db 5176 TGAAGCTGTTGAAGATGCTGTGGCATGCGGCACCTGTGCACACGGGTGATGAGGCC 5235
QY 1740 euProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaL 1760

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QY 1760 euGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuG 1780
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Db 5296 TGGCGGTGAGACTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGTGAGGGCTTGG 5355
QY 1780 IyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerT 1800
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Db 5356 GTGGCATGCCACCTTTAGGAACCTTGGTATGGCTTTTCTGACCCCTCTTCGAGTCTCCA 5415
QY 1800 hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSerT 1820
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Db 5416 CTGTTGACAACTGGAATGTTATTAAGAAGACACCCCTCCGGACTGTGACCAAGACTCCA 5475
QY 1820 hrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValIleuThrAlaGlnP 1840
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Db 5476 CCGTGTACACACTGTCACTTCCCTATCTACTTGTGTCTTGTGCTGACGCGCCAGT 5535
QY 1840 heValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysG 1860
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Db 5536 TTGTGCTGTCAACGTGTGTATAGCTGTGTGCTGATGAAGCACTTGAAAGAAAGCAACAAG 5595
QY 1860 IuAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerP 1880
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Db 5596 AGGCCAAGAGAGAGCCGAGCTCGAGGCCGAGCTGGAAGTGAAGACCGCTCAGCC 5655
QY 1880 roGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnS 1900
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Db 5656 CGCAGCCCCACTCCCGCTGGGACAGCCCTTCTCTGGCCCCGGGGTGAGGGTGTCAACA 5715
QY 1900 erThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerG 1920
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Db 5716 GTACTGACAGCCCTTAAGCCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCCTCGG 5775
QY 1920 IyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuG 1940
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Db 5776 GCTTCTCCCTTGAAGCACCCCAAGATGTATCCCCACCCGAGAGAGTGCAGTCCCCCTAG 5835
QY 1940 IyProAspLeuLeuThrValArgLysSerGlyValLserArgThrHisSerLeuProAsnA 1960
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Db 5836 GACCAGACTGCTGACTGTGAGGAAGTCTGTGTCAAGCCGAGCAGCACTCTTGTCCCAATG 5895
QY 1960 spSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpG 1980
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Db 5896 ACAGCTACATGTGCCGAATGGAGCACTGCTGAGAGATCCCTAGACACAGGGGCTGGG 5955
QY 1980 IyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrS 2000
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Db 5956 GGCTCCCCAAAGCCAGTCAAGGCTCATCTTGTCCGTTCACTCCCAACCAAGACACACA 6015
QY 2000 erCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProt 2020
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Db 6016 GCTGCATCTTACAGCTTCCCAAGATGTGACTATGTCTCCAGCCTCATGGGGCTCCA 6075
QY 2020 hrTrpGlyAlaIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProL 2040
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Db 6076 CCTGGGGCGCATCCCTAAACTTACCCCCACCTGGCGGCTCCCTCTGGCTCAGAGGCTTC 6135
QY 2040 euArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgG 2060
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Db 6136 TCAGGCGCGAGCACAATTAAGACTGACTCCCTGATGTGCAAGGCGCTGGGTAGCCGGG 6195
QY 2060 IuAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheT 2080
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Db 6196 AAGACCTGTTGTCAAGGTGAGTGGGCCCTCTCTGCTGACCCGCTCATCTTCT 6255
QY 2080 rpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysH 2100
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Db 6256 GGGGCGGGTGAGCATCCAGGTGACAGCAGCGTTCGGGCATCCAGACAAAGTCTCCAAGC 6315
QY 2100 iSileArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProg 2120
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Db 6316 ACATCCGCTGCGAGCCCTTGCCAGCGCTGGAACCCAGCTGGGCCAAGACCCTCCAG 6375
QY 2120 luthrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuP 2140
Db 6376 AGACCAGAAGCAGCTTAGAGCTGGACACGAGCTGAGCTGGATTTCAGAGAACCTCCTTC 6435
QY 2140 roSerSerGlnGluGluProLeuPheProArgAspLeuLysCysTyrSerValGluT 2160
Db 6436 CCAGCAGCCAGGAAGACCCTGTTCCACCGGAGCTGAAGAAGTGTACAGTGTAGAGA 6495
QY 2160 hrcGlnSerCysArgArgProGlyPheTrpLeuAspGlnArgArgHisSerIleA 2180
Db 6496 CCCAGAGCTGCAGCGCGAGGCTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCATTG 6555
QY 2180 laValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeuG 2200
Db 6556 CTGTCAAGCTGTCTGACACAGCGGCTCCCAACCCCGCTATGTCCAAGCCCTCAAGCCTCG 6615
QY 2200 lylGlnProLeuGlyGlyProGlySerArgProLysLysLeuSerProProSerI 2220
Db 6616 GGGGCCCAACCTCTGGGGGTCTCTGGAGACCGGCTTAAGAAAAAAGTCAAGCCCAAGCTA 6675
QY 2220 leSerIleAspProProGlnSerGlnGlySerArgProProCysSerProGlyValCysL 2240
Db 6736 TCAGAGAGAGGCGCGCGGAGTGAAGTCTTAAGGATCCCTCGGTCTCCAGCCCTTGACA 6795
QY 2260 eTrhAlaAlaSerProSerProLysAspThrLeuSerLeuSerGlyLeuSerSera 2280
Db 6796 GCACGGCTGCCTCACCCCTCCCAAGAAGACACGCTGAGTCTCTGTGTTGTTCTTCTG 6855
QY 2280 sProThrAspMetAspPro 2286
Db 6856 ACCCAACAGACATGGAACCC 6875

RESULT 2
US-09-383-894-3
: Sequence 3, Application US/09383894
: Publication No. US20030125269A1
: GENERAL INFORMATION:
: APPLICANT: Li, Ming
: TITLE OF INVENTION: T-Type Calcium Channel
: FILE REFERENCE: 004, 00191
: CURRENT APPLICATION NUMBER: US/09/383, 894
: CURRENT FILING DATE: 1999-08-26
: EARLIER APPLICATION NUMBER: US 60/098, 004
: EARLIER FILING DATE: 1998-08-26
: EARLIER APPLICATION NUMBER: US 60/117, 399
: EARLIER FILING DATE: 1999-01-27
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 7285
: TYPE: DNA
: ORGANISM: Rattus sp.
US-09-383-894-3

Alignment Scores:
Pred. No.: 0 Length: 7285
Score: 11829.00 Matches: 2270
Percent Similarity: 97.72% Conservative: 1
Best Local Similarity: 97.68% Mismatches: 15
Query Match: 98.35% Indels: 38
DB: 10 Gaps: 2

US-09-611-257A-24 (1-2287) X US-09-383-894-3 (1-7285)

QY 1 MetLeuProHisArg-ValProArg-CysValArgThrProProLeuArgGlySerAlaA 20
Db 57 ATGCTCCCCACCGGGGTCCCCCGTTGCGTGAGGACACTCTCTGAGGGGCTCCGCTC 116

QY 20 rgProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetG 40
Db 117 GCCCCCTCTCGAACCCCCCGGGGCCCCGGCTGGCCAGAGGATGACGAGAGAGATGG 176
QY 40 luArgAlaProArgSerArgAspSerProValAlaSerArgSerSerThrCysProG 60
Db 177 AGCGGGCGCGAGAGTGGGACAGCCCGTAGCTTACAGCACTCAACGACCTGTCCGG 236
QY 60 lYProGlyAla-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerG 79
Db 237 GGCCGGGGGCGGAGGGCGCGGGTGCACGAAAAAGACCCGGGACGCGGACTCCGA 296
QY 79 uAlaGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAs 99
Db 297 GCGGAGGGGCTGCCGTACCCGGCGCTACCCGGTGTTCCTTCTACTTGAGCCAGGA 356
QY 99 pSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSe 119
Db 357 CAGCCGCGCGGAGCTGTGTCTCCGACGGTCTGTAAACCCGTGTTGAGCGAGTCA 416
QY 119 rMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspI 139
Db 417 TATGCTGTATTCTTCTCAACTGTGTACTCTGGTATGTTCAGGCCGTGTGAGGACAT 476
QY 139 eAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaP 159
Db 477 TGCCCTGTACTCCAGCGCTGCCGATCTGCAGGCTTCGATGACTTCATCTTGCTT 536
QY 159 ePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTy 179
Db 537 CTTTGTGTGGAATGTGTGTGAAGATGTGGCTTGAGCATCTTGGGAAGAATGTTA 596
QY 179 rLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGluTy 199
Db 597 CTTGGAGACACTTGGAAACCGGCTTGACTTTTTCATTGTGATTCAGGGATGCTGAGTA 656
QY 199 rSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArgPr 219
Db 657 TTGCTGACCTGCAGAACGTGAGCTTCTCCGACAGTACAGACAGTCCGTGTGCGACC 716
QY 219 oLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAspTh 239
Db 717 GCTCAGGGCCATTACCGGGGTGCCAGCATGCGCATTCCTGTCACATTACTGTGACAC 776
QY 239 rLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyI 259
Db 777 CTGCTATATGCTGGGCAACGTCCTGCTCTGTTCTTCTGCTTTTCATCTTGGCAT 836
QY 259 eValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPh 279
Db 837 CGTGGCGCTCCAGCTGTGTGGCAGGACTGCTTCGCAACCGATGCTTCCCGAGACTT 896
QY 279 eSerLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSe 299
Db 897 CAGCCTCCCGCTGAGCGTGAACCTGAGCCTTATTACAGACAGAGATGAGACGAGAG 956
QY 299 rProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProTh 319
Db 957 CCCCTTCATCTGCTCAGCCTCGGAGATGGCATGAGATCCTGCAAGAGTGTGCCAC 1016
QY 319 rLeuArgGlyGluGlyGlyGlyGlyProProCysSerSerLeuAspTyrGluThrTyrAsnSe 339
Db 1017 ACTGCGTGGGAGAGCGGTGTGGCCACCTGCAGTGTGACATAGAGACCTATAACAG 1076
QY 339 rSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyG 359
Db 1077 TTCCAGCAACACCACTGTGTCAACTGGAACCACTACTATACCACTGCTGCGGCGA 1136
QY 359 uHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaI 379
Db 1137 GCACAAACCCCTTCAAGGCGGCATCAACTTTGACAAACATTGGCTTAGCTGATCGCCAT 1196

QY	379	epheGlnValIleThrLeuGluGlyTrpValAspIleMetYrPheValMetAspAlaHi	399
Db	1197	CTTCCAGGTCATCACACTGGAGGGCTGGGTGCACATCATGTACTTCGTAATGACGCTCA	1256
QY	399	sSerPheTyrAsnPhelIeTyrPheIleLeuLeuIleIleValGlySerPhePheMetI	419
Db	1257	CTCCTTCTACAACTTCATCTACTTCATTTCTCATCATCGTGGGCTCCTTCTTCATGAT	1316
QY	419	eAsnLeuCysLeuValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerG	439
Db	1317	CAACCTGTGCCTGGTGTGATTGCCACGCAGTTCTCCGAGACCAACAGCGGAGAGTCA	1376
QY	439	nLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSe	459
Db	1377	GCTGATGCGGAGCAGCGGTATGCAATTCTGTCCAAATGTAACACCCCTGGCAAGCTTCTC	1436
QY	459	rGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgIysAl	479
Db	1437	TGAGCCAGGAGCTGCTATAGAGAGCTACTCAAGTACCTGGTGTACATCCTCCGAAGAAGC	1496
QY	479	aAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSe	499
Db	1497	AGCCCGAAGGCTGGCCCAAGTCTTAGGGCTATAGCGGTGCGGGCTGGGCTGCTCAGCAG	1556
QY	499	rProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisAr	519
Db	1557	CCCACTGGCCCGTAGTGGGACAGAGCCCAAGCCAGCTGGCAGCTGCACCTGCACACCG	1616
QY	519	gArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisHisTyrHisLe	539
Db	1617	TGCTGTCTGTCTCCACCACCTGGTCCACCACCATCACCACCACTACCACTACCACT	1676
QY	539	uGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAs	559
Db	1677	GGGTAATGGAGCGCTCAGAGTTCCCCGGGCCAGCCCAAGATCCAGACAGGAGATGCCAA	1736
QY	559	nGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProPr	579
Db	1737	TGGGTCTCGCGGCTCATGTACCAACCACTTACACCACTCCCTCTGGGGGCCCTCC	1796
QY	579	oArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValAr	599
Db	1797	GAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGACTGCCACTTGAGCCAGTCCG	1856
QY	599	gCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGl	619
Db	1857	TTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCTGTAGGACTGTGGGTAGTGG	1916
QY	619	ylYsValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLe	639
Db	1917	GAAAGTGTACCCCACTGTGCTACCAAGCCCTCCACACAGATACGAAAGATAAAGCACT	1976
QY	639	uValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGl	659
Db	1977	AGTGAAGGTGGCCCCAGCCCTGGGGCCCCCACCCTCACAGCTTCAACATCCCACTGG	2036
QY	659	yProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSe	679
Db	2037	GCCCTTCAGCTCCATGCACAAAGCTCCTGGAGACACAGAGTAACGGGAGCCTGCCATAGCTC	2096
QY	679	rCysLysIleSerSerProCysSerLysLysAlaAspSerGlyAlaCysGlyProAspSerCy	699
Db	2097	CTGCAAAATCTCCAGCCCTTGTCTCCAAGGCAGACAGTGGAGCCTGCGGGCCGGACAGTTG	2156
QY	699	sProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAs	719
Db	2157	TCCCTACTGTGCCCCGACAGAGACAGAGAGCCAGAGTCCGCTGACCATGTATGCTCTGA	2216
QY	719	pSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAs	739
Db	2217	CTCAGACAGCGAGGCTGTGTATGAGTTCAACACAGGACGCTCAGCACAGTGAACCTCCGGGA	2276
QY	739	pProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValIle	759

Db	2277	TCCCACAGCCGGCGCGACAGCGGAGCCTGGGCCACAGATGACAGACCTAGTCTGTGCT	2336
Qy	759	uAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheG1	779
Db	2337	GGCTTTCTGGAAGCTGATCTGTGACACATTCCGGAAGATCGTAGATAGCAAAATACTTTGG	2396
Qy	779	yArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisG1	799
Db	2397	CCGGGAATCATGATCGCATCTGTGTCATACACTCAGCATGGGCATCGAGTACCACGA	2456
Qy	799	uGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPh	819
Db	2457	GCAGCCCGAGGAGCTCACCAACGCCCTGGAATCAGCAACATCGTCTCACACGCCCTCT	2516
Qy	819	eAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnPr	839
Db	2517	CGCCTTGGAGATGCTGCTGAACCTGCTGTCTACGGTCCCTTTGGCTACATTAGAATCC	2576
Qy	839	oTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGlyGlnG1	859
Db	2577	CTACACATCTTTGATGGTGTCATTGTGTGTCATCAGTGTGTGGAGATTGGGCCAGCA	2636
Qy	859	ngIyGlyIleuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValAr	879
Db	2637	GGAGAGTGGCCTGTGCGTGTGCGGACCTTCCGCTGATGCGGGTGTGAAGCTGTGCG	2696
Qy	879	gPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAl	899
Db	2697	CTTCTGCGCCGCCCTGCAGCGCCAGCTCGTGGTGCTCATGAAGACCATGGACACGTGGC	2756
Qy	899	aThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLe	919
Db	2757	CACCTTCTGCATGCTCCTTCATGCTGTTCATCTTCATCTTCAGCATCTTGCGCATGCACT	2816
Qy	919	uPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPh	939
Db	2817	CTTTGGTTGCAAGTTCGCACTCTGAACGGAGTGGGGAACAGTTGCCAGACCGAAGAATT	2876
Qy	939	eAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAs	959
Db	2877	CGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATTCTGACTCAGGAAGACTGGA	2936
Qy	959	nLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAl	979
Db	2937	TAAAGTCTCTACAAACGGCATGGCCTCCACATCGTCTTGGGCTGCTCTTACTTCATCGC	2996
Qy	979	aLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluG1	999
Db	2997	CCTCATGACTTTTGGCACTATGTGCTCTTTAACTGCTGTGGCCATTCTTGTGAAGG	3056
Qy	999	yPheGlnAlaGlu-----	1003
Db	3057	ATTCCAGCGCAGAGAAATCGGCAAAACGGGAAGATGCGAGTGACACTTAAGCTGTATTCA	3116
Qy	1004	-----GlyAspAlaThrLysSerGluSerGluProAspPhePh	1016
Db	3117	GCTGCTGTCAACTCTCAGGGGGGAGATGCCACCAAGTCTGAGTCAAGACCTGATTTCTT	3176
Qy	1016	eSerProSerValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuG1	1036
Db	3177	TTTCGCCAGTGTGATGTGATGGGACAGAAAGAAGCGCTTGGCCCTGTGGCTTTGGG	3236
Qy	1036	yGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThr	1056
Db	3237	AGAACACGCGGAACACTACGAAGAAGCCTTTTGGCACCCCTCATCATCAACGGCTGCGAC	3296
Qy	1056	rProMetSerHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySe	1076
Db	3297	ACCAATGTCACTACCCAGAGCTCCAGCACAGGTGTGGGGGAAGCACTGGGCTCTGGGCTC	3356
Qy	1076	rArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCy	1096

Db 3357 TCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCACCATGAGATGAATC 3416
Qy 1096 sProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrse 1116
Db 3417 TCCGCCAAGTGCCTCGCAGCTCCCGCACAGTCCCTGGAAGTGGGCAAGCAGCTGGACCAG 3476
Qy 1116 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProse 1136
Db 3477 CAGGCGCTCCAGCAGGAACAGCCTGGGCGCGGCCCCACGCTAAAGCGAGAGACCCGAG 3536
Qy 1136 rGlyGlyArgArgSerLeuLeuSerGlyGlyGlyGlnGlyLeuSerGlnAspGlyGlyLeuSe 1156
Db 3537 CGGGAGCGGAGGTCCCTGCTGCTGGAGAGGGCCAGAGAGTCAAGATGAGAGGAAG 3596
Qy 1156 rSerGlyLysAspArgLaserProAlaGlySerAspHisArgHisArgGlySerLeuGly 1176
Db 3597 TTCAGAAAGAGACCGGGCCAGCCACGAGGCAAGTCAATCGCCACAGGGGTTCCTTGA 3656
Qy 1176 uArgGlyAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisAr 1196
Db 3657 ACGTAGGCCAAGAGTTCCTTTGACCTGCTGACACTCTGCAGGTGCGGGGCTGCACCG 3716
Qy 1196 gThrAlaSerGlyArgSerSerAlaSerGlyHisGlnAspCysAsnGlyLysSerAlase 1216
Db 3717 CACAGCCAGCGCGCGAGCTCTGCTCTGAGCACCAAGACTGTAATGGCAAGTCGGCTTC 3776
Qy 1216 rGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAs 1236
Db 3777 AGGGCGTTTGGCCCCGACCTGAGAGACTGATGACCCCACTGGATGGGATGATGACAA 3836
Qy 1236 nAspGlyGlyAsnLeuSerLysGlyGlyLysArgGlyGlnAlaTrpValArgSerArgLeuPr 1256
Db 3837 TGATGAGGGAATCTGAGCAAAGGGGAACGATACAGCCTGGGTCAATCCCGGCTTCC 3896
Qy 1256 oAlaCysCyAspArgLysArgAspSerTrpSerAlaTyrllePheProProGlnSerArgPh 1276
Db 3897 TGCCTGTTGCCGAGAGCGAGATTCTGTGTCGGCTATATCTTCTCCTCACTCAAGGTT 3956
Qy 1276 eArgLeuLeuCySHisArgIleIleThrHisLysMetPheAspHisValValLeuValIl 1296
Db 3957 TCGTCTCCTGTGCACCGGATCATCACCCACAAAGATGTTGACCATGTGTCTCTGCAT 4016
Qy 1296 eIlePheLeuAsnCysIleThrIleAlaMetGlyArgProLysIleAspProHisSerAl 1316
Db 4017 CATCTTCTCAACTGTATCACCATCGTATGAGCGGCCCAAAATTGACCCCAACAGCGC 4076
Qy 1316 aGlyuArgIlePheLeuThrLeuSerAsnTyrllePheThrAlaValPheLeuAlaGlyLeu 1336
Db 4077 TGAGCGCATCTTCTTGACCCCTCTCCAACTACATCTTCAAGGAGTCTTCTAGCTGAAT 4136
Qy 1336 tThrValLysValValAlaLeuGlyTrpCysPheGlyGlyGlnAlaTyrlleuArgSerSe 1356
Db 4137 GACAGTGAAGGTGTGTGGCACTGGGCTGTGTGGGAGCAAGGCTTACCTGCGCAGCAG 4196
Qy 1356 rTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMe 1376
Db 4197 CTGGAATGTGCTGACCGGCTTGTGTGCTCATCTCCGTATCGACATCTGTGCTTCAT 4256
Qy 1376 tValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgTh 1396
Db 4257 GGTCTCCGACAGCGGACCAAGATCCTTGGCATGTGAGGGTGTGCGGCTGTGCGGAC 4316
Qy 1396 rLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLe 1416
Db 4317 CCTGCGTCCACTCAGGGTCAACGCCGGGCCCAAGGACTGAAGTGTGTAGAGACTCT 4376
Qy 1416 uMetSerSerLeuLysProIleGlyAsnIleValValIleCysCyAspAlaPhePheIleIl 1436
Db 4377 GATGTCACTCCCTCAAAACCATTTGGCAACATTGTGTCAATTGTGCTGTCTTCATCAT 4436
Qy 1436 ePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyLys 1456
Db 4437 TTTTGAATTCTCGGGGTGACGCTTTCAAAGGGAAGTTCTTGTGTGTACGGGTGAGGA 4496

Qy 1456 pThrArgAsnIleThrAsnLysSerAspCysAlaGlyAlaSerTyrrArgTrpValArgHis 1476
Db 4497 CACCAGGAACATCACTAACAATCCGACTGCGCTGAGGCCAGCTTACCATGGGTCCGGCA 4556
Qy 1476 sLysTyrrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLy 1496
Db 4557 CAAGTACAACCTTGAACAACCTGGGCCAGGCTGTATGTCCCTGTTGTCTGGCTCCAA 4616
Qy 1496 sAspGlyTrpValAspIleMetTyrrAspGlyLeuAspAlaValGlyValAspGlnGlnPr 1516
Db 4617 GGATGTTGGGTGACATCATGTATGATGGGCTGGATGCTGGGTGTGATCAGACGCC 4676
Qy 1516 oIleMetAsnHisAsnProTrpMetLeuLeuTyrrPheIleSerPheLeuLeuIleValAl 1536
Db 4677 CATCATGAACCAACACCCCTGGATGCTGTCTATCTTCACTCTCCTCCTCATCGTGGC 4736
Qy 1536 aPhePheValLeuAsnMetPheValGlyValValValGlyLysAsnPheHisLysCysArgGly 1556
Db 4737 CTTCTTGTCTGAAATGTTGTGGGCGTGTGTGTGAGAACTTCCATTAAGTGACAGACA 4796
Qy 1556 nHisGlnGlyGlyGlyGlyAlaArgArgArgGlyGlyLysArgLeuArgArgLeuGlyLy 1576
Db 4797 GCACCAAGAGAGAGAGGAGCGGCGGTGAGAGAGAAAGCACTACGAGGCTGAGAA 4856
Qy 1576 sLysArgArg-----SerLysGlyLysGlnMe 1585
Db 4857 AAAGAGAAGAAATGTAATGTTGACGATGTAATTGCTTCCGGCAGCTCACCGCGCTGC 4916
Qy 1585 tAlaGlyAlaGlnCysLysProTyrrTyrrSerAspTyrrSerArgPheArgLeuLeuValHi 1605
Db 4917 GTCAGAAGCCCAAGTGAAGCCCTACTACTCTGACTACTCGAGATTCCGGCTCCTTGCCA 4976
Qy 1605 sHisLeuCysThrSerHisIleTyrrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnVa 1625
Db 4977 CCACCTGTGTACCAGCACTACCTGGAACCTTTCATCACTGGTGTCACTCGGGCTGAACGT 5036
Qy 1625 lValThrMetAlaMetGlnHisTyrrGlnGlnProGlnIleLeuAspGlyAlaLeuLysIl 1645
Db 5037 GGTCACTATGGCCATGGAACATTACACAGCAGGCCCAAGATCCTGACGAGGCTTGAAAGAT 5096
Qy 1645 eCysAsnTyrllePheThrValIlePheValPheGlySerValPheLysLeuValAlaph 1665
Db 5097 CTGCAATTACATCTTACCCTCATCTTGTGCTTGAAGTTCAACTTGTGGCCTT 5156
Qy 1665 eAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLe 1685
Db 5157 TGGCTTCCGCCGTTTCTTCCAGGACAGGTGGAACCAAGCTGGAACCTGTGCTTCT 5216
Qy 1685 uSerIleMetGlyIleThrLeuGlyGlyIleGlyValAsnLeuSerLeuProIleAsnPr 1705
Db 5217 GTCCATCATGGGCATACACTGGAGGAGATTGAGGTCAATGCTTCGCTGCCCATCAACCC 5276
Qy 1705 oThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMe 1725
Db 5277 CACCATCATCCGTATCAGAGGGTGTCTCCGCATTGCTCGAGTTCTGAAGCTGTGAAGAT 5336
Qy 1725 tAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAs 1745
Db 5337 GGTGTGGGCATGCGGGCACTGTGACACGGGTGATGACGCCCTGCCAGGTGGGAA 5396
Qy 1745 nLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPh 1765
Db 5397 CCTGGACTTCTCTTCATGTATTATTGTTTTCATCTTGGACGCTCTGGGCGGTGAAGCTCTT 5456
Qy 1765 eGlyAspLeuGlyCysAspGlyThrHisProCysGlyGlyLeuGlyLysArgHisAlaThrPh 1785
Db 5457 TGAAGACCTGAGTGTATGAGACACACCCCTTGTGAGGGCTTGGGTGGCATGCCACCTT 5516
Qy 1785 eArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAs 1805
Db 5517 TAGGACTTGTGTATGGCTTCTTGACCCCTCTCCGAGTCTCCACTGTGTGACAACTGAA 5576

QY	1805	nglYlIeMeLysAspProSerArGAspGlnGluSerThrCysTyrAsnThrVa	1825
Db	5577	TGGTATTATGAAGACACACCTCCGGGACTGTGACCAGAGTCCACTGTACACACTGT	5636
QY	1825	lIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnVa	1845
Db	5637	CATCTCCCTTATCTACTTTGTGTCTTCCTGTGCTGACGGCCCACTTTGTGCTGGTCAAGT	5696
QY	1845	lValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAl	1865
Db	5697	GGTCATAGCTGTGCTGATGAAGCACCTGGGAAGAACAAAGAGGCCAAGGAGGAGGC	5756
QY	1865	agluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerPr	1885
Db	5757	CGAGCTCGAGGCCGAGCTGAGCTGGAAGACGCTCAGCCCGCAGCCCACTCC	5816
QY	1885	oleuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrAspSerProLy	1905
Db	5817	GCTGGGACAGCCCTTCTCTGTGCCCCGGGGTGAGGGTGTCAACAGTCTTGACAGCCCTAA	5876
QY	1905	sProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerGlyPheSerLeuGluHi	1925
Db	5877	GCCTGGGGCTCCACACACCACTGCCCATTTGAGAGAGCCCTCGGCTTCTCCCTTGAGCA	5936
QY	1925	sProThrMetValProHisProGluGluValProValProLeuGlyProAspLeuLeuTh	1945
Db	5937	CCCCACGATGGTACCACCCACCCGAGAGGTGCAGTCCCCCTTAGAACCAAGACCTGTGAC	5996
QY	1945	rValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysAr	1965
Db	5997	TGTGAGGAAGTCTGGTGTGTCAGCCGGACGCACTCTGTGCCAATGACAGCTACATGTGCGG	6056
QY	1965	gAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaG1	1985
Db	6057	CAATGGAGCACTGTGAGAGATCCCTTAGAACACAGGGGCTGGGGGCTCCCAAAAGCCA	6116
QY	1985	nSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLe	2005
Db	6117	GTCAGGCTCCATCTTGTCCGTTCACTCCCAACAGACAGACAGACTGCATCCTACAGCT	6176
QY	2005	uProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIlePr	2025
Db	6177	TCCCAAGATGTGCACTATCTGTCTCCAGCTCATGGGGCCCCCACCCTGGGGCCCATCCC	6236
QY	2025	olysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAl	2045
Db	6237	TAAACTACCCCACTGGCCGCTCCCTCTTGCTCAGAGGCTCTTCAGGCGCCAGGCAAGC	6296
QY	2045	aiIeArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerG1	2065
Db	6297	AATAAGACTGACTCCCTGGATGTGAGGGCCTGGTAGCCGGGAAGACCTGTTGTGAGA	6356
QY	2065	uValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSer11	2085
Db	6357	GGTAGTGGGCCCTCTGCCCCCTGTGACCCGGTCTCATCTTCTGGGGCGGGTGCAGCAT	6416
QY	2085	eGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAl	2105
Db	6417	CCAGGTGACGACGCTTCCGGCATCCAGAGCAAGTCTCCAAGCACATCCGCTGCCAGC	6476
QY	2105	aProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerle	2125
Db	6477	CCCTTGCCCAAGGCTTGAACCCAGCTGGGCCAAGGACCCCTCCAGAGACCAAGAAAGCAGTT	6536
QY	2125	ugluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGluG1	2145
Db	6537	AGAGCTGACACGAGAGCTGAGCTGATTTCAGAGAACCTCTTCCAGCAGCCAGGAGAAGA	6596
QY	2145	uProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrGlnSerCysArgAr	2165
Db	6597	ACCCCTGTCCCAAGGAGCCTGAAGAAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGGG	6656
QY	2165	gArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAs	2185

Db	6657	CAGGCTGGGCTCTGGCTAGATGAACAGCGGAGACTCCATTGCTGTCACTGTCTGGA	6716
QY	2185	pSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlyGlnProLeuG1	2205
Db	6717	CAGGGCTCCCAACCCCGCTTATGTCCAAGCCCTTCAGGCTCGGGGCCAACCCTTTGG	6776
QY	2205	yGlyProGlySerArgProLysLysLysLeuSerProProSerIleSerIleAspProPr	2225
Db	6777	GGGTCTGGGAGCCGGCCTTAGAAAAAACTCAGCCCAACAGTATCTTATAGACCCCCC	6836
QY	2225	ogluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgAlaPr	2245
Db	6837	GGAGAGCCAGGGCTCTCGGCCCATGACGTCTGGTGTCTGCTCAGAGAGGAGGGCGCC	6896
QY	2245	oAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerPr	2265
Db	6897	GGCCAGTGACTTAAGATCCCTCGGTCTCCAGCCCCCTTGACAGACGGCTGCCCTCAC	6956
QY	2265	oSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMetAs	2285
Db	6957	CTCCCAAGAAAGACACGCTGAGTCTCTGTGTTTGTCTTGACCCCAAGACATGGA	7016
QY	2285	pPro 2286	
Db	7017	CCCC 7020	

RESULT 3

US-09-383-894-1
; Sequence 1, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004,00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7129
; TYPE: DNA
; ORGANISM: Rattus sp.
; US-09-383-894-1

Alignment Scores:
Pred. No.: 0 Length: 7129
Score: 11673.00 Matches: 2237
Percent Similarity: 97.77% Conservative: 1
Best Local Similarity: 97.73% Mismatches: 15
Query Match: 97.05% Indels: 36
DB: 10 Gaps: 2

US-09-611-257A-24 (1-2287) x US-09-383-894-1 (1-7129)

QY	34	TrpThrArgArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg	53
Db	2	TGAGCAGAGGAGGATGAGCGGGCGCCGAGAGTGGGACAGCCCGTAGCTTCACGC	61
QY	54	SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAspP	73
Db	62	AGCTCAACGACCTGTCCGGGGCGGGGGCCGGCAGGGGCGGGGTGCAGCGAAAGAAC	121
QY	73	roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP	93
Db	122	CGGGCAGCGGGACTCCGAGCGGAGGGGCTGCCGTACCGCGCTAGCCCGGTGTTT	181
QY	93	hePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP	113

Db 182 TCCTCTACTTGAGCCAGACAGCCGCCGAGCTGGTGTCTCCGACGGTCTGTAAACC 241
Qy 113 roTTPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CGTGGTTCGAGCGAGTCAGTATGCTGGTCAATTCTTCAACTGTGTGACTCTGGGTATGT 301
Qy 133 heaArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhea 153
Db 302 TCAGGCCGCTGTGAGGACATTCCTGTGACTCCAGCGCTGCCGATCTCGACAGGCCCTTCG 361
Qy 153 sPaSPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTCATCTTGGCTTCTTGGCTGTGAAATGGTGTGAAGATGGTGGCTTGGCA 421
Qy 173 lePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
Db 422 TCCTTGGGAAGAATGTTACTCGGAGACACTTGAACCGGCTTGACTTTTCATTGTCA 481
Qy 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAAGCTTCCGACATCAGGA 541
Qy 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTCGACCCGCTCAGGGCCATTAAACGGGTGCCACGATGCCGCAATTCTCG 601
Qy 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACATTACTGTGTCGACACCTTGCTTATGTCTGGGCAAGCTGCTGTCTGTCTTCTCG 661
Qy 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCCTTTTCATCTTGGCATCGTGGGCGCTCCAGCTGTGGCAGAGACTGTGCAACCGAT 721
Qy 273 ysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGAACCTGAGCCTTATTACCAGA 781
Qy 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGATGAGGACGAGAGCCCTTCATCTGCTTCAGCCTCGGAGAAATGGCATGAGAT 841
Qy 313 exCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAGTGTGCCCACTGCGTGGGGAAGCGGTGTGGCCCACTGCAGTCTGG 901
Qy 333 spTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGACCTATAACAGTTCACAGCAACACCACTGTGTCAACTGGAACCACTACTATA 961
Qy 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCTGCGGGCGAGCAACCCCTTCAAGCGGCCCATCACTTGCACAACATTG 1021
Qy 373 lyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetT 393
Db 1022 GCTATGCTGGATCGCCATCTTCCAGGTCACTGACATGGAAGGGCTGGGTGCACATCATGT 1081
Qy 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACTTCGTAATGAGCGCTCACTCTTCTACAACACTTCACTTCACTTCTCATCATCG 1141
Qy 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGATTGCCACGCACTTCCGAGA 1201
Qy 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAAACAGCGGAGAGTACGCTGATCGGGGAGCAGCGGTGTACGATTCTGTCCAATGCTA 1261
Qy 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCCCTGGCAAGCTTCTCTGAGCCAGGCAAGCTGTATGAGGAGCTACTCAAGTAACTCTGG 1321

Qy 473 alTyrIleLeuAlaGlyAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCAGGTCCTTAAGGGCTATAGGCGGTGC 1381
Qy 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGCTGGCTGCTCAGCAGCCAGTGGCCGTAGTGGCAGAGAGCCCAAGCCAGTGCA 1441
Qy 513 erCysThrArgSerHisArgArgLeuSerValHisIleuValHisHisHisHisHis 533
Db 1442 GCTGCACTCGCTCACACCGCTCGTGTGTGTCCACCACTGTGTCCACCACTCACACCACC 1501
Qy 533 iSH 553
Db 1502 ACCATCACCACTACCACTGGGTATGGGACGCTCAGAGTTCCCCGGGCCAGCCAGAGA 1561
Qy 553 leGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrProT 573
Db 1562 TCCAGACAGGATGCCAATGGGTCTCGCCGGCTCATGTACCAACCACTCTACACCCA 1621
Qy 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CTCCCTCTGGGGCCCTCCGAGGGTGGAGTCTGTACACAGCTTCTACATGTGACT 1681
Qy 593 ySHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSHiSH 613
Db 1682 GCCACTTGAGCCAGTCCGCTTGCCAGGCAACCCCTCCAGATGCCATCGAGGATCTG 1741
Qy 613 lyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI 633
Db 1742 GTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAACCCCTCCACAGAGA 1801
Qy 633 leLeuLysAspIleAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653
Db 1802 TACTGAAGATAAAGCACTAGTGAAGTGGCCCCCAGCCCTGGGCCCCCAACCTCACCA 1861
Qy 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSert 673
Db 1862 GCTTCAACATCCCACTGGGCCCTTCACTTCATGCACAAAGCTCTGGAAGACACAGAGTA 1921
Qy 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTGTCTCCAAAGGACAGAGTGAG 1981
Qy 693 laCysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera 713
Db 1982 CCTGCGGGCCGAGAGTTGTTCCTACTGTGTGCCCGGACAGAGAGCAGAGAGTCCG 2041
Qy 713 laAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CTGACCATGTATGCTGACTGAGACAGAGGAGGTGTATGAGTTCAACAGAGCGCTC 2101
Qy 733 lnHisSerAspLeuArgAspProHisSerArgArgGlnArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCAGAGTGACCTCGGGATCCCAACAGCCGGCGGAGCAGCGGAGCCTGGGCCAGATG 2161
Qy 753 laGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2162 CAGAGCCTAGTCTGTGCTGGCTTCTGAGGCTGATCTGTGACACATTCCGGAAGATCG 2221
Qy 773 alAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2222 TAGATAGCAAAATACTTTGGCCGGGAATCATGATGCCATCCTGTGTCAATACACTCAGCA 2281
Qy 793 etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2282 TGGGCATCGAGTACACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAATACAGCAACA 2341
Qy 813 leValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProp 833
Db 2342 TCGTCTTCAACCAAGCTTCTGCGCTTGAGATGTCTGTGAACGTGTTGTCTACGCTCCCT 2401

QY	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT	853
Db	2402	TTGGCTACATTAAAGATCCCTACAACATCTTTGATGGTGTCAATTGTGCATCAGTGT	2461
QY	853	rpGluIleValGlyGlnGlnGlyGlyLeuSerValIleuArgThrPheArgLeuMetA	873
Db	2462	GGGAGATTGTGGCCAGCAGGAGGTGGCTGTGGGTCTGCGGACCTTCGGCTGATGC	2521
QY	873	rgValIleuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValIleuMetI	893
Db	2522	GGGTGCTGAAGCTGTGTGGCTTCTGCGGCCCTGCAGCGCCAGCTCGTGTGTCATGA	2581
QY	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
Db	2582	AGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCA	2641
QY	913	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL	933
Db	2642	GCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCCGACTTGAAACGGGATGGGACACGT	2701
QY	933	eupProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL	953
Db	2702	TGCCAGACCGGAAGAAATTGCACTCCCTGCTCTGGGCATCGTCACTGTCTTTCAGATTTC	2761
QY	953	euThrGlnGluAspTrpAsnLysValIleuTyrAsnGlyMetAlaSerThrSerSerTrpA	973
Db	2762	TGACTCAGGAAGACTGGAAATAAGTCTCTACAACGGCATGGCTCCACATCGTCTTGGG	2821
QY	973	IaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV	993
Db	2822	CTGCTCTTACTTCACTCGCCCTCATGACTTTTGGCACTATGTGCTCTTTAACCTGTGG	2881
QY	993	aAlaIleLeuValGluGlyPheGlnAlaGlu-----	1003
Db	2882	TGGCCATTCTTGTGGAAGATTTCCAGGCAGAGAAATCCGCCAAACGGGAGATGCCAGTG	2941
QY	1004	-----GlyAspAlaThrLysSerg	1010
Db	2942	GACAGTTAAGCTGTATTACGCTGCTCTCACTCTCAGGGGGGAGATGCCACCAAGTCTG	3001
QY	1010	IuSergLuproAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgL	1030
Db	3002	AGTCAGAGCCTGATTTCTTTTCGCCACAGTGTGATGTGATGGGACAGAAAGACGCT	3061
QY	1030	euaIaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuI	1050
Db	3062	TGGCCCTGTGGCTTTGGGAGAACACGCGGAACACTACGAAGACCTTTTGCCACCCCTCA	3121
QY	1050	IeIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG	1070
Db	3122	TCATCCATACGGCTGCGACACCAATGTCACTACCAACCAAGACTCCAGCACAGGTGTGGGG	3181
QY	1070	IuaIaLeuGlySergLysSerArgArgThrSerSerSergLysSerAlaGluProGlyAlaA	1090
Db	3182	AAGCACTGGGCTCTGGCTCTTCACAGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGACCTG	3241
QY	1090	IaHisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTyrSera	1110
Db	3242	CCCAACCATGAGATGAATCTCCGCCAAGTGCCCCGACGTCCCCGCCACAGTCCCTGGAGTG	3301
QY	1110	IaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL	1130
Db	3302	CGGCAAGCAGCTGGACCAAGCGCTCCAGCAGGAACAGCTGGGCCCGGCCCCCAAGCC	3361
QY	1130	eulYsArgArgSerProSergLysLysArgArgSerSerLeuLeuSergLysGlyGlnGlnLus	1150
Db	3362	TAAAGCGGAGAGCCCGAGCGGGGAGCGGAGTCCCTGTCTGTGAGAGGCGCAGAGGA	3421
QY	1150	erGlnAspGluGluGluSergLysGluLysAspArgAlaSerProAlaGlySerAspHisA	1170
Db	3422	GTCAAGATGAGGAGGAAGTTTCAAGAAGAACCGGGGCCAGCCCAAGCAGGACGTGACCATC	3481
QY	1170	rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG	1190

Db	3482	GCCACAGGGGTTCTTGAACGTGAGGCCACAGAGTTCTTTGACCTGCTGACACTCTGC	3541
QY	1190	lNvalProglYleuHIsArgThrAlaSerGlYArgSerSerAlaSerGlHIsGlAspC	1210
Db	3542	AGGTGCCCCGGCTGCACCGCACAGCCAGCGCGGAGCTCTGCTCTGAGCACCAAGACT	3601
QY	1210	yEaSnGlYLySSerAlaSerGlYArgLeuAlaArgThrLeuArgThrAspAspProGlInL	1230
Db	3602	GTAATGGCAAGTCGCTTCAGGGCGTTTGGCCCCGCAACCTGAGGACTGATGACCCCCAAC	3661
QY	1230	eUaSPGlYAspAspAspAsnAspGlUGlYAsnLeuSerLySGlYGlUArgtlleglNalAT	1250
Db	3662	TGGATGGGATGATGACAATGATGAGGAAATCTGAGCAAAAGGGGAACGCATACAAAGCCT	3721
QY	1250	rPValArgSerArgLeuProAlaCysCySArgGlUArgAspSerTrpSerAlaTyrlleP	1270
Db	3722	GGGTACAGATCCCGGCTTCCTGCTGTGTCGAGAGCGAGATTCTTGTCGGCTATATCT	3781
QY	1270	heProProGlInSerArgPheArgLeuLeuCysHIsArglllelThrHIsLySMetPhea	1290
Db	3782	TTCCTCCTCAGTCAAGGTTTGTCTCTCTGTGTCAACGGATCATCACCCACAAGATGTTTG	3841
QY	1290	sPHisValValLeuValllelPheLeuAsnCyslleThrllleAlaMetGlUArgProL	1310
Db	3842	ACCATGTGGTCTCTCATCATCTTCTCTCACTGATACCATCGCTATGAGCGCCCA	3901
QY	1310	ySllEaSPProHIsSerAlaGlUArgtllePheLeuThrLeuSerAsnTyrllePheThra	1330
Db	3902	AAATTGACCCCCACAGCGCTGAGCGCATTTCTTGACCTCTCCAATACATCTTCACGG	3961
QY	1330	lAValPheLeuAlaGlUmetThrValLySValValAlaLeuGlYTrpCySPhelYGlUG	1350
Db	3962	CAGTCTTCTAGCTGAATGACAGTGAAGTGTGGCACTGGGCTGTCTTTGGGGAGC	4021
QY	1350	lNalATyrLeuArgSerSerTrpAsnValLeuAspGlYLeuLeuValLeuIleSerValI	1370
Db	4022	AGGCCTACCTGCGCAGCAGCTGGAATGTGTGAGCGGCTGTGCTGTCAATCTCGTCA	4081
QY	1370	lEaSPllleLeuValSerMetValSerAspSerGlYThrLySllleLeuGlYMetLeuArgV	1390
Db	4082	TCGACATCCTGGTCTCCATGTTCTCCGACAGCGGCACCAAGATCCTTGCACTGAGGG	4141
QY	1390	alLeuArgLeuLeuArgThrLeuArgProLeuArgVallleSerArgAlaGlInGlYLeuL	1410
Db	4142	TGCTGCGGCTGCTGCGGACCTGCGTCCACTCAGGGTCAATCAGCCGCGCCAGGACTGA	4201
QY	1410	ySLeuValValGlUThrLeuMetSerSerleuLySProilleGlYAsnllleValVallleC	1430
Db	4202	AGCTGTGTTAGACTCTGATGTATCTCCCTCAAAACCATTTGGCAACATTTGTGTCATTT	4261
QY	1430	ySCysAlaPhePheIlellePheGlYllleLeuGlYValGlInLeuPheLySGlYLySPheP	1450
Db	4262	GCTGTGCTTCTTCATCATTTTGTGAATTTCTGGGGGTGCAAGCTCTTCAAAAGGAAATTCT	4321
QY	1450	heValCySGlInGlYGlUaSPThrArgAsnllleThrAsnLySSerAspCySAlaGlUAlaS	1470
Db	4322	TGCTGTGTCAAGGTGAGACACCAAGAACATCACTAACAATCCGACTGCGTGAAGCCA	4381
QY	1470	eTrYrArgTrpValArgHIsLySTyrAsnPhaSPaSnLeuGlYGlInAlaLeuMetSerL	1490
Db	4382	GCTACCGATGGGTCCGGCACAAAGTACAACCTTGCGCAGGCTCTGATGTCCC	4441
QY	1490	eUPheValLeuAlaSerLySAspGlYTrpValaSPllleMetTyraSPGlYLeuAspAlaV	1510
Db	4442	TGTTTGTGCTGGCTTCCAAGATGTTGGGTGACATCATGTATGATGGGCTGGATGCTG	4501
QY	1510	aGlYValaSPGlInGlInProilleMetAsnHIsaSnProTrpMetLeuLeuTyrrPheIleS	1530
Db	4502	TGGGTGTGATCAGCAGCCCATCATGAACCAACCCCTGGATGCTGTACTTCACTCT	4561
QY	1530	eRheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlYValValGlUa	1550

Db 4562 CCTTCCTCATCGTGGCTTCTTGTCTCTGAACATGTTGTGGCGGTGTGTGAGA 4621
Qy 1550 snPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysA 1570
Db 4622 ACTTCATAGTGCAGACACCAAGAGAGAGAGGCGGCGGTGAGAGAAC 4681
Qy 1570 rgLeuArgArgLeuGluLysLysArgArg----- 1579
Db 4682 GACTACGAGGCTGAGAAAAGAGAGAAATCTAATGTTGACGATGTAATGCTTCCG 4741
Qy 1580 --SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerA 1599
Db 4742 GCAGCTCAGCCAGCGCTGCGTCAGAGCCAGTGACAGCCCTACTACTGTGACTACTCGA 4801
Qy 1599 rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrg 1619
Db 4802 GATTCCGGCTCTTGTCTCCACCACCTGTGTACCGACCACTACCTGGACCTTTCATCACTG 4861
Qy 1619 lYValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIlel 1639
Db 4862 GTGTCAATCGGGCTGAACGTGTCTACTATGCCCATGGAACTATTACAGACGCCCAAGATCC 4921
Qy 1639 euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV 1659
Db 4922 TGGACGAGGCTCTGAAGATCTGAATTAATCATCTTTACCGTCATCTTGTCTTGAAGTCAG 4981
Qy 1659 alPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTTPAsnGlnLeuA 1679
Db 4982 TTTTCAAACTTGTGCGCTTGGCTTCCGCCGTTTCTTCCAGGACAGGTGAACCAAGCTGG 5041
Qy 1679 spLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnL 1699
Db 5042 ACCTGGCTATTGTGCTTGTTCATCATGCGGCATCACACTGGAGAGATTGAGTCAATG 5101
Qy 1699 euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV 1719
Db 5102 CTTCGCTGCCATCAACCCCACTCATCTCGTATCATGAGGGTCTCCGCAATTGCTCGAG 5161
Qy 1719 alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739
Db 5162 TTCTGAAGCTGTGAAGATGGCTGTGGGCATGCGGCATGCTGACACCGTGATGCAGG 5221
Qy 1739 lalLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaA 1759
Db 5222 CCCTGCCCCAGGTGGGGAACCTGGACTTCTCTTCATGTTATTGTTTTCATCTTTCAG 5281
Qy 1759 lalLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyL 1779
Db 5282 CTCTGGCGCTGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCTGTGAGGGCT 5341
Qy 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValS 1799
Db 5342 TGGGTGGCATGCCACCTTGAAGACTTTGGTAIGGCTTTCTGACCCTCTTCGAGTCT 5401
Qy 1799 erThrgLysAspAsnTTPAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS 1819
Db 5402 CCACGTGGTGAACAATGGAATGATTATGAAGACACCCTCCGGACTGTGACCAAGAGT 5461
Qy 1819 erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
Db 5462 CCACCTGTGTACAACACTGTCACTCCCTATCTACTTGTGTCTTGTGTGACGGCCC 5521
Qy 1839 lnpHeValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnL 1859
Db 5522 AGTTTGTCTGTCAACAGTGTCTATAGCTGTGTGATGAAGCACCTGGAAGAAACAACA 5581
Qy 1859 ysgLualalysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeus 1879
Db 5582 AAGAGGCCAAGAGAGAGCGCGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCA 5641
Qy 1879 exProGlnProHisSerProLeuGlySerProPheLeuTTPProGlyValGluGlyValA 1899
Db 5642 GCCCGCAGCCCCACTCCCGCTGGCAGCCCCCTTCTTGGCCCCGGGGTGGAGGTTGTCA 5701

Qy 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlas 1919
Db 5702 ACAGTCTGTACAGCCCTTAAGCCTGGGGCTTCCACACACCACTGTGCCCATTTGGAGCAGCTT 5761
Qy 1919 ergLysPheSerLeuGluHisProThrMetValProHisProGluGluValProValProL 1939
Db 5762 CGGGCTTCTCCCTTGAGCACCCCAAGATGTACCACCCCGAGAGGTGCAGTCTCCCC 5821
Qy 1939 euGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProA 1959
Db 5822 TAGGACCAGACCTGTGACTGTGAGGAAGTCTGTGTCAAGCCGAGCAGCACTCTGCCCCA 5881
Qy 1959 snAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyT 1979
Db 5882 ATGACAGCTACATGTGTCCGCAATGGAGGACCTGTGAGAGATCCCTAGACACAGGGGCT 5941
Qy 1979 rpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspT 1999
Db 5942 GGGGGCTCCCAAGCCAGTCAGGCTTCATCTTGTCCGTTCACTTCCCAACAGCAGACA 6001
Qy 1999 hrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaP 2019
Db 6002 CCAGCTGCATCCTACAGCTTCCCAAGATGTGCATATCTGTCTCAGCCTCATGGGGCC 6061
Qy 2019 roThrTTPGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArgP 2039
Db 6062 CCACCTGGGGCGCATCCCTAACTACCCCACTGGCGGCTCCCTGTGGCTCAGAGGC 6121
Qy 2039 roLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerA 2059
Db 6122 CTCTCAGCGCGCAGGACCAATAAGACTACTCCCTGGATGTGCAGGGCTGGTAGCC 6181
Qy 2059 rgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerp 2079
Db 6182 GGGAAACCTGTGTTCAGAGGTGAGTGGGCCCTCTGCCCCCTTGACCCGGTCTCATCTCT 6241
Qy 2079 heTTPGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerL 2099
Db 6242 TCTGGGGCGGCTCGAGCATCCAGGTGACAGCGTTCGGGCATCCAGAGCAAAAGTCTCCA 6301
Qy 2099 yshIleArgLeuProAlaProCysProGlyLeuGluProSerTTPAlaLysAspProp 2119
Db 6302 AGCACATCCGCTGCAGCCCTTGCCAGGCTTGAAACCAAGCTGGGCCAAGAGACCTTC 6361
Qy 2119 roGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTTPIleSerGlyAspLeuL 2139
Db 6362 CAGAGAACCAAGACAGCTTGAAGCTGGACACAGGAGCTGAGCTGGAATTTCAGAGACCTCC 6421
Qy 2139 euProSerSerGlnGluGluProLeuPheProArgAspLeuLysLysCysTyrSerValG 2159
Db 6422 TTCCAGCAGCAGAGAAAGAACCCCTGTCTCCCAAGGGAACCTGAAGAGTGCTAACAGTGA 6481
Qy 2159 luthrGlnSerCysArgArgArgProGlyPheTTPLeuAspGluGlnArgHisSerI 2179
Db 6482 AGAACCAAGCTGCAGGCGCAGCCTGGGTCTGGCTAGATGAACAGCGGAGACACTCCA 6541
Qy 2179 leAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerProSerSerL 2199
Db 6542 TTGTGTACAGTGTGTGACAGCGGCTCCCAACCCCGCTATGTCCAAGCCCTCAAGCC 6601
Qy 2199 euGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPros 2219
Db 6602 TCGGGGGCCAACTCTTGGGGGTCTCGGAGCGGCTTAAGAAAAAACTCAAGCCACCCA 6661
Qy 2219 erIleSerIleAspProProGluSerGlnGlySerArgProProCysSerProGlyValC 2239
Db 6662 GTATCTCTATAGACCCCCGAGAGCCAGGGCTCTCGGCCCCCATGCAGTCTGTGTCT 6721
Qy 2239 yseLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerProLeuA 2259
Db 6722 GCCTCAGAGAGAGGCGCGCGCCAGTGACTTAAGGATCCCTCGGTCTCCAGCCCTTGTG 6781

QY	542	LYThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerA	562
Db	1901	GGACGCTCAGGGCCCCCGGGCCAGCCCGAGATCCAGACAGGAGTGCCTAATGGGTCCC	1960
QY	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	1961	GCCGGCTCATGCTGCCACCACCTCGACGCGCTGCCCTCTCCGGGGCCCCCTGTGGCG	2020
QY	582	laGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
Db	2021	CAGAGTCTGTGACAGCTTTTACCATGCCGACTGCCACTTAAAGCCAGTCCGCTGCCAGG	2080
QY	602	laProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2081	CGCCCCCTCCAGGTCCCATCTGAGGCATCCGGCAGACTGTGGCAGCGGAAGGTGT	2140
QY	622	yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2141	ATCCCAACCGTGACACACCGCCCTCCACCGGAGACGCTGAAGAGAAGACACTAGTAGAGG	2200
QY	642	alAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
Db	2201	TGGTGCCAGCTCTGGGCCCCCAACCTCACCAGCCTCAATCCACCCGGGCCCTACA	2260
QY	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2261	GCTCCATGCACAAAGCTGCTGGAGACACAGAGTACAGGTGCTGCCAAAGCTCTTGCAAGA	2320
QY	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	2321	TCTCCAGCCCTTGCTGTAAGAAGACAGACAGTGGAGCCTGTGTTCAGACAGCTGCCCTACT	2380
QY	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspS	722
Db	2381	GTGCCCCGGGCGGGGAGGGAGGTGAGCTCGCCGACCGTGAATGCTGACTCAGACA	2440
QY	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS	742
Db	2441	GCGAGGCAAGTTATGAGTTCAACAGATGCCAGCACAGGCACTCCGGGACCCCA	2500
QY	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762
Db	2501	GC--CGGGCGCAACGAGCCTGGGCCCAAGATGCAGAGCCCACTGTGCTGGCCTTCT	2557
QY	762	rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI	782
Db	2558	GGAGGCTAATCTGTGACACCTTCCGAAGATTGTGACAGCAAGTACTTTGGCCGGGGA	2617
QY	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG	802
Db	2618	TCAATGATCGCCATCCTGTGTAACAACACTCAGCATGGGCATGCAATACACAGAGACCCG	2677
QY	802	luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	822
Db	2678	AGGAGCTTAACCAACGCCCTGAATCAACAACATCGTCTTACCAAGCCTTTTGCCCTGG	2737
QY	822	luMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI	842
Db	2738	AGATGCTGCTGAAGCTGCTTGTAATGTCCTTGGCTATCAAGAATCCCTACAACA	2797
QY	842	lePheAspGlyValIleValValIleSerValTyrGluIleValGlyGlnGlnGlyGlyG	862
Db	2798	TCTTCGATGTGTCAATGTGTGTCATCAGCTGTGGAGATCGTGGGCCAGAGGGGGCG	2857
QY	862	lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP	882
Db	2858	GCCGTGCGGTGCTGCGGACCTTCCGCTGATGCGTGTGCTGAAGCTGGTGGCTTCTGCG	2917
QY	882	roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC	902
Db	2918	CGGCGCTGCAGCGGCAAGCTGTGTGCTCATGAAGACCATGGACAACGTGGCCACCTTCT	2977
QY	902	ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC	922

Db	2978	GCATGCTGCTTATGCTCTTTCATCTTTCATCTTCAGCATCTGGGCATGCATCTCTGGGCT	3037
Qy	922	ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL	942
Db	3038	GCAAGTTTGCTCTTGAGCGGGATGGGGACACCCCTGCCAGACCGGAAGATTTTGACTCCT	3097
Qy	942	euleuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL	962
Db	3098	TGCTCTGGGCCATCGTCACTGTCTTTCAGATCCTGACCAGAGAGACTGGAACAAAAGTCC	3157
Qy	962	eutYraenGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrrPheIleAlaLeuMetT	982
Db	3158	TCTACAATGGTATGGCCTCCACGTGCTCTGGGGGCCCTTATTTCATTGCCCTCATGA	3217
Qy	982	hrPheGlyAsnTyrrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA	1002
Db	3218	CCTTCGGCACTACGTGCTCTTCAATTGTGCTGCCATTCTGTGGAGGGCTTCAGG	3277
Qy	1002	IaGlu-----	1003
Db	3278	CGAGAGAAATCAGCAACGGGAAGATGCGAGTGACAGTTAAGCTGATTTCAGCTGCCTG	3337
Qy	1004	-----GlyAspAlaThrLysSerGluSerGluProAspPheSerProS	1019
Db	3338	TCGACTCCCAAGGGGGAGATGCCAACAAAGTCCGAATCAGAGCCCGATTCTTCTCACCCA	3397
Qy	1019	erValAspGlyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyLuhIbA	1039
Db	3398	GCCTGATGTGATGGGACAGAGAAGAGTGTGGCTTGCTGTGCTTGGGAGAGCACACC	3457
Qy	1039	IaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetS	1059
Db	3458	CGAGCTGCGGAAGAGCCTGCTGCCCTCTCATCATCCACACGCCGCCACATCATGT	3517
Qy	1059	erHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgT	1079
Db	3518	CGCTGCCCAAGACACACAGACGGGCTGGGGCAGGGCGCTGGCCCTGCCGCCGCCA	3577
Qy	1079	hrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProS	1099
Db	3578	CCAGCAGCAGCGGGTCGGCAGAGCCTGGGGCGGCC--CACGAGATGAAGTCACTGCCCA	3634
Qy	1099	erAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgS	1119
Db	3635	GCGCCCGCAGCTCTCCGACACAGCCCTGAGCGCTGCAAGCAGCTGCACCAAGCGCT	3694
Qy	1119	erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluA	1139
Db	3695	CCAGCCGGAACAGCCTCGGCCCTGCACCCAGCCTGAAGCCGAGAAAGCCCAAGTGAGAGC	3754
Qy	1139	rgArgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluG	1159
Db	3755	GGCGGTCCCTGTTGTGCGGAGAAAGCCAGAGAGCCAGATGAAGAGAGAGCTCAGAAG	3814
Qy	1159	IuAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA	1179
Db	3815	AGGAGCGGGCCAGCCCTGCGGCAAGTGAACATCGCCACAGGGGCTCCCTGAGCGGAGG	3874
Qy	1179	IaLysSerSerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaS	1199
Db	3875	CCAAGATTCTTTGACTGCGCAACACACTGCAGGTGCCAGGGCTGCATCGCACTGCCA	3934
Qy	1199	erGlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgL	1219
Db	3935	GTGCGCGAGGGTCTGCTTCTGAGCACAGGACTGCAATGGCAAGTCCGGCTTCAGGGCGCC	3994
Qy	1219	euaIaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluG	1239
Db	3995	TGGCCCGGGCCCTGCGGCTGATGACCCCCCACTGATGGGAGATGACGCCGATGACGAGG	4054
Qy	1239	IyAsnLeuSerLysGlyLuhArgIleGlnAlaTrpValArgSerArgLeuProAlaCysC	1259

Db 4055 GCAACCTGAGCAAGGGGACGGGTCCGGCGGTGATCCGAGCCCGACTCCCTGCTGCT 4114
QY 1259 ySARgLUARgAspSerTrpSerAlaTyrIlePheProProGlnSerArgpHeArgLeuL 1279
Db 4115 GCCTCGAGCGAGACTCCTGGTCAGCCFACATCTCCCTCCCTCAGTCCAGGTTCCGGCTCC 4174
QY 1279 eUCySHisArgIleIleThrHisLysMetPheAspHisValIleuValIleIlePheL 1299
Db 4175 TGTGTACCGGATCATCACCCACAAGATGTTCCAGCACGTGGTCTTGTATCATCTTCC 4234
QY 1299 euAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgI 1319
Db 4235 TTAACTGCATCACCATCGCCATGGAGCGGCCCAAATTGACCCCCACAGCGCTGAACGCA 4294
QY 1319 lePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValL 1339
Db 4295 TCTTCCTGACCCCTCCCAATTACATCTTCACCGCAGTCTTCTGGCTGAATGACAGTGA 4354
QY 1339 ySVAlValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnV 1359
Db 4355 AGGTGTGACACTGGGCTGTGCTTCGGGAGACAGCGTACCTCGGAGCAGTTGGAACG 4414
QY 1359 alLeuAspGlyLeuLeuValleuIleSerValIleAspIleLeuValSerMetValSerA 1379
Db 4415 TGCTGGACGGGCTGTGGTGTCTCATCTCCGTCATCGACATTCTGTGTCCATGTCTCTG 4474
QY 1379 spSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgp 1399
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QY 1419 erLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyI 1439
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QY 1439 leLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgA 1459
Db 4655 TCTTGGGGGTGACGCTTCAAGGGAAGTTTTCGTGTGCCAGGGCGAGATACCAAGA 4714
QY 1459 snIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrA 1479
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QY 1499 rpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetA 1519
Db 4835 GGGTGGACATCATGTACGATGGGCTGATGTGTGGCGTGACCAAGCCCATCATGA 4894
QY 1519 snHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheV 1539
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QY 1559 luGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgA 1579
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QY 1579 rg-----SerLysGluLysGlnMetAlaGluA 1588
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QY 1588 laGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuc 1608
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QY 1608 ySThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrm 1628
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QY 1928 -----MetValProHisProGluGluV 1935
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QY 1935 aLProValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrH 1955
Db 6455 TGCCA-----GGACCAGACTTACTGACTGTGGGAAGTCTGGGGTCAGCCGAACGC 6505
QY 1955 iSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuG 1975
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RESULT 5
US-10-786-148-120
; Sequence 120, Application US/10786148
; Publication No. US20050191634A1
; GENERAL INFORMATION:
; APPLICANT: LIN, SHIU-RU
; APPLICANT: WANG, JAW-YUAN
; TITLE OF INVENTION: GENES FOR DIAGNOSING COLORECTAL CANCER
; FILE REFERENCE: BHT/3230-85
; CURRENT APPLICATION NUMBER: US/10/786,148
; CURRENT FILING DATE: 2004-02-26
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 7825
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-786-148-120
Alignment Scores:
Pred. No.: 0 Length: 7825
Score: 10963.50 Matches: 2128
Percent Similarity: 89.56% Conservative: 34
Best Local Similarity: 88.15% Mismatches: 117
Query Match: 91.15% Indels: 135
Gaps: 7
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QY 23 SerAspProProGlyProArgLeuAlaArgGlyTTrpThrArgArgArgMetGluArgAla 42
Db 341 CCGGATCGCCCGGGCCCGGCTGGCCAGAGATGACGAGAGGAGATGAGCGGGCG 400
QY 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGly 62
Db 401 CCGAGGAGTGGGAGACGCCCGGAGCTTCAATCGGCTCAACGACCTTGGGGGCGGGG 460
QY 63 Ala-AlaGlyAla-glySerThrGluLysAspProGlySerAlaAspSerGluAlaGluG 82
Db 461 GCCGGCCGGGGCGGGGTCAGCAGAAAAGACCCGGGGCAGCGCGGACTCCGAGGCGAGG 520
QY 82 lYleuProTyrProAlaLeuAlaProValPhePheTyrLeuSerGlnAspSerArgP 102
Db 521 GGCTGCCGTACCCGCGCTGGCCCCCGGTGTTTCTTCTACTTGAGCCAGACAGCGGCC 580
QY 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV 122
Db 581 CGCGGAGCTGTGTCTCGCAACGCTGTGAACCCCTGTTGAGCGGATCAAGCATGTTGG 640
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[illegible]

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QY	562	rgArgLeuMetLeuProProProSerThrProThrProSerGlyGlyProProArgGlyA	582
Db	1961	GCCGGCTCATGTGTCACACCACTTCGACGCTTCCTCTCCGGGGCCCCCTGTGGCG	2020
QY	582	IaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
Db	2021	CAGAGTCTGTGCACAGCTTCTACCATGCGCACTGCCACTTAGAGCCAGTCCGCTGCAGG	2080
QY	602	IaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2081	CGCCCCCTCCAGGTCCCATCTGAGGCATCCGCGCAGACTGTGGCGACGGGAAGTGT	2140
QY	622	yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2141	ATCCCAACCGTGACACCAAGCCCTCCACCGAGACCGCTGAAGAGAGAGGCACTAGTAGAG	2200
QY	642	aAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
Db	2201	TGGCTGCCAGCTCTGGGGCCCCCAACCTCACCAGCCTCAACATCCACCCGGGCTTACA	2260
QY	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2261	GCTCCATGACACAAGCTGCTGGAGACACAGAGTACAGGTGCTGCCAAAGCTCTTGCAAGA	2320
QY	682	IeSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	2321	TCTCCAGCCCTTGCTTGAAAGACAGACAGTGGAGCTGTGTCCAGACAGCTGCCCTACT	2380
QY	702	ysAlaArgThrGlyValaGlyGluProGluSerAlaAspHisValMetProAspSerAsps	722
Db	2381	GTGCCCCGGGGCGGCGAGGGAGGTGGAGCTCGCGGACCGTGAATGCTGACTCAGACA	2440
QY	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS	742
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QY	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762
Db	2501	GC---CGGCGCAACGAGCCCTGGGCCAGATGCAAGCCCAAGCTCTGTGCTGGCTTCT	2557
QY	762	rPArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI	782
Db	2558	GGAGGCTAATCTGTGACACCTTCGAAAGATTGGACAGCAAGTACTTTGGCCGGGAA	2617
QY	782	IeMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG	802
Db	2618	TCATGATCGCCATCTGTGTCAACACACTCAGCATGGGCATCGAATACCAAGCAGCCCG	2677
QY	802	IuGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	822
Db	2678	AGGAGCTTACCAACGCCCTAGAATCAGCAACATCTTCCACCAGCCTCTTGCCCTGG	2737
QY	822	IuMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI	842
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QY	842	IepHeAspGlyValIleValValIleSerValTyrGluIleValGlyGlnGlnGlyG	862
Db	2798	TCTTCGATGTGTCAATTGTGTGCATCAGCGTGTGGAGATCGTGGCCAGCGGGGGCG	2857
QY	862	IyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP	882
Db	2858	GCCTGTGCTGCTGGGACCTTCCGCTGATGCGTGTGCTGAAGCTGTGCGCTTCCCTGC	2917
QY	882	roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC	902
Db	2918	CGGCGCTGACGGCGGCACTGTGTGTGCTCATGAAGACCATGGACAACGTGGCCACTTCT	2977

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Db 7346 CCAGCCCTGTATCTGCCCGGAGGAGGCGCTCCGTCACGACTCCAGGATCCCTTG 7405
QY 2254 aLSerSerProLeuAspSerThrAlaAlaSerProSerProIlySlyAspThrLeuSerL 2274
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 7406 CCTCTGGCCCCCTGACAGCATGGCTGCTCGCCCTCCCAAGAAAGATGTGCTGAGTC 7465
QY 2274 euSerGlyLeuSerSerAspProThrAspMetAspPro 2286
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Db 7466 TCTCCGGTTATCTCTGACCCAGCAGACCTGACCCC 7503
RESULT 6
US-10-377-139-10
: Sequence 10, Application US/10377139
: Publication No. US20040175761A1
: GENERAL INFORMATION:
: APPLICANT: Mackinnon, Roderick
: APPLICANT: Jiang, Youxing
: APPLICANT: Lee Mackinnon, Alice
: APPLICANT: Ruta, Vanessa
: TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
: FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
: CURRENT APPLICATION NUMBER: US/10/377,139
: CURRENT FILING DATE: 2003-03-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 10
: LENGTH: 7648
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-377-139-10

Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 10845.50 Matches: 2105
Percent Similarity: 89.72% Conservative: 33
Best Local Similarity: 88.33% Mismatches: 110
Query Match: 90.17% Indels: 135
DB: 19 Gaps: 7

US-09-611-257A-24 (1-2287) x US-10-377-139-10 (1-7648)
QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 2 TGGACGAGAGGAGATGAGCGGGCGCCGAGAGTCGGACAGCCCCGGAGCTTCATGC 61
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 62 GGCTCAACGACCTGTGCGGGCGCGGGCGCGCGGGCGGGGTACAGCAAGAAAGACC 121
QY 73 roGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValValP 93
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 122 CGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCGCGGCTGGCCCCGGTGTT 181
QY 93 hepHeTyrlLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 113
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 182 TCTTCTACTTGAGCCAGGACAGCCGCCCGGAGCTGTGTCTCCGCACGGTCTTAACC 241
QY 113 roTyrPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 242 CCTGGTTGAGCGCATCAGCATGTGGTCATCTTCTTCAACTGCGTGAACCTGGGCATGT 301
QY 133 hepArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhea 153
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Db 302 TCCGGCCATCGAGGACATCGCCTGTGACTCCAGCGCTGCCGATCCTGCAGGCTTTG 361
QY 153 sPAspPheIlePheAlaPhePheAlaValGluMetValIlySlyMetValAlaLeuGlyI 173
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Db 362 ATGACTTCATCTTGCTTCTTTCGCGTGAGATGATGTGTAAGATGTGTGGCTTGGGCA 421

QY 173 lePheGlyIlySlyCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValI 193
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Db 422 TCTTTGGAAAAAGTGTTAACTGTGGAGACACTTGGAACCGGCTTCACTTTTCATCGTCA 481
QY 193 leAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
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Db 482 TCGCAGGATGCTGAGTACTCGCTGGACCTGCAGAACGTCAAGTCTTCAGCTGTCAAGA 541
QY 213 hrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuV 233
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Db 542 CAGTCCGTGTGTGCAACCGCTCAGGGCCATTAAACGGGTGCCACGATGCCATCCTTG 601
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 253
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Db 602 TCACGTTGCTGTGATACGCTGCCCATGTGGGCAACGTCCTGTGCTTCTTCTTCG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 662 TCTTCTTCATCTTGGGATCGTCCGCGTCCAGCTGTGGCAGGGCTGCTTCGGAACCGAT 721
QY 273 ySPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
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Db 722 GCTTCTTACTGAGAAITTTCAAGCTTCCCTTGAAGCTGGACCTGGACGCTATTACAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
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Db 782 CAGAGAAAGAGATGAGAGCCCTTCATCTGTCTCCAGCCACGCGAGAACGGCATGCGGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProProCysSerLeuA 333
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Db 842 CCTGCAGAAAGCGTCCACGCTGCGGGAGACGGGGCGGTGGCCCACTTGGCTTGG 901
QY 333 sPTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
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Db 902 ACTATGAGGCCTACACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTACA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
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Db 962 CCAACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGCCATCACTTGACAACATTG 1021
QY 373 lYTyrlAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 393
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1022 GCTATGCTTGATCGCATCTTCCAGGTCAATCAGCTGAGAGGGCTGGGTGACATCATGT 1081
QY 393 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1082 ACTTTGTGATGATGATTCATCTTCTTCAATTTTCATCTTCACTTCTTCATCATCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1142 TGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGATTGCCACGCAGTTCACAGA 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1202 CCAAGCAGCGGGAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTCTCTCAACGCCA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1262 GCACCTGGCTAGCTTCTCTGAGCCCGGACGCTGTATGAGAGCTGTCTCAAGTACCTGG 1321
QY 473 alTyrlleLeuArgIlyAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1322 TGTACATCCTTCTGTAAGGAGCCCGCAGGCTGGCTCAGGTTCTTCCGGCAGCAGGTGTC 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlys 513
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Db 1382 GGGTTGGGCTGTCTCAGAGCCCAAGACCCCTCGGGGGCCAGAGACCAAGCCAGCAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisIleLeuValHisIleHisIleSH 533
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1442 GCTGCTCTGCTCCACCGCGGCTATCCGTCAACCACTGTGTACACCAACCAACACC 1501
QY 533 iSHIleHisIleTyrHisIleLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553

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Db 1502 ATCACCACCACCTAGCCTGGCAATGGAGCGCTCAGGGCCCCCGGGCCAGCCGGAGA 1561
QY 553 IeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProT 573
Db 1562 TCCAGGACAGGATGCCAATGGGTCCCGCAGGCTCATGTGTCACACCCCTCGACGGCTG 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CCCTCTCCGGGGCCCCCTGGTGGCGCAGAGTGTGACACAGCTTCTACCATGCCGACT 1681
QY 593 ySHisLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCACTGTAGGCAATCCG 1741
QY 613 lYArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI 633
Db 1742 GCAGGACTGTGGGCAAGCGGGAAGGTGTATCCACCGTGACACCAAGCCCTCCACCGGAGA 1801
QY 633 lLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653
Db 1802 CGCTGAAGAGAGCACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAAAGCTGTGAGACACAGATA 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGTGCCCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGAAGACAGACAGTGAG 1981
QY 693 lAcysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSera 713
Db 1982 CCTGTGGTCCAGACAGCTGCCCTACTGTGTGCCGGCGGGCCAGGGGAGGTGAGACTCG 2041
QY 713 lAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGGTGAATGCTCTGACTCAGACAGGAGGCAAGTTATGATGATTCAACAGGATGCC 2101
QY 733 lnhisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCACAGCGACCTCCGGGACCCCCACAGC--CGGGCGCAACGAGCCTGGGCCCATG 2158
QY 753 lAGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleV 773
Db 2159 CAGAGCCCAAGCTGTGTCTGGCCTTCTGAGGGCTAATCTGTGACACTTCCGAAAGATTG 2218
QY 773 aLAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerM 793
Db 2219 TGGACAGCAAGTACTTTGGCCGGGAATCATGATGCCATCCTGTCAACACACTCAGCA 2278
QY 793 etGlyIleGlyTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI 813
Db 2279 TGGGCATCGAATACCAAGAGCAGCCCGAGAGCTTACCACGCCCTAGAATCAGCAACA 2338
QY 813 lValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp 833
Db 2339 TCGTCTTACCAAGCCTCTTTGGCCCTGAGATGCTGTGAAGCTGCTGTGTATGTTCCCT 2398
QY 833 heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValT 853
Db 2399 TTGGCTACATCAAGAAATCCCTACAAACATCTTCAGTGTGTATGTGTGCATCAGCGTGT 2458
QY 853 rPGluIleValGlyGlnGlnGlyGlyLysLeuSerValLeuArgThrPheArgLeuMetA 873
Db 2459 GGGAGATCGTGGGCGAGCAGGGGGCGGCTGTGCGTGTGCGGACCTTCCGCTGATGC 2518
QY 873 rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetL 893
Db 2519 GTGTGCTGAAGCTGTGTGCGCTTCTGCGGCGCTGCAGCGGCACTGTGTGCTCATGA 2578
QY 893 ySThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS 913
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Db 2579 AGACCATGGACAACGCTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTTCA 2638
QY 913 erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL 933
Db 2639 GCATCTTGGGCATGCATCTCTTCGGCTGCAGATTGTGCTTGAGCGGAGATGGGAGACACC 2698
QY 933 euProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleL 953
Db 2699 TGCCAGACCGGAAGAAATTTTGACTCTTGCTCTGGGCCATCGTCACTGTCTTCAGATCC 2758
QY 953 euThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpA 973
Db 2759 TGACCCAGAGGACTGGAACAAAGTCTCTACAAATGGTATGGCTCCACGTGCTCTGGG 2818
QY 973 lAAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuV 993
Db 2819 CGGCCCTTATTTCATTGCCCCCTCATGACCTTCGGCACTACGTCCTTCAATTGTGCTGG 2878
QY 993 aLAlaIleLeuValGlyGlyPheGlnAlaGlu-----GlyAspAlaThrLysSerG 1003
Db 2879 TCGCAATCTGTGTGAGGGCTTCCAGCGGAGAAATCAGCAACCGGAAGATGCGAGTGTG 2938
QY 1004 -----GlyAspAlaThrLysSerG 1010
Db 2939 GACAGTTAAGCTGTATTTCAGCTGCCTGTGACTCCCAAGGGGGAGATGCCAACAAAGTCCG 2998
QY 1010 luserGluProAspPhePheSerProSerValAspGlyAspGlyAspArgLysLysArgL 1030
Db 2999 AATCAGAGCCCGATTCTTCTTACCCAGCCTGGATGTGATGGGACAGGAAGAGTGTCT 3058
QY 1030 euAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuI 1050
Db 3059 TGGCCTTGTGTCTCTGGAGAGCAACCGGAGCTGCGGAAGAGCCTGCTGCCCTCTCA 3118
QY 1050 lElIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG 1070
Db 3119 TCATCCACAGCGCGCCACACCATGTGCTGCTGCCAAGACACAGCACGGGCTGGGCG 3178
QY 1070 lValaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaA 1090
Db 3179 AGCGCTGGGCCCTGCGTCCGGCGGACCAAGAGAGCGGGTCCGACAGAGCTTGGGGCGG 3238
QY 1090 lAhisHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSera 1110
Db 3239 CC--CACGAGATGAAGTCAACGCCCAAGCGCCGCGAGCTCTCCGACAGCCCTGGAAGCG 3295
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Db 3296 CTGCAAGCAGCTGGACCAAGAGCGGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCC 3355
QY 1130 euLysArgArgSerProSerGlyLysArgSerLeuLeuSerGlyGlyGlnGluS 1150
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QY 1150 erGlnAspGluGluGluSerSerGluGluAspArgAlaSerProAlaGlySerAspHisA 1170
Db 3416 GCCAGATGAAGAGAGAGAGCTCAAGAGAGAGCGGGCCAGCCCTCGGGCAGTGAACCATC 3475
QY 1170 rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuG 1190
Db 3476 GCCACAGGGGGTCCCTGAGCGGGAGGCCAAGAGTTCTTTGACCTGCCAGACCACTGC 3535
QY 1190 lInValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC 1210
Db 3536 AGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTGAAGCACAGAGACT 3595
QY 1210 ySAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL 1230
Db 3596 GCAATGGCAAGTGGCTTCAAGGGCGCTGCGCCGGGCCCTGCGGCTGATGATGACCCCCAC 3655
QY 1230 euAspGlyAspAspAspAsnAspGluGlyAsnLeuSerLysGlyLysArgIleGlnAlaT 1250
Db 3656 TGGATGGGATGACGCCGATGACGAGGGCAACCTGAGCAAAAGGGGAACGGGTCCGGCGGT 3715
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QY 1250 rpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTrpSerAlaTyrIleP 1270
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Db 3716 GGATCCGAGCCCGACTCCCTGCTGCTGCTCGAGCAGACTCCCTGGTCAGCCTACATCT 3775
QY 1270 heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheA 1290
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Db 3776 TCCCTCCTCAGTCCAGGTTCCGCTCCTGTGTACCCGATCATCACCCACAAGATGTTCCG 3835
QY 1290 sPHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL 1310
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Db 3836 ACCACGTGCTCTGTTCATCATCTTCTTAAGTCATCACCATCCGCCATGGAGCGCCCA 3895
QY 1310 ysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrA 1330
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Db 3896 AAATGACCCCCACAGCGCTGAAGCATCTTCTGACCCTCTCCAAATTACATCTTCACCG 3955
QY 1330 laValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluG 1350
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Db 3956 CAGTCTTCTGCTGAATGACAGTGAAGTGGTGGCACTGGGCTGTCTTCGGGAGC 4015
QY 1350 lnaIaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleSerValI 1370
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Db 4016 AGCGCTACCTGCGAGCAGCTTGGAACTGCTGACGGGCTGTGTGCTCATCTCCGTC 4075
QY 1370 leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV 1390
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Db 4076 TCGACATTCTGGTGTCCATGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGG 4135
QY 1390 alleuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL 1410
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Db 4136 TGCTGCGGCTGCTGCGGACCTGCGCCGCTCAGGGTGATCAGCCGGGCGCAGGGGCTGA 4195
QY 1410 ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleC 1430
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Db 4196 AGCTGGTGTGAGAGCGCTGATGTCTCACTGAACCCATCGGCAACATTTGATCATCT 4255
QY 1430 yeCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP 1450
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Db 4256 GCTGTGCTTCTTTCATCATTTCCGCATCTTGGGGTGCAGCTCTTCAAGGGAAGTTT 4315
QY 1450 heValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS 1470
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Db 4316 TCGTGTGCCAGGGCGGAGGATACAGGAACATCACCAATAATCGGACTGTGCCAGGCCA 4375
QY 1470 erTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerL 1490
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Db 4376 GTTACCGGTGGTCCGGCACAAAGTAACTTTGACAACTTGCCAGGCCCTGATGTCCC 4435
QY 1490 eupheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaV 1510
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Db 4436 TGTTCGTTTTGGCTCCAAAGGATGTTGGGTGACATCATGTACGATGGCTGGATGCTG 4495
QY 1510 aIcGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleS 1530
|||||
Db 4496 TGGGGGTGGACCAAGCCCATCATGAACCAACCCCTGGATGCTGTACTTCATCT 4555
QY 1530 erPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluA 1550
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Db 4556 CGTTCCTCTCATTTGTGGCTTTCTTGTCTCTGAACATGTTTGTGGTGTGTGGTGAAGA 4615
QY 1550 snPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysA 1570
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Db 4616 ACTTCCACAAGTGTCCGGCAGCACCAAGAGGAAGAGGCCCGGGCGGAGAGGAAGC 4675
QY 1570 xgLeuArgArgLeuGluLysLysArgArg----- 1579
Db 4676 GCCTAGGAAGACTGAGAAAAAGAGAAGAAATCTAATGCTGAGCATGTAATTGCTTCCG 4735
QY 1580 --SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSera 1599
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Db 4736 GCAGCTCAGCCAGCGCTGCTCAGAAAGCCCAAGTGCAAACCTTACTACTCCGACTACTCCC 4795

QY 1599 rgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrG 1619
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Db 4796 GCTTCCGGCTCCTCGTCCACCACCTTGACACCAAGCCACTACTGGAACCTTTCATCAG 4855
QY 1619 lyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleL 1639
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Db 4856 GTGTCAATCGGGCTGAAGCTGTGTACCATGGCCATGGAGCATTACAGACAGCCCAAGATT 4915
QY 1639 euAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerV 1659
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Db 4916 TCGATGAGGCTTGAAAGATCTGCAACTACATCTTCACTGTCTTTGCTTGGAGTCAAG 4975
QY 1659 alPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuA 1679
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Db 4976 TTTTCAAACTTGCGCTTTGTTTCCGTCCGTTCTTCAGAGCAGGTGAACCAAGCTTGG 5035
QY 1679 sPLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGluIleGlyValAlaSnL 1699
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Db 5036 ACCTGGCCATTGTGCTGTCTTCATCATGGGCATCACGCTGGAGGAATCGAGTCAACG 5095
QY 1699 euSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgV 1719
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Db 5096 CCTCGCTGCCATCAACCCCAACCATCATCCGATCATGAGGGTGTGCGCATTGCCCGAG 5155
QY 1719 alleuLysLeuLeuLysMetAlaValAlaGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739
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Db 5156 TGCTGAAGCTGTGAAGATGGCTGTGGGCATCGGGCGCTGTGGAACAACGGTGTGACGG 5215
QY 1739 laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaA 1759
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Db 5216 CCCTGCCCCAGGTGGGAAACCTGGGACTTCTTTCATGTTGTTTTCATCTTTGGCAG 5275
QY 1759 laLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGlnGlyL 1779
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Db 5276 CTCTGGGCGTGAAGCTCTTGGAGACCTGGAAGTGTGACGAGACACACCCCTGTAGGGCC 5335
QY 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValS 1799
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Db 5336 TGGGCGCTCATGCACTTTCGGAACCTTGGCATGGCTTCCTAACCTCTCCGAGTCT 5395
QY 1799 erThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluS 1819
|||||
Db 5396 CCACAGGTGACAAATTGGAATGGCATTTATGAAGACACCCCTCCGGACTGTGACAGAGT 5455
QY 1819 erThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
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Db 5456 CCACTGTCTACAACGGTCACTCTGCTTAATCTACTTGTGTCTTCTGCTGACGGGCC 5515
QY 1839 lnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnL 1859
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Db 5516 AGTTCGTCTAGTCAAGCTGTGATCGCGTGTGATGAAGCACTGGAGAGACAACA 5575
QY 1859 ysgLualalysGlnGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuS 1879
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Db 5576 AGGAGGCCAAGAGAGGCCGAGCTAGAGCTGAGCTGAGCTGAGATGAAGACCTCA 5635
QY 1879 erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValA 1899
|||||
Db 5636 GCCCCCAGCCCACTTCCCACTGGGACAGCCCTTCTCTGTGGCTGGGCTCGAGGGCCCCG 5695
QY 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaS 1919
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Db 5696 ACAGCCCCGACAGCCCCCAAGCTGGGGCTTGTGCACCAGCGGCCCAAGCATCAGCCT 5755
QY 1919 erGlyPheSerLeuGlnHisProThr----- 1927
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Db 5756 CCCACTTTTCCCTGGAGCACCCCACGAGACAGGAGCTGTTTGACACCATATCCCTGCTGA 5815
QY 1927 ----- 1927
Db 5816 TCCAGGGCTCCCTGAGTGGAGTGAAGCTGATGAGCAGAGCTGGCAGGCCAGGGGGCC 5875
QY 1927 ----- 1927

Db 5876 AGCCCTCTGCTTCCCTTCTGCCCCAGCCTGGAGGCTCCGACCACAGATCCCTCTAG 5935
QY 1927 -----
Db 5936 CTGAGATGAGGCTGTGTCTGTGACGTGAGAGATTGTGTGAACCGTCTGTCTTAG 5995
QY 1927 -----
Db 5996 CTCTGACGATGACTTTGCTGTATGATGACATGACACACTCTTACTTAGTGCCCTGGAGA 6055
QY 1928 -----MetValProHisProGluGluValProValProLeuGlyProAspLeuLeuThrV 1946
Db 6056 GCATATATGACGCCCCACCCACGAGCTGCCA-----GGACCAGACTTACTGACTG 6106
QY 1946 aAlArgLySerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA 1966
Db 6107 TCGGGAAGTCTGGGGGTACGCCGAGCGACTCTGTGCCCAATGACAGCTACATGTGTCCGC 6166
QY 1966 snGlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnS 1986
Db 6167 ATGGGAGCACTGCGAGGGGCCCTGGGACACAGGGGCTGGGGGCTCCCAAAAGCTCAGT 6226
QY 1986 ergLySerIleuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuP 2006
Db 6227 CAGGCTCCGTCGTGTCCGTTCACTCCACGACAGACATACAGACTACATCCTGACGCTTC 6286
QY 2006 roLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProL 2026
Db 6287 CCAAAGATGACACTCATCTGCTCCAGCCCCACAGCGCCCCCAACCTGGGGCACCATCCCCA 6346
QY 2026 ysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaI 2046
Db 6347 AACTGCCCCACGAGGAGCGCTCCCTTGCGCTCAGAGGCCACTCAGGCGCCAGGACGACAA 6406
QY 2046 leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluV 2066
Db 6407 TAAGGACTGACTCTTGACGTTCAAGGCTCTGGGCAAGCCGGGAAGACCTGTGCGCAGAG 6466
QY 2066 alSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIleG 2086
Db 6467 TGAGTGGGCCCTCCCGCCCTGTGGCCCGGCTACTCTTTCTGGGGCCAGTCAAGTACCC 6526
QY 2086 lnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaP 2106
Db 6527 AGGCACAGCAGCACTCCCGCAGCCACAGAAATCTCCAAGCACATGACCCCGCCAGCCC 6586
QY 2106 roCysProGlyLeuGlnProSerTrpAlaLysAspProProGluThrArgSerSerLeuG 2126
Db 6587 CTTGCCCAGGCCAGAACCCCACTGGGGCAAGGGCCCTCCAGAGACCAGAAGCAGCTTAG 6646
QY 2126 luleuAspThrGluLeuSerTrpIleSerGlyAspLeuLeu---ProSerSerGlnGlu 2145
Db 6647 AGTTGGACACGGAGCTGAGCTGATTTCAGGAAGACCTCTGCCCTGGCGGCGCAGAGAG 6706
QY 2145 luProLeuPheProArGAspLeuLysLysCysTyrSerValGluThrGlnSerCysArgA 2165
Db 6707 AGCCCCCATCCCCACGGGACCTGAAGAACTGTACAGCGTGGAGGCCCCAGAGCTGCCAGC 6766
QY 2165 rgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuA 2185
Db 6767 GCCGGCCTACGTCCTGGCTGATGAGCAGAGAGACACTCTATGCGCGTCAAGCTGCTGG 6826
QY 2185 spSerGlySerGlnProArgLeuCysProSerProSerSerLeuGlyGlnProLeuG 2205
Db 6827 ACAGCGGCTCCCAACCCCACTGGGACAGACCCCTTAACCTTGGGGGCCAGCCTCTTG 6886
QY 2205 lyGlyProGlySerArgProLysLysLeuSerProProSerIleSerIleAspProp 2225
Db 6887 GGGGGCCTGGAGCGGGCCCAAGAAAAAATCAGCCCGCTAGTATCACCATAGACCCCC 6946
QY 2225 roGluSerGlnGlySerArgProProCysSerProGlyValCysLeuArgArgArgAlaP 2245

Db 6947 CCGAGAGCCAAAGTCTCTGGAGCCCCCGCCAGCCCTGTATCTGCTCCGGAGGAGGGCTC 7006
QY 2245 roAlaSerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSerP 2265
Db 7007 CGTCAGCGACTCCAAAGGATCCCTTGGCCTGTGCCCCCTGTACAGACATGAGCTGCCCTGC 7066
QY 2265 roSerProLysLysAspThrLeuSerLeuSerGlyLeuSerSerAspProThrAspMeta 2285
Db 7067 CCTCCCAAGAAAGATGTGTGAGTCTCTCCGGTTATCCTCTGACCACGACAGACCTGG 7126
QY 2285 spPro 2286
Db 7127 ACCCC 7131
RESULT 7
US-10-757-262-15
; Sequence 15, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2518, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MP103-007P1RNMNMIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(7134)
US-10-757-262-15
Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 10845.50 Matches: 2105
Percent Similarity: 89.72% Conservative: 33
Best Local Similarity: 88.33% Mismatches: 110
Query Match: 90.17% Indels: 135
DB: 19 Gaps: 7

US-09-611-257a-24 (1-2287) x US-10-757-262-15 (1-7648)

QY 34 TrpThrArgArgMetGluArgAlaProArgSerArgAspSerProValAlaSerArg 53
Db 2 TGGACGAGGAGGAGATGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGAGCTTCATGC 61
QY 54 SerSerThrThrCysProGlyProGlyAla-AlaGlyAla-GlySerThrGluLysAsp 73
Db 62 GGCTCAACGACCTGTCCGGGGGCCGGGGGCCGGGGGGGGGGGTCTAGCAGAAAGGACC 121
QY 73 roGlySerAlaAspSerGluAglGlyLeuProTyrProAlaLeuAlaProValValP 93
Db 122 CGGGCAGCGCGGACTCCGAGCGGGAGGGGCTGCGTACC GGCGCTGGCCCCGGTGTGTT 181
QY 93 hepHeTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnP 113
Db 182 TCTTCTACTTGAGCCAGGACAGCCGCCCGGAGCTGTGTCTCCGACGGTCTGTAAAC 241
QY 113 roTrpPheGluArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetP 133
Db 242 CCTGGTTTGAGCGCATCAGCATGTTGGTCATCCTCTCAACTGCGTGACCTGGGCATGT 301
QY 133 hepArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhea 153
Db 302 TCCGGCCATGCGAGGACATGCGCTGTGACTCCACGCGCTCCGGATCCTGCAGGCCCTTG 361
QY 153 sPaSPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyI 173
Db 362 ATGACTTCATCTTGCCTTCTTTGCGGTGAGATGTGTGAAGATGTGTGCGCTTGCGCA 421
QY 173 IepheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValI 193
Db 422 TCTTTGGGAAAAAGTTACTCGGAGACACTTGGAACCGGCTTGACTTTTCATCGTCA 481
QY 193 IeAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgT 213
Db 482 TCGCAGGAGATGCTGAGTACTCGCTGGAACCTGCAGAACGTCAAGTCTCAAGTGTCAAGA 541
QY 213 hrValArgValLeuArgProLeuAlaIleAsnArgValProSerMetArgIleLeuV 233
Db 542 CAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCCATCCTTG 601
QY 233 alThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheV 253
Db 602 TCACGTTGCTGCTGATACGCTGCCATGCTGGGCAACGTCTGCTGCTTCTTCTCG 661
QY 253 alPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgC 273
Db 662 TCTTCTTCATCTTGGCATCGTGGCGCTCCAGCTGTGGGCAAGGCTGCTCGAAACCGAT 721
QY 273 ySPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluProTyrTyrGlnT 293
Db 722 GCTTCTAAGCTGAGAAATTACAGCTCCCTGAGCGTGGAACCTGAGCGCTATTACAGA 781
QY 293 hrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgS 313
Db 782 CAGAGAACGAGGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGGCATGCCGT 841
QY 313 erCysArgSerValProThrLeuArgGlyGlyGlyGlyGlyProProCysSerLeuA 333
Db 842 CCTGCAGAAAGCGTGCCACGCTGCGGGGAGCGGGGGGGGTGCCACCTTGCGGCTTG 901
QY 333 sPTyrGluThrTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrT 353
Db 902 ACTATGAGGCTTACAACAGCTCCAAGCAACACACCTGTGTCAACTGGAACCACTTACA 961
QY 353 hrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleG 373
Db 962 CCAACTGCTCAGCGGGGAGACAAACCTTCAAGGGCGCATCAACTTGAACAACATTG 1021
QY 373 lYTrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMetT 393

Db 1022 GCTATGCTGATCGCCATCTTCCAGGTCAACGCTGAGGGCTGGGTGCACATCATGT 1081
QY 393 yrpPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleV 413
Db 1082 ACTTGTGATGATGCTCATTCCTTCTTACAAATTTCATCTTCACTCTCATCATTCG 1141
QY 413 alGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluT 433
Db 1142 TGGGCTCCTTTCATGATCAACCTGTGCTGTGTGTGATGTCCACGAGTTCTCAGAGA 1201
QY 433 hrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaS 453
Db 1202 CCAAGCAGCGGGAAGCCAGCTGATGCGGAGACAGCGTGTGCGGTTCCTGTCCAACGCCA 1261
QY 453 erThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuV 473
Db 1262 GCACCTGAGTACTTCTCTGAGCCCGGACGCTGCTATGAGGAGCTGCTCAAGTACCTGG 1321
QY 473 alTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValA 493
Db 1322 TGTAACATCCTTCGTAAGGACAGCCCGGAGGTGGCTCAGGTCTCGGGCAGCAGGTGTG 1381
QY 493 rgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGluProGlnProSerGlyS 513
Db 1382 GGGTTGGGCTGCTACAGACCCAGCACCCCTCGGGGGCCAGGAGACCCAGCCACAGCA 1441
QY 513 erCysThrArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHisH 533
Db 1442 GTGCTCTCGCTCCACCGCGCTATCGCTTCCACCACTGTGTGACCAACCAACCAACC 1501
QY 533 IShISHisISTyrHisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluI 553
Db 1502 ATCACCAACCACTACCACTGGCAATGGACCTCAGGCCCCCGGGCCAGCCCGGAGA 1561
QY 553 IeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrProt 573
Db 1562 TCCAGGACAGGATGCCAATGGTCCCGGAGCTCATGTGCGCACCACTCGAGCGCTG 1621
QY 573 hrProSerGlyGlyProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspC 593
Db 1622 CCTCTCCGGGGCCCCCTGCTGTGGCGCAGAGTCTGTGACAAGCTTCTACCATGCCGACT 1681
QY 593 ySHISLeuGluProValArgCysGlnAlaProProProArgCysProSerGluAlaSerG 613
Db 1682 GCCACTTAGAGCAGTCCGCTGCGCCAGCGCCCCCTCCAGGTCCCATCTGAGGCATCCG 1741
QY 613 lYArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGluI 633
Db 1742 GCAGGACTGTGGGAGCGGGAAGGTGTATCCACCGTGACACACCAAGCCCTCACCGAGA 1801
QY 633 IeLeuLysAspLysAlaLeuValGluValAlaProSerProGlyProProThrLeuThrs 653
Db 1802 CGCTGAAGAGAGAAGGACTAGTAGAGTGGCCAGCTGTGGGCCCAACCTCACCA 1861
QY 653 erPheAsnIleProProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerT 673
Db 1862 GCCTCAACATCCACCGGGGCTTACAGCTCATGCACAAAGCTGCTGGAGACACAGAGTA 1921
QY 673 hrGlyAlaCysHisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyA 693
Db 1922 CAGGTGCTGCCAAAGCTCTTGCAAGATCTTCAGCCCTTGCTTGAAGACAGACAGTGAAG 1981
QY 693 IACysGlyProAspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerA 713
Db 1982 CCTGTGCTCAGACAGCTGCCCTTACTGTGCCCCGGGCGGAGGAGGTGAGCTCG 2041
QY 713 IAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaG 733
Db 2042 CCGACCGTGAATGCTGACTCAGACAGCGAGGCAATTATGAGTTCAACACAGATGCC 2101
QY 733 lnhISerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspA 753
Db 2102 AGCAGCGACCTCCGGGACCCCAACAGC---CGGGGCAACGAGCTGGGCCAGATG 2158

QY	753	laGluproSerSerValleuAlaPheTyrArgleuIleCysAspThrPheArgLysIleV	773
Db	2159	CAGAGCCAGACTCTGTGCTGGCCCTTCTGGAGGCTAACTGTGACACACCTCCGAAAGATTG	2218
QY	773	aLAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleuValAsnThrLeuSerM	793
Db	2219	TGGACAGCAAGTACTTTGGCCGGGAATCATGATCGCATCTGTCAACACACTCAGCA	2278
QY	793	etGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	813
Db	2279	TGGGCATCGAATACCAAGACAGACCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACA	2338
QY	813	IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProp	833
Db	2339	TCGCTCTTACCAGCCTCTTTGCCCCTGGAGATGCTGCTGAAGCTGCTGTGTATGTCTCCT	2398
QY	833	heGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValT	853
Db	2399	TTGGCTACATCAAGAAATCCCTACAAACATCTTCGATGTGTCAATTGTGTATCAGCGTGT	2458
QY	853	rpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValleuArgThrPheArgLeuMetA	873
Db	2459	GGGAGATCGTGGCCAGAGGGGGCGGCTGTGGGTGCTGCGACCTTCGCTCATGTC	2518
QY	873	rgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValleuMetL	893
Db	2519	GTGTGCTGAAGCTGTGTGCGCTTCTGCGCGCGCTGCAGCGGCAGCTGTGTGTCTATGA	2578
QY	893	ysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheS	913
Db	2579	AGACCATGACCAACGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTCACTTCA	2638
QY	913	erIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrL	933
Db	2639	GCATCCTGGGCATGCATCTCTTGGCTGCAAATTGCTCTGAGCGGATGGGACACCC	2698
QY	933	euProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleL	953
Db	2699	TGCCAGACCGGAAGAAATTTGACTCCTGTGCTCTGGGCCATCGTCACGTCTTTACAGATCC	2758
QY	953	euThrGlnGluAspTyrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrP	973
Db	2759	TGACCCAGAGGAGCTGGAACAAGTCCCTTACAATGTATGGCCTCCACGTCGTCTGGG	2818
QY	973	IaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuV	993
Db	2819	CGGCCCTTATTATTCAATGCCCTCATGACCTTCGGCACTACGTGCTCTCAATTGCTGG	2878
QY	993	aLAlaIleLeuValGluGlyPheGlnAlaGlu-----	1003
Db	2879	TCGCCATTCTGTGGAGGCTTCCAGGCGAGAAATCAGCAACGGGAAGATGCGAGTG	2938
QY	1004	-----GlyAspAlaThrLysSerG	1010
Db	2939	GACAGTTAAGCTGATTTCAGCTGCTGCGACTCCAGGGGGGAGATGCCAACAGATCCG	2998
QY	1010	IuSerGluProAspPhePheSerProSerValAspGlyAspGlyAspArgLysArgL	1030
Db	2999	AATCAGAGCCCGATTCTTCTCACCCAGCCTGGATGTGATGGGGACAGGAAGAAGTCT	3058
QY	1030	euAlaLeuValAlaLeuGlyGluHisAlaGluLeuValGlySerLeuLeuProPoleuI	1050
Db	3059	TGGCCTTGTGTCTCCCTGGAGAGCACCCGAGCTGCGGAAGAGCCTGCTGCGCTTCA	3118
QY	1050	IeIleHisThrAlaAlaThrProMetSerHisProLysSerSerSerThrGlyValGlyG	1070
Db	3119	TCATCCACACGCGCCGCAACCCATGTGCTGCCCAAGACACACGACGCGCTGGGCG	3178
QY	1070	IuAlaLeuGlySerGlySerArgArgThrSerSerSerSerGlySerAlaGluProGlyAlaA	1090
Db	3179	AGCGCGTGGGCGCTGCGTGGCGCCGACACGACGACGCGGCTCGGACAGCCTTGGGCGG	3238

QY	1090	laHsihGIuMeLysCysProProSerAlaArgSerProHisSerProTyrSera	1110
Db	3239	CC--CACGAGATGAAGTCAACCGCCACAGCCTCTCCGACAGCCCTTGAGCG	3295
QY	1110	laAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerL	1130
Db	3296	CTGCAAGCAGCTGCACACGAGCGCTCCAGCCGGAACAGCCTCGGCCGTGCACCCAGCC	3355
QY	1130	eulysArgArgSerProSerGlyLuarArgSerLeuLeuSerGlyGluGlyGlnLus	1150
Db	3356	TGAAGCGAGAGACCCCAAGTGAGAGCGCGGTCCTGTGTGCGAGAAAGCCAGAGAGA	3415
QY	1150	ergLnaSPgluGluSerSerSerGluLnaSPArgAlaSerProAlaGlySerAspHisA	1170
Db	3416	GCCAGGATGAAGAGAGAGACTCAGAGAGAGACGGGCCAGCCCTGCGGGCAGTGACCATC	3475
QY	1170	rgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeug	1190
Db	3476	GCCACAGGGGGTCCCTTGAGCGGAGGCCAAGAGTTCCTTGACCTGCCAGACACACTGC	3535
QY	1190	lnValProGlyLeuHisArgThrAlaSerGlyArgSerSerAlaSerGluHisGlnAspC	1210
Db	3536	AGGTGCCAGGGCTGCATCGCACTGCAGTGGCCAGGGTCTGCTTGAGCACCAAGACT	3595
QY	1210	ysAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAspAspProGlnL	1230
Db	3596	GCAATGCAAGTCGGCTTCAGGGCGCTGGCCCGGCCCTGCGGCTGTAGTACCCCCAC	3655
QY	1230	euaSPglYaspaSPaspaSPasnAspGluGlyAanLeuSerLysGlyLuarGlyLeGlnAlaT	1250
Db	3656	TGGATGGGGATGACGCCGATGACGAGGGCACTGAGCAAGGGGAACGGGTCCGGCGT	3715
QY	1250	rpValArgSerArgLeuProAlaCysCysArgGluArgAspSerTyrSeraL TyrLeP	1270
Db	3716	GGATCCGAGCCCCGACTCCCTGCTGCTGCCTCGAGCGAGACTCCTGGTCAGCCTACATCT	3775
QY	1270	heProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhea	1290
Db	3776	TCCCTCCTCAGTCCAGGTTCCGCCCTCTGTGTCACCGATCATCACCCACAAGATGTTGG	3835
QY	1290	spHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProL	1310
Db	3836	ACCACGTGTCCTTGCATCATCTTCTTAATGCATCACCATCGCCATGAGCGCCCA	3895
QY	1310	ysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThra	1330
Db	3896	AAATTGACCCCCACAGCGGTGAACGCATCTTCTGACCCTCTCCAATTACATCTTCACCG	3955
QY	1330	laValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluG	1350
Db	3956	CAGTCTTCTGGCTGAATGACAGTGAAGTGTGTGGCACTGGGCTGTGCTTCGGGGAGC	4015
QY	1350	lnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValI	1370
Db	4016	AGGCGTACCTGCGGACAGTTGGAACGTGCTGACCGGCTGTGTGCTCATCTCCGTCA	4075
QY	1370	leAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgV	1390
Db	4076	TCGACATTCTGTGTTCATGTGTTCTTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGG	4135
QY	1390	alleuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuL	1410
Db	4136	TGCTGCGGCTGTCGGGACCTGCGCCCGCTCAGGGTGATCAGCCGGCGCAGGGGGCTGA	4195
QY	1410	ysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleC	1430
Db	4196	AGCTGTGTGTGAGACGCTGATGTCTCTACTGAACCATCGGCAACATTGTATCATCT	4255
QY	1430	ysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPheP	1450
Db	4256	GCTGTGCTTCTTCATCATTTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGGAAGTTT	4315
QY	1450	heValCysGlnGlyLusProThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaS	1470

Db 4316 TCGTGTGCAGGCGGAGGATACAGGAACATCAATAATCGAGCTGCGGAGCCA 4375
QY 1470 eTyrArgTrpValArgHisLysTyrAsnPhaAspAsnLeuGlyGlnAlaLeuMetSerL 1490
Db 4376 GTTACCGGTGGTCCGGCACAAGTACAACATTGTGACAACTTGGCCAGGCCCTGATGTCCC 4435
QY 1490 euPheValLeuAlaSerLysAspGlyTrpValAspLleMetTyrAspGlyLeuAspAlaV 1510
Db 4436 TGTTCGTTTGGCCTCCAAGATGGTTGGGTGACATCATGTACGATGGGCTGGATGCTG 4495
QY 1510 aIGlyValAspGlnGlnProLleMetAsnHisAsnProTrpMetLeuLeuTyrPheLleS 1530
Db 4496 TGGGCGGTGACCAAGCAAGCCCATCATGAACCAACACCCTGGATGCTGCTTAATTCTCT 4555
QY 1530 exPheLeuLeuLleValAlaPhePheValLeuAsnMetPheValGlyValValGlnVal 1550
Db 4556 CGTTCCTGCTCATTTGTGGCCTTCTTTGCTGAACATGTTGTGGGTGTGGTGGAGA 4615
QY 1550 snPheHisLysCysArgGlnHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1570
Db 4616 ACTTCCACAAGTGTCCGACAGCAACAGAGAAGAGAGGCCCGCGCGGAGAGAAGC 4675
QY 1570 rglLeuArgArgLeuGlnLysLysArgArg----- 1579
Db 4676 GCCTACGAAGACTGGAGAAAAAGAGAAGGAATCTAATGCTGGACGATGTAATGCTTCCG 4735
QY 1580 --SerLysGlnLysGlnMetAlaGlnAlaGlnCysLysProTyrTyrSerAspTyrSerA 1599
Db 4736 GCAGCTCAGCCAGCGCGTGCCTGACGAAGCCCAAGTGCAAACCTTACTACTCCGACTCTCC 4795
QY 1599 rgpPheArgLeuLeuValHisHisLysLeuCysThrSerHisTyrLeuAspLeuPheLleThrg 1619
Db 4796 GCTTCCGGCTCCTCGTCCACCACTTGTGCACCAGCCACTAAGCTTGCATCTTGCATCAG 4855
QY 1619 lYValIleGlyLeuAsnValValThrMetAlaMetGlnHisTyrGlnGlnProGlnLleL 1639
Db 4856 GTGTCAATCGGGCTGAACGTGTGCACCATGCGCATGAGCACTAACAGCAGCCCAAGATT 4915
QY 1639 euAspGlnAlaLeuLysLleCysAsnTyrLlePheThrValLlePheValPheGlnSerV 1659
Db 4916 TGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCATCTTGTCTTGGAGTCA 4975
QY 1659 alPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuA 1679
Db 4976 TTTTCAAACCTTGTGGCCTTTGGTTTCCGTCGTTCTTCCAGGACAGGTGGAACCAAGCT 5035
QY 1679 spLeuAlaLleValLeuLeuSerLleMetGlyLleThrLeuGlnGlnLleGlnValAsnL 1699
Db 5036 ACCGTGCATTTGTGCTGCTGCATCATGGGCATCACGCTGAGAGGAATCGAGGTCAACG 5095
QY 1699 euSerLeuProLleAsnProThrLleLleArgLleMetArgValLeuArgLleAlaArgV 1719
Db 5096 CCTCGTGCCTCATCAACCCCAACCATCATCCGCATCATGAGGGTCTGCGCATTGCCCGAG 5155
QY 1719 alLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnA 1739
Db 5156 TGTGTGAAGCTGCTGAAGATGGCTGTGGGCATGCGGCGCTGCTGGACAACGGTATGCA 5215
QY 1739 laLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheLlePheAlaA 1759
Db 5216 CCTGTCCCAAGGTGGGGAACCTGGGACTTCTCTTCATGTTGTTGTTTTCATCTTTGCA 5275
QY 1759 laLeuGlyValGlnLeuPheGlyAspLeuGlnCysAspGlnThrHisProCysGlnGlyL 1779
Db 5276 CTCTGGGCGGTGAGCTCTTGGAGACTGTGAGTGTGACGAGACACACCCCTGTGAGGGCC 5335
QY 1779 euGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValS 1799
Db 5336 TGGGCGGTATGCAACCTTTCGGAATTTGGCATGCGCTTCTTAACCTCTTCGAGTCT 5395
QY 1799 erThrGlyAspAsnTrpAsnGlyLleMetLysAspProSerArgAspCysAspGlnGlnS 1819

Db 5396 CCACAGGTGACAAATTGAATGGCATTTAAGAAGACACCCCTCCGGGACTGTGACAGAGT 5455
QY 1819 erThrCysTyrAsnThrValLleSerProLleTyrPheValSerPheValLeuThrAlaG 1839
Db 5456 CCACCTGTACAACACGGTCACTCCGCTATCTACTTGTGTCTTGTGCTGACGGGCC 5515
QY 1839 lnPheValLeuValAsnValValLleAlaValLeuMetLysHisLeuGlnLysSerAsnL 1859
Db 5516 AGTTGCTAGTCAACGTGTGATCGCCGTCTGTATGAAGCACTTGAGAGAGACCAACA 5575
QY 1859 ysgLValAlaYsgGlnGlnAlaGlnLeuGlnAlaGlnLeuGlnMetLysThrLeus 1879
Db 5576 AGAGGCCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTGAGAGATGAAGACCTTCA 5635
QY 1879 erProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlnGlyValA 1899
Db 5636 GCCCCCAGCCCCACCTCGCCACTGGCAGACGCCCTTCTCTGCGCTGGGGGTGAGGGCCCCG 5695
QY 1899 snSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisLleGlyAlaAlaS 1919
Db 5696 ACAGCCCCGACAGACCCCCAAGCCTGGGGCTCTGCACACCAGCGGCCACGAGATCAGCCT 5755
QY 1919 ergLysPheSerLeuGlnHisProThr----- 1927
Db 5756 CCCACTTTTCCCTGGAGCAACCCACGAGACGACAGCTGTTTGACACCATATCCCTGCTGA 5815
QY 1927 ----- 1927
Db 5816 TCACAGGCTCCCTGAGTGGAGCTGAAGCTGATGACGAGCTGGCAGGCCCAAGGGGGCC 5875
QY 1927 ----- 1927
Db 5876 AGCCCTGCTGCTTCCCTTCTGCCCCCAGCCTGGGAGGCTCCGACCAAGATCCCTTAG 5935
QY 1927 ----- 1927
Db 5936 CTGAGATGAGGCTGTCTCTGACGTCAAGATTGTGTGAACCGTCTGCTCTAG 5995
QY 1927 ----- 1927
Db 5996 CTCTGACGGATGACTCTTTGCTGCTGATGACATGCACACACTCTTACTTAGTCCCTGAGA 6055
QY 1928 -----MetValProHisProGlnGlnValProValProLeuGlyProAspLeuLeuThrV 1946
Db 6056 GCATATATGACGCCCAACCCCAAGAGCTGCCA-----GGACCAGACTTACTGACTG 6106
QY 1946 alArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgA 1966
Db 6107 TGGCGAAGTCTGGGGTCAACGCAAGCACTCTGCCCCAATGACAGCTACATGTGTGGC 6166
QY 1966 snGlySerThrAlaGlnArgSerLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnS 1986
Db 6167 ATGGAGCACTGCGGAGGGCCCCCTGGGACACAGGGGCTGGGGCTCCCAAAAGCTCAGT 6226
QY 1986 ergLysSerLleLeuSerValHisSerGlnProAlaAspThrSerCysLleLeuGlnLeuP 2006
Db 6227 CAGGCTCCGTCTTGTTCGTTCACTCCCAAGCCACAGATACCAAGCTACATCTGCAGCTTC 6286
QY 2006 roLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaLleProL 2026
Db 6287 CCAAGATGACCTCATCTGCTCCAGCCCAAGCGGCCCAACCTGGGGCAACATCCCCA 6346
QY 2026 yseLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaI 2046
Db 6347 AACTGCCCCCACCAGAGCGCTCCCTTGGCTCAGAGGCCACTCAGGGCCAGGCAAGCAA 6406
QY 2046 leArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlnAspLeuLeuSerGlnV 2066
Db 6407 TAAGACTGACTCCTTGAAGCTTCAAGGTCTGGGACAGCCGGAAAGACTGTGCGAGAGG 6466
QY 2066 alSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyLysSerSerLleG 2086
Db 6467 TGAAGTGGGCCCTCCCGGCCCTGGGCCGCTACTTTCTGGGGCAAGTCAAGTACCC 6526

[illegible]

Db	2361	TCTCCAGCCCTTGCTTGAAGCAGACAGTGGAGCCTGTGTCCAGACAGCTGCCCTACT	2420
Qy	702	ysAlaArgThrGlyAlaGlyGluProGlnSerAlaAspHisValMetProAspSerAspS	722
Db	2421	GTGCCCCGGGGGGGGCAGGGAGGTGGAGCTTCGCCAGCCGTGAATGCTGACTCAGACA	2480
Qy	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS	742
Db	2481	GCGAGGCAGTTTATGAGTTCACACAGAGATGCCAGCACAGCAACTTCGGGAACCCCAA	2540
Qy	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762
Db	2541	AGCGGG--GGGCAACGGAGCCTGGGCCAGATGCAGAGCCAGCTCTGTGTGGCTTCT	2598
Qy	762	rpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI	782
Db	2599	GGAGGCTAATCTGTGACACCTTCGAAAGATTGTGGACAGCAAGTACTTTGGCCGGGAA	2658
Qy	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG	802
Db	2659	TCATGATCGCCATCTCTGTCAACACACTCAGCATGGGCATCGAATACCAAGAGACCCG	2718
Qy	802	luGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	822
Db	2719	AGGAGCTTACCAACGCCCTAGAAATCAGCAACATCGTCTTACACAGCCTTTTGCCCTG	2778
Qy	822	luMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI	842
Db	2779	AGATGCTGCTGAAGCTGCTGTGTATGCTCCCTTTGGCTACATCAAGAATTCCTACACA	2838
Qy	842	lePheAspGlyValIleValValIleSerValTrpGluIleValGlyGlnGlnGlyG	862
Db	2839	TCTTCGATGGTTCATTTGTGTGTCATCAGCGTGGGAGATCGTGGCCAGCAGGGGGCG	2898
Qy	862	lyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP	882
Db	2899	GCCTGTGGGTGCTGGGACCTTCGGCTGATGGCTGTGCTGAAGCTGTGCGCTTCTTGC	2958
Qy	882	roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC	902
Db	2959	CGGCGCTGCAGCGGCAAGCTGGTGTGCTCATGAAGCATGGACACAGTGCCACCTTCT	3018
Qy	902	ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC	922
Db	3019	GCATGCTGCTTATGCTCTTCATCTTCATCTTCAGCATCTGGGCATGCATCTCTTGGCT	3078
Qy	922	ysLysPheAlaSerGlnArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL	942
Db	3079	GCAAGTTTGCTCTGAGCGGGATGGGACACCCCTGCCAGACCGAAGAATTTGACTCTT	3138
Qy	942	euleuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValL	962
Db	3139	TGCTCTGGGCCATCTCACTGCTCTTTCAGATCTTCAGACCCAGAGAGACTGAAACAAGTCC	3198
Qy	962	eutTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetT	982
Db	3199	TCTACAATGTATGGCTCCACGTCGTCTGGGGGGCCCTTTATTTCATTGCCCTCATGA	3258
Qy	982	hrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA	1002
Db	3259	CCTTCGGCACTACGTGCTCTTCATTTGTGTGGCCATTCTGTGAGGGCTTCCAGG	3318
Qy	1002	laGluGlyAspAlaThrLysSerGlnSerGluProAspPhePheSerProSerValAspG	1022
Db	3319	CGGAGGAGATGCCACAACAAGTCCGAATCAGAGCCCAATTCTTCACCCAGCCTGGATG	3378
Qy	1022	lyAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyLuhHisAlaGluLeuA	1042
Db	3379	GTGATGGGGACAGGAAGAAGTCTTGGCCTTGTGTCTTGGGAGAGACCCCGAGCTGC	3438
Qy	1042	rgLysSerLeuLeuProLeuIleIleHisThrAlaAlaThrPrometSerHisProL	1062

Db 3439 GGAAGACCTGTCGCCGCTCTCATCATCCACACGCGCCGACACCCATGTGCTGCCCA 3498
QY 1062 ySerserSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSersers 1082
Db 3499 AGAGCACCAAGCAGCGGCCCTGGGCGAGCGCTGGGCCCTGCGTCGCGCCGACACGACGA 3558
QY 1082 ergLySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgS 1102
Db 3559 GCGGGTCGGCAGACGCTGGGGCGGCC--CACGAGATGAAGTCACCGCCCAAGCGCCCGCA 3615
QY 1102 erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArg 1122
Db 3616 GCTCTCCGACAGCCCTTGAGCGCTGCAGACAGCTGAGCCAGCAGGCGCTCCAGCCGGA 3675
QY 1122 snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerL 1142
Db 3676 ACAGCCTCGCGCCGTGCACCCAGCCTGAAGCGGAGAAAGCCCAAGTGAAGAGCGCGCTCC 3735
QY 1142 euLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluLysAspArg 1162
Db 3736 TGTGTGCGGAGAGGCCAGAGAGCCAGATGAAGAGAGAGCTCAGAAGAGAGCGGG 3795
QY 1162 laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerS 1182
Db 3796 CCAGCCCTGCGGGCAGTGAACCATCGCCACAGGGGGTCCCTGAGCGGGAGGCCAAGATT 3855
QY 1182 erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS 1202
Db 3856 CTTTGACCTGCGACACACACTGCAAGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAG 3915
QY 1202 erSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT 1222
Db 3916 GGTGTGCTTGTGAGCACAGGACTGCATGCGCAAGTGGCTTCAGGGCGCTGCGCCGG 3975
QY 1222 hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAspGluGlyAsnLeuS 1242
Db 3976 CCCTGCGCGCTGATGACCCCCCACTGGAATGGAGTGAACGCCGATGACGAGGCAACTGA 4035
QY 1242 erLysGlyGluArgLleGlnAlaTrpValArgSerArgLeuProAlaCysCysArgGlu 1262
Db 4036 GCAAGGGGAACGGGTCCGCGCGTGGATCGAGCCGCACTCCCTGCTGCTCGAGC 4095
QY 1262 rgAspSerTrpSerAlaTyrllePheProProGlnSerArgPheArgLeuLeuCysHis 1282
Db 4096 GAGACTCCTGGTCAAGCTACATCTCCCTCTCAGTCCAGGTTCCGCCCTCTGTGTACC 4155
QY 1282 rgLlelleThrHisLysMetPheAspHisValValLeuVallellePheLeuAsnCysI 1302
Db 4156 GGATCATCACCCACAGAATGTTGCAACCACTGGTCTTGTTCATCATCTTCTTAACGTGA 4215
QY 1302 leThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgllePheLeuT 1322
Db 4216 TCACCATCGCCATGAGCGCCCAAAATGACCCCAAGCGGTGAACGCATCTTCTCTGA 4275
QY 1322 hrLeuSerAsnTyrllePheThrAlaValPheLeuAlaGluMetThrValLysValVal 1342
Db 4276 CCCTCTCCAATTACATCTTCAACGCACTTCTGGCTGAATGACAGTGAAGTGTGG 4335
QY 1342 laLeuGlyTrpCysPheGlyGlyGlnAlaTyrlleuArgSerSerTrpAsnValLeuAspG 1362
Db 4336 CACTGGGCTGTGTCTTCGGGGAGCAGGCGTACTGCGGAGCAGTTGGAACGTGTGAGC 4395
QY 1362 lyleuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyT 1382
Db 4396 GGCTGTTGTGTCTATCTCCGTCAATCGACATTTGTGTTCATGTCTCTGACAGCGGCA 4455
QY 1382 hrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgGlnLeuArgProLeuArgV 1402
Db 4456 CCAAGATCCTGGGCAATGCTGAGGGGTGTGCGGCTGTGCGGACCTGCGCCGCTCAGGG 4515
QY 1402 alIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysP 1422
Db 4516 TGATCAGCCGCGGCGAGGGGCTGAAGCTGTGTGTGAGACGCTGATGTCTCACTGAAC 4575

QY 1422 rolleGlyAsnIleValValIleCysCysAlaPhePheIlellePheGlylleLeuGlyV 1442
Db 4576 CCATCGGCAACATTGTAGTCACTGTGCTGCTTCTTCAATCATTTTCGGCATCTTGGGG 4635
QY 1442 alGlnLeuPheLysGlyLysPhePheValCysGlnGlyLysPThrArgAsnIleThra 1462
Db 4636 TGACGCTCTCAAGGGAAGTTTTCGTGTGCGAGGCGAGGATACAGGAACATCACCA 4695
QY 1462 snLysSerAspCysAlaGluAlaSerTyrrArgTrpValArgHisLysTyrrAsnPheAsp 1482
Db 4696 ATAAATCGACTGTGCCGAGCCAGTTACCGGTGGTCCGGCACAAAGTACAACTTGACA 4755
QY 1482 snLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspI 1502
Db 4756 ACCTTGCCAGGCCCTGATGTCCCTGTTGTTGGCTCCAAAGATGTTGGTGAGACA 4815
QY 1502 leMetTyrrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsn 1522
Db 4816 TCATGTACGATGGGCTGATGCTGTGGCGGTGAGACCAAGCCATCATGAACCAACC 4875
QY 1522 roTrpMetLeuLeuTyrrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsn 1542
Db 4876 CCTGATGCTGCTGTACTTCACTCTGTTCTCTGCTCATTTGTGGCTTCTTGTCTGAACA 4935
QY 1542 etPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluG 1562
Db 4936 TGTTTGTGGGTGTGTGTGTGAAGAACTTCACAAGTGTGGCAGCACAGGAGGAAGAG 4995
QY 1562 luAlaArgArgArgGlu-GluLysArgLeuArgArgLeuGluLysLysArgArgSerLys 1581
Db 4996 AGGCCCGGCGGGAGCGAGCCAGAGCCCTACGAAGACTGGCGAAAGAGAGCGAGCTAG 5055
QY 1582 GluLysGlnMetAlaGluAlaGlnCysLysProTyrrTyrrSerAspTyrrSerArgPheArg 1601
Db 5056 GAGAAGCAGATGGCTGAAGCCAGTGCAAACTTACTCCGACTACTCCGCTTCCGG 5115
QY 1602 LeuLeuValHisHisLeuCysThrSerHisTyrrLeuAspLeuPheIleThrGlyValIle 1621
Db 5116 CTCCTGTCACCACTTGTGTGACCAAGCACTACCTGGAACCTTTCATCACAGGTGCATC 5175
QY 1622 GlyLeuAsnValValThrMetAlaMetGluHisTyrrGlnGlnProGlnIleLeuAspGlu 1641
Db 5176 GGGTGAACTGTGTACCATGCGCATGAGACACTACAGACAGCCCAAGATTCTGGATGAG 5235
QY 1642 AlaLeuLysIleCysAsnTyrllePheThrValIlePheValPheGluSerValPheLys 1661
Db 5236 GCTGTGAAGATCTGCAACTACATCTTCACTGTCACTTGTGTTGTGGAGTCACTTTCAA 5295
QY 1662 LeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAla 1681
Db 5296 CTGTGGCTTGTGTTCCGTGGTCTTCCAGAGACAGGTGAACCAAGCTGACCTGGCC 5355
QY 1682 lleValleuLeuSerIleMetGlylleThrLeuGluGluIleGluValAsnLeuSerLeu 1701
Db 5356 ATTGTGCTGTGCTCATCATGCGCATCACGCTGAGAGAAATCGAGTCAACGCTCGCTG 5415
QY 1702 ProIleAsnProThrIlelleArgIleMetArgValLeuArgIleAlaArgValleuLys 1721
Db 5416 CCCATCAACCCCAACATCATCCGATCATGAGGGGTGCTGCGCATTTGCCGAGTGTGAAG 5475
QY 1722 LeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuPro 1741
Db 5476 CTGTGAAGATGGCTGTGGGCAATGCGGGCGCTGCTGACACAGGTGATGACGCGCTGCC 5535
QY 1742 GlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGly 1761
Db 5536 CAGGTGGGGAACCTGGACTTCTTTCATGTGTGTTTTCATCTTGGAGCTCTGGGC 5595
QY 1762 ValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArg 1781
Db 5596 GTGAGCTCTTTTGAGACCTGGAAGTGTGACGAGACACACCCCTGTGAGGGGCTGGCGCT 5655


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Db      2031 GCAGCCACTGCGCTGCAGCCTCAGGCTGGCCACAGCGCTGGCACCATGAACTACCCC 2090
QY      624 ThrVal-----HisThrSerProProGluIle 633
Db      2091 ACCGATCCTGCCCTCAGGGGTGGGCAGCGGCAAAGCAGCACACCCCGGACCCCAAG--- 2147
QY      634 LeuIysAspIysAlaLeuValGluValAlaProSerPro-----Gly 647
Db      2148 -----GGGAAGTGGGGCCGGTGGACCGCCAGGACCGGGGGGGCAGCGC 2189
QY      648 ProProThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHisLysLeu 667
Db      2190 CCGTTGAGCTTGAAACAGC-----CCTGATCCCTACGAGAAGATCCCGCATGTG 2237
QY      668 LeuGluThrGlnSerThrGlyAlaCys-----HisSerSer-----Cys 680
Db      2238 GTGGGGAGCATGACTGGGCGCAGCCCTGGCCATCTGTGGGCGCTCAGTGTGCCCTGC 2297
QY      681 LysIleSerSerProCysSerIysAlaAspSerGlyAlaCysGlyProAspSerCysPro 700
Db      2298 CCGCTGCCCAAGCCCC-----CCAGCGGGCACACTGACTGTGAGCTGAAGAGCTGCCCG 2351
QY      701 TyrCysAlaArgThr--GlyAlaGlyGluProGluSerAlaAspHisValMetProAsp 719
Db      2352 TACTGCACCCCGTGCCTTGAGGACCCGGAGGGGTGAGCTCAGCGGCTCGGAAAGTGAGAC 2411
QY      720 SerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 739
Db      2412 TCAGATGGCCGTGGCGTGTATGATTCACGCAGAGAGCTCCGGCACGGGTGACCGCTGGAC 2471
QY      740 Pro-----HisSerArg 743
Db      2472 CCCACGCGACCAACCCCGTGCAGCGACACACACAGGCCCGAGCCCGCAGCGCCCGAGCGG 2531
QY      744 ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheTrpArg 763
Db      2532 CGGGCACAAGCAGAGGGCAGCCCG--GGCGAGCCAGCGCTGATGGCGCGCTCTGGGTT 2588
QY      764 LeuIleCysAspThrPheArgIysIleValAspSerIysTyrPheGlyArgGlyIleMet 783
Db      2589 ACCTTACAGCGGCAAGCTGCCCGCATCTGTGACAGCAAGTACTTACGCCGTGCATCATG 2648
QY      784 IleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGlu 803
Db      2649 ATGGCATCTTGTCAACACCGCTGAGCATGGCGGTGAGTACCATGAGCAGCCCGAGGAG 2708
QY      804 LeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMet 823
Db      2709 CTGACTAATGCTCTGAGATCAGCAACATCGTGTTCACCAACATGTTGCCCTGGAGATG 2768
QY      824 LeuLeuIysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePhe 843
Db      2769 CTGCTGAAGCTGTGCGCTGCGGCCCTCTGGGCTACATCCGGAACCCGTACAAACATCTTC 2828
QY      844 AspGlyValIleValIleSerValTrpGluIleValGlyGlnGlnGlyGlyLeu 863
Db      2829 GACGGCATCATCGTGTGTCATCAGCGTCTGGAGATCGTGGGGCAGCGGAGCGTGGCTTG 2888
QY      864 SerValLeuArgThrPheArgLeuMetArgValLeuIysLeuValArgPheLeuProAla 883
Db      2889 TCTGTGTGCGCACCTTCGGGTGTGCTGCTGTAAGCTGTGCGCTTCTGCCAGCC 2948
QY      884 LeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMet 903
Db      2949 CTGCGGCGCAGCTCGTGTGTGTGAAGACCATGACAACTGGCTACTTCTGCACG 3008
QY      904 LeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLys 923
Db      3009 CTGCTCATGCTCTTCATTTCATCTTACATCTCAGCATCTGGGCATGCACTTTCCGCTGCAAG 3068
QY      924 PheAlaSerGluArgAsp--GlyAspThrLeuProAspArgLysAsnPheAspSerLeu 942

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Db      3069 TTCAGCCTGAAGACAGACACCGGAGACCGTGCTGACAGAGAAGACTTCGACTCCCTG 3128
QY      943 LeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeu 962
Db      3129 CTGTGGCCATCGTTCACCGGTGTTCCAGATCTGACCCAGAGAGACTGGAACGTGTCTCTG 3188
QY      963 TyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThr 982
Db      3189 TACAACGGCATGCGCTCCACCTCTCTGGGCGCCCTCTACTTCTGTGGCCCTCATGACC 3248
QY      983 PheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGlyGlyPheGlnAla 1002
Db      3249 TTCGCCAATATGCTCTTCAACCTGTGTGGTGCATCTCGTGAAGGCTTCAGGCG 3308
QY      1003 GluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspGly 1022
Db      3309 GAGGGCGATGCCAACAGATCCGACAGCAGACAGACAAGACGTGGTCCACTTCAGAGAG 3368
QY      1023 AspGlyAspArgLysIysArgLeuAlaLeuValAlaLeu----- 1035
Db      3369 GACTTCCACAAGCTCAGAGAACTCCAGACCACAGAGCTGAAGATGTCCCTGGCCGTG 3428
QY      1036 -----GlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThr 1053
Db      3429 ACCCCCAACGGGCACCTGGAGGAGCAGGACCGCTGTCCCTCCCTCATCATGTGCACA 3488
QY      1054 AlaAlaThrProMetSerHisProLysSerSer--ThrGlyValGlyGluAlaLeu 1072
Db      3489 GCTGCCACGCCCATGCTTACCCCAAGAGCTCACATCTCTGATGACAGCCCGACGCTC 3548
QY      1073 GlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHis 1092
Db      3549 CCAGACTCTCGCGTGGCAGCAGCAGCTCGGGGACCCGCCACTGGGA----- 3596
QY      1093 GluMetLysCysProProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSer 1112
Db      3597 GACCAGAAGCTCCGGGCAAGCTCCGAAGTCTCCCTGTGCCCCCTGGGGCCCCAGTGCG 3656
QY      1113 SerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArg 1132
Db      3657 GCCTGAGCAGCGCGGCTCCAGCTGGAGCAGCTGGGCGCTGCCCGCCCTCAAGCGC 3716
QY      1133 ArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlnSerGlnAsp 1152
Db      3717 CGCGGCCAGTGTGGGAACGTGAGTCCCTGTGTGGCGAGGGCAAGGGCAGCACCGAC 3776
QY      1153 GluGluGluSerSerGluAspArgAlaSerProAla-----GlySerAspHisArg 1170
Db      3777 GACGAA-----GCTAGGAGACGCGAGCGCGCCGCGGCCCGTGCACCCCACTGCGG 3830
QY      1171 HisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu-- 1189
Db      3831 CGGGCCGAGTCCCTGGAACCCACGCGCCCTGGCGCGCGCGCCCTCCCGCTACCAAGTGC 3890
QY      1190 -----GlnValProGlyLeuHis-----ArgThrAlaSer 1199
Db      3891 CGCGATCGCGACGGGAGGTGTTGGCCCTGCCACGCACTTCTTCTGCGCATCGACAGC 3950
QY      1200 GlyArgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db      3951 CACCGTAGGATGACGCGAGCTTGACGACGACTCGGAGACAGACTGTGCTCGCCTG 4010
QY      1220 AlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAsnAspGluGly 1239
Db      4011 CATAAAGTGTGAGCCCTTACAAGCCCCAG----- 4040
QY      1240 AsnLeuSerLysGlyLysArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCys 1259
Db      4041 -----TGC-----TGC 4046
QY      1260 ArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeu 1279
Db      4047 CGGAGCCCGCAGGCGCTGGCCCTTACTCTCTCCACAGAACCGGTTCCGCGTCTCC 4106

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QY	1280	CysHisArgIleIleThrHisLysMetPheAspHisValLeuValIleIlePheLeu	1299
Db	4107	TGCCAAGAAGTCATGACACACACAAGATGTTGATGACAGTGCTTCATCTTC	4166
QY	1300	AsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIle	1319
Db	4167	AACTGCGTCACCATCGCCCTGGAGAGCGCTGACATGACCCCGCAGCACCGAGCGGGTC	4226
QY	1320	PheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLys	1339
Db	4227	TTCTTCAGCGCTCCAAATTACATCTTCACGCGCCATCTTCGTGGCGGAGATGATGTGAAG	4286
QY	1340	ValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTyrAsnVal	1359
Db	4287	GTGTGGCCCTGGGGCTGCTGCTCCGGCAGACCGCTTACTGACAGACGTGGAACCTG	4346
QY	1360	LeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAsp	1379
Db	4347	CTGGATGGGCTGCTGGTGTGTCCTGATGACATTTGCTGGCCATGGCTCGGCT	4406
QY	1380	SerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgPro	1399
Db	4407	GGTGGCGCCAAGATCTGGGTGTCTGCGCGTGCCTGCTGCGGACCTGCGGCT	4466
QY	1400	LeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSer	1419
Db	4467	CTAAGGTCATCAGCCGGGCCCGGGCTCAAGCTGGTGGAGACGCTGATATCTGCG	4526
QY	1420	LeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIle	1439
Db	4527	CTCAGGCCCATTTGGGAACATGCTCTCATCTGCGCCTTCTCATCATTTTGGCATC	4586
QY	1440	LeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyLysAspThrArgAsn	1459
Db	4587	TTGGGTGTGAGCTCTTCAAGGGAAGTTCTACTACTCGAGGGCCCCGACACCAAGAAAC	4646
QY	1460	IleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLysTyrAsn	1479
Db	4647	ATCTCCACCAAGGCACAGTCCGGCCGGCCGCCCACTACCGCTGGGTCCGACGCAAGTACAAC	4706
QY	1480	PheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyr	1499
Db	4707	TTTGACAACCTGGGCCAGGCCCTGATGTGCTGTCTGTCATCCAAAGATGATGG	4766
QY	1500	ValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsn	1519
Db	4767	GTAACATCATGTACGACGGGCTGATGCCGTGGGTGTCACACGACCTGTGCAGAAC	4826
QY	1520	HisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheVal	1539
Db	4827	CACAACCCCTGATGCTGCTGACTTCATCTCTCTGCTCATGTCAGCTTCTTCGTG	4886
QY	1540	LeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGlu	1559
Db	4887	CTCAACATGTTCTGGGCGTCTGTCGAGAACCTTCCACAAGTCCCGGCAACCAAGAG	4946
QY	1560	GluGluGluValaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArg	1579
Db	4947	GCGAGAGAGCGCGCGGAGAGAGAAAGCGGCTGCGGCGCTTAGAGAGAGGCGCAGG	5006
QY	1580	SerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArg	1599
Db	5007	AGCACTTTCCCCAGC--CCAGAGGCCACAGCGCGGCTTACTATGCGGACTACTCGCC	5063
QY	1600	PheArgLeuLeuValHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleThrGly	1619
Db	5064	ACGCGCGGCTCCATTCACTCGCTGTGCACCAAGCCACTATCTGACCTTTCATCACTTC	5123
QY	1620	ValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeu	1639
Db	5124	ATCATCTGTCTCAACGTCATCAACATGTCATGAGCACTATAACCAACCAAGTCGCTG	5183

QY	1640	ASpGIuAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerVal	1659
Db	5184	GACGAGCCCTCAAGTACTGCAACTACGCTTCAACCATCGTGTTCCTTCGAGGCTGCA	5243
QY	1660	PhelLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAsp	1679
Db	5244	CTGAAGCTGTGATCATTTGGGTTCCGTCGGTCTTCAAGACACAGGTGGAAACAGCTGGAC	5303
QY	1680	LeuAlaIleValIleLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeu	1699
Db	5304	CTGGCCATCGTGTCTGTCTACTCATGTGGGATCACGCTGAGAGATGAGATGAGCGCC	5363
QY	1700	SerLeuProIleAsnProThrIleIleArgIleMetArgValIleuArgIleAlaArgVal	1719
Db	5364	GCGCTGCCATCAACCCCAACCATCATCCGCATCATGGCGGTCTTCGCATTGCCCGTGTG	5423
QY	1720	LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAla	1739
Db	5424	CTGAAGCTGTGAAGATGGCTACGGGCAATGCCGCCCTGTGTGACACATGTGTGCAAGCT	5483
QY	1740	LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAla	1759
Db	5484	CTCCCCCAGGTGGGAACTGGGCTTCTTTTCATGTCTCCTGTTTATTATATGCTGCG	5543
QY	1760	LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu	1779
Db	5544	CTGGAGTGTGAGCTGTTCCGGAGGCTGGAGTGCAGTGAAGACAAACCCCTGCGAGGCTG	5603
QY	1780	GlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer	1799
Db	5604	AGCAGGCACGCCACTTCAGCAACTTCGGCATGGCTTCCTCACGCTGTCCGCGTGTCC	5663
QY	1800	ThrGlyAspAsnTyrAsnGlyIleMetLysAspProSerArgAspCys-----Asp	1816
Db	5664	ACGGGGGACAACCTGGAACGGGATCATGAAGACACGCTGCCGCAGTGCTCCCGTGAGGAC	5723
QY	1817	GlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeu	1836
Db	5724	AAGCACTGCTGAGCTACCTGCCGGCCCTGTGCCCCGCTACTTCGTGACCTTCGTGCTG	5783
QY	1837	ThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGlu	1856
Db	5784	GTGCCCCAGTTCTGTCTGTGTGAACGTGTGTGTGCGCTGCATGAAGACCTGGAGGAG	5843
QY	1857	SerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLys	1876
Db	5844	AGCAACAAGAGGACGCGGAGGATGCGGAGCTGGACGCCGAGATCGAGCTGGAAGATGGCG	5903
QY	1877	ThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTyrProGlyValGlu	1896
Db	5904	-----CAGGGCCCCGGG	5915
QY	1897	GlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGly	1916
Db	5916	AGTGCAACGCCGGGTGGACGGGACAGAGGCT-----	5945
QY	1917	AlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValPro	1936
Db	5946	-----CCCTTGCCCCAGAGAGTCCG	5966
QY	1937	ValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSer	1956
Db	5967	GGCGCCAGGATGCCCAAACTGTGTGCACGCAAGGTGTCCGTGTCCAGGATGCTCTCG	6026
QY	1957	LeuProAsnAspSerTyrMetCysArgAsnGlySerThrAla-----	1970
Db	6027	CTGCCCCAAGACAGTACATGTTCAGGCCCCGTGTGCTCCTCGCGGCCCAACCCCGCG	6086
QY	1971	-----GluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGly	1987
Db	6087	CCGCTGCAGAGGATGAGATGGAACCTATGGGCGCGGCAACCCCG-----TTGGGGC	6137
QY	1988	SerIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLys	2007

Db 6138 TCCGTTGCCTCTGTGCACTCTCCGCCGACAGATCTGTGCTCCCTCCAGATCCCACTG 6197
QY 2008 AspValHis-----TyrLeuLeuGlnProHisGlyAla 2018
Db 6198 GCTGTGTGCTCCCGACGAGCGGCGGAGCCCTCCACGCCCTGTCTCCCTCGGGGACACA 6257
QY 2019 ProThrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuAlaGlnArg 2038
Db 6258 -----GCCCGCTCCCGACGTCTCAGCCGG 6281
QY 2039 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2058
Db 6282 CTGCTCTGCACAGACAGAGGCTGTGCACACCGATTCTTGAAGGGAAG---ATTGACAGC 6338
QY 2059 ArgGluAspLeuLeuSerGluVal-----SerGlyProSerCysProLeuThr 2074
Db 6339 CCTAGGGACACCCCTGGATCCTGCACAGACCTGGTGAGAAACC CGGTGAGGCCGTGACC 6398
QY 2075 ArgSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGln 2094
Db 6399 CAG-----GGGGGCTCCCTGCAGTCCCAACCAACCGCTCCCAACGGGCC 6440
QY 2095 SerLysVal-----SerLysHis-----IleArgLeuProAlaPro 2106
Db 6441 GCCAGCGTCCGCACTCGTAAGCATACCTTCGACAGACACTGCGTCTCCAGCGCGCGCG 6500
QY 2107 CysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeuGlu 2126
Db 6501 GCCCCAGGCGGAGAGAGGCGGAGCCTCGAGCCCA----- 6536
QY 2127 LeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuPro---SerSerGlnGluGlu 2145
Db 6537 GCCGACGAGAGAGGTCAAGCATCACAGCTCCGCTGCCCCCTGACAGCCACAGCCGAG 6596
QY 2146 ProLeuPhePro-----ArgAspLeuLysLysCysTyr 2156
Db 6597 CCCCATGCCCCGGAAGCCTCTCCGGTGGCCGCGGCGGAGCCTGCGGAGGCTCTAC 6656
QY 2157 SerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGluGlnArgArg 2176
Db 6657 AGCTTGAGCGCTCAGGGCTTCTTGGAACAAGCCGGGC---CGGGCAGACGAGCAGTGGCGG 6713
QY 2177 HisSerIleAlaValSerCysLeuAspSerGlySerGlnProArgLeuCysProSerPro 2196
Db 6714 CCTTCGCGGAG-----CTGGGCGAGCGGGAG-----CCTGGGAG 6749
QY 2197 SerSerLeuGlyGlyGlnProLeuGlyGlyPro-----GlySerArgProLysLys 2214
Db 6750 GCGAAGGCTGGGGC---CCTAGAGCGGAGCCCGCTGTGGGTGCGCGAAGAAAGAAAG 6806
QY 2215 LeuSerProProSerIleSerIleAspProPro---GluSerGlnGlySer---ArgPro 2232
Db 6807 ATGAGCCCCCTGCATCTCGGTGAACCCCTCGGAGGACGAGGCTCTGCGCGGGCC 6866
QY 2233 ProCysSerProGly-----ValCysLeuArgArgAlaProAla----- 2246
Db 6867 TCCGCGGAGAGGCGGCGGACACCACTGAGGCGGAGACCCCGTCTGTGAGGCCACG 6926
QY 2247 -----SerAspSerLysAspProSerValSerSerProLeuAspSerThrAlaAlaSer 2264
Db 6927 CCTCACAGGACTCCCTGAGCCCAAGAGGCTCAGGCGCGGGGGGAGCCCTGCAGCC 6986
QY 2265 -----ProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6987 AAGGGGAGCGCTGGGCGCAGGCTCTGCGGCTGAGCACTGACCGTCCCAAGCTTT 7046
QY 2278 SerSerAspProThrAspMet-----AspPro 2286
Db 7047 GCCTTTGAGCCGCTGAGCCTCGGGGTCCCAAGTGAGACCT 7088

RESULT 10
US-10-930-301-51

; Sequence 51, Application US/10930301
; Publication No. US20050026207A1
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JHU1590
; CURRENT APPLICATION NUMBER: US/10/930,301
; PRIOR FILING DATE: 2004-08-30
; PRIOR APPLICATION NUMBER: US/09/398,522
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 3993
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CACNA1G - a gene encoding a T-type calcium channel
; NAME/KEY: CDS
; LOCATION: (373)...(3993)
US-10-930-301-51

Alignment Scores:
Pred. No.: 0 Length: 3993
Score: 6103.00 Matches: 1173
Percent Similarity: 95.49% Conservative: 12
Best Local Similarity: 94.52% Mismatches: 52
Query Match: 50.74% Indels: 4
DB: 21 Gaps: 2

US-09-611-257a-24 (1-2287) x US-10-930-301-51 (1-3993)

QY 3 ProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArgProSer 22
Db 281 CCGCGGGGGCCCCGGGTTGCGTGAGGACACCTCTCTGAGGGGCGCGCTTGCCCCCT 340
QY 23 SerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAla 42
Db 341 CCGGATCGCCCGGGGCGCGGCTGGCCAGAGATGACGAGAGAGATGAGAGCGGCGG 400
QY 43 ProArgSerArgAspSerProValAlaSerArgSerSerThrCysProGlyProGly 62
Db 401 CCGAGAGTGGGAGACCCCGGAGCTTACGCGCTCAACGACCTGTGCGGGCGGGG 460
QY 63 Ala-AlaGlyAla-GlySerThrGluLysAspProGlySerAlaAspSerGluAlaGlu 82
Db 461 GCGGCGGGGCGCGGGGTACAGAGAAAAGACCCGGGCGAGCGCGGACTCCGAGCGGAG 520
QY 82 LysLeuProTrpProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgP 102
Db 521 GGCTGCCGTACCCGGCGCTGGCCCCCGGTGTTCTTCTACTGTAGCAGACAGACCGGCC 580
QY 102 roArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuV 122
Db 581 CCGGAGCTGTGTCTCCGACAGGTCTGTAACTCTGTTGAGCGCATCAACATGTTGG 640
QY 122 alileLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysA 142
Db 641 TCATCTTCTCAACTGCGTGACCTGGGCAATGTCGGCCATGCGAGCATCGCTGTG 700
QY 142 spSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaV 162
Db 701 ACTCCAGCGCTGCCGATCTGCAGAGCCTTGATGACTTCATCTTGCCCTTCTTGCCG 760
QY 162 alGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyA 182
Db 761 TGGAGATGTGTGAAGATGTGTGGCTTGGGCACTTTGGGAAAAGTGTAACTGGAG 820
QY 182 spThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuA 202
Db 821 ACACTTGAAACCGGCTTGACTTTTTCATCGTCATCGCAGGAGATGCTGAGTACTCGCTGG 880

[illegible]

QY	562	rgArGlueuMeLLeuProProProSerThrProThrProSerGlyGlyProProArGGLyA	582
Db	1961	GCCGGCTCATGTCTGCACACCCTCGAGCCTGCCCTCTCCGGGGCCCCCTTGTTGGCG	2020
QY	582	laGlueSerValHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnA	602
Db	2021	CAGAGTCTGTGCACAGCTTCTTACCATTGCGCACTGCCACTTAGAGCCAGTCCGCTGCCAGG	2080
QY	602	laProProProArGcCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValT	622
Db	2081	CGCCCCCTCCAGAGTCCCATCTGAGGCATCCGGCAGGACTGTGGGCAGCGGGAAGTGT	2140
QY	622	yrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluV	642
Db	2141	ATCCCAACCGTGCAACACGACCCCTCCACCGGAGACGCTGAAGAGAGAAGGCACTAGTAGAGG	2200
QY	642	alAlaProSerProGlyProProProThrLeuThrSerPheAsnIleProProGlyProPheS	662
Db	2201	TGGCTGCCAGCTCTGGGGCCCCCAACCTCAACGCTCAACATCCACCCGGGCCCTTACA	2260
QY	662	erSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysI	682
Db	2261	GCTCCATGCACAGCTGCTGGAGACACAGAGTACAGTGCCTGCCAAGCTCTTGCAAGA	2320
QY	682	leSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrC	702
Db	2321	TCTCCAGCCCTTGCTTGAAAGCAGACAGTGAAGCTGTGTTCCAGACAGCTGCCCTACT	2380
QY	702	ysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAsps	722
Db	2381	GTGCCCCGGCGGGGAGGGAGGTGAGCTGCCGACCGTGAATGCTGACTCAGACA	2440
QY	722	erGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisS	742
Db	2441	GCGAGGCAGTTTATGAGTTCACACAGAGATGCCACAGCACAGGACCTCCGGACCCCCACA	2500
QY	742	erArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheT	762
Db	2501	GC--CGGGCGCAACGGAGCCTGGGCCCATGCAAGCCCAAGCTCTGTGCTGGCTTCT	2557
QY	762	rPArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyI	782
Db	2558	GGAGGCTAATCTGTGCACCTTCGAAAGATTGTGACAGCAAGTACTTTGGCGGGGAA	2617
QY	782	leMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProG	802
Db	2618	TCATGATCGCCATCTCTGTGTCAACACACTCAGCATGGGCATCGAATACCAGCAGACCCG	2677
QY	802	IuGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuG	822
Db	2678	AGGAGCTTACCACGCGCCTAGAAATCAGCAACATGCTTTCACCAAGCCTCTTGGCCCTGG	2737
QY	822	IuMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnI	842
Db	2738	AGATGCTGCTGAAGCTGCTGTGTATGTCCTTTGGCTACATCAAGAAATCCCTAACACA	2797
QY	842	lePheAspGlyValIleValIleValIleSerValTrpGluIleValGlyGlnGlnGlyG	862
Db	2798	TCTTCGATGCTGTCTATGTGTGTCATCAGCGTGTGGAGATCGTGGCCAGCGGGGGCG	2857
QY	862	IyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuP	882
Db	2858	GCCTGTGCTGCTGCGGACCTTCGCGCTGATGCTGTGCTGAAGCTGTGTCGCTTCTGC	2917
QY	882	roAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheC	902
Db	2918	CGGCGCTGCAGCGGCGAGCTGTGTGCTCATGAAGACCATGGAACAAGTGGCCACTTCT	2977
QY	902	ysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyC	922
Db	2978	GCATGCTGCTTATGCTTTCATCTTCATCTTCAGCATCCTGGGCATGCATCTCTGGGCT	3037
QY	922	ysLysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerL	942

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Db 3038 GCAAGTTTGCTCTGAGCGGATGGGACACCCCTGCCAGACCGGAAGATTGTGACTCCT 3097
QY 942 euleuTrpAlaIleValThrValPheGlnIleLeuThrGlnIuAspTrpAsnLysValI 962
Db 3098 TGCTCTGGGCCATCGTCACTGTCTTTCAGATCCGTGACCCAGAGAGATGGAACAAGTCC 3157
QY 962 eUTyrAsnGlyMetAlaSerThrSerSerTrpAlaIleuValIleuTyrPheIleAlaLeuMet 982
Db 3158 TCTACAATGGTATAGCCCTCCACGTCTCTGCGGCGCCCTTATTTCATTGCCCTCATGA 3217
QY 982 hrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeuValGlyPheGlnA 1002
Db 3218 CCTTCGGCAACTACGTGCTCTTCAATTGTCTGTGTCGCAATTCTGTGAGGGCTTCCAGG 3277
QY 1002 laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG 1022
Db 3278 CGAGGGAGATGCCAACAAAGTCCGAATCAGAGCCCGATTCTTCTCACCCAGCCTGGATG 3337
QY 1022 lYAspGlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA 1042
Db 3338 GTGATGGGGACAGAGAAGATGCTTGCCCTGTGTCTGAGAGACACCGGAGCTGC 3397
QY 1042 rGlySerLeuLeuProProLeuIleIleHisThrAlaAlaThrPrometSerHisProl 1062
Db 3398 GGAAGACCTGCTGCCCGCTTCATCATCCACACGCGCCACACCCCATGTCGCTGCCCA 3457
QY 1062 ySerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSers 1082
Db 3458 AGAGCACACGACGCGGCTGGGCGAGGCGCTGGGCGCTGCGCGCCGACACGACGACA 3517
QY 1082 eRgLySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgS 1102
Db 3518 GCGGGTCGCGAGAGCCTGGGCGGCC--CACGAGATGAAGTCAACGCCACGCGCCGCA 3574
QY 1102 eRserProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgA 1122
Db 3575 GCTTCGCGACAGACCCCTGAGCGCTGCAAGCAGCTGACACGAGCGCTCCAGCCGGA 3634
QY 1122 snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyLysArgSerL 1142
Db 3635 ACAGCCTCGGCGCTGCACCCAGCCTGAAGCGGAGAGCCCAAGTGAGAGCGCGGTCCC 3694
QY 1142 euleuSerGlyGlyGlyGlnGluSerGlnAspGlyGluGluSerSerGlyLysAspArgA 1162
Db 3695 TGTGTTCGGGAGAAAGGCCAGGAGAGCCAGGATGAAGAGAGAGCTCAGAAAGAGAGCGGG 3754
QY 1162 laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSers 1182
Db 3755 CCAGCCCTGCGGGCAGTAGCACCAATGCCACAGGGGGTCCCTGGAGCGGAGGCCAAGATT 3814
QY 1182 erPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgS 1202
Db 3815 CCTTGACCTGCCAGACACACTGAGGTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAG 3874
QY 1202 eRserAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgT 1222
Db 3875 GGTCTGCTTCTGAGCACACGAGACTGCAATGGCAAGTCCGCTTCAGGGCGCTGCCGGG 3934
QY 1222 hrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGlyLysnLeu 1241
Db 3935 CCCTGCGGCTGATGACCCCCCACTGATGGGATGACCGCCGATGACGAGGGCAACCTG 3993

RESULT 11
US-10-377-139-8
; Sequence 8, Application US/10377139
; Publication NO. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee Mackinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins

;; TITLE OF INVENTION: Uses Thereof
;; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
;; CURRENT APPLICATION NUMBER: US/10/377,139
;; CURRENT FILING DATE: 2003-03-01
;; NUMBER OF SEQ ID NOS: 21
;; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 6990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-377-139-8

Alignment Scores:
Pred. No.: 0 Length: 6990
Score: 5432.50 Matches: 1234
Percent Similarity: 62.21% Conservative: 241
Best Local Similarity: 52.05% Mismatches: 514
Query Match: 45.17% Indels: 387
DB: 19 Gaps: 62

US-09-611-257A-24 (1-2287) x US-10-377-139-8 (1-6990)
QY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
Db 16 TCCCCGCCCTCCTCATCTGCAGACGCCCGCTGAGCCAGAGACTCACCGAGAGCAG 75
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
Db 76 CCGGAGACCCCG----- 87
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
Db 88 -----AGCCCCCATCTCCCGCCGACGCGCTGAGAGAGCTTGATGAGACT----- 135
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
Db 136 -----GATCCT-----CATGTCCACAC 153
QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
Db 154 CCAGACCTGGCGGCTATTGCTCTTCTGTGCTGCACAGACACCAACGCCCCGGAAGTGG 213
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
Db 214 TGCATCAAGATGTTGTCAACCCGTTGTTGAATGTGTCAAGCATGCTGTGATCCTGTG 273
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
Db 274 AACTGCGTGACACTGGCATGTACACAGCCGTCGACGACATGAGACTGCTGCCAGCCGC 333
QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
Db 334 TGCAGATCCTCGCAGGTCCTTGATGACTTCATTATCTTCTTGCCATGAGATGATG 393
QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrIleuGlyAspThrTrpAsn 185
Db 394 CTCAGATGTGCGCCCTGGGGATTTTGGCAGAGAAGTGCTACTCGGGACACATGGAAC 453
QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
Db 454 CGCTGGAATTTCTTCATGTCATGTCAGAGGATGTCGAGTACTCCCTCGACCTTCAGAAC 513
QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
Db 514 ATCAACCTGTGAGCCATCCGACCGTGCGGCTGAGGCCCTCAAGCCATCAACCGC 573
QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuPrometLeuGlyAsn 245
Db 574 GTGCCAGTATGCGGATCTGTGTAACCTGTCTCGACACACACTGCCATGCTGGGAAT 633
QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
Db 634 GTCTGCTGCTCTGCTTCTTGTCTTCTTCACTTTGGCATCATAGGTGTGAGCTCTGG 693

QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheserLeuProLeuSerVal 285
Db 694 GCGGGCCTGCTGCTAACCGCTGCTTCTGGAGAGAACTTACCATACAAAGGGGATGTG 753
QY 286 AsPLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
Db 754 GCCTTGCCCCCATACTAACAGCCGGAGAGATGATGAGATGCCCTTCACTGCTCCTG 813
QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGly 325
Db 814 TCGGGCGACAATGGATATAGGCTGCCATGAGATCCCCCGCTCAAGAGCAG----- 867
QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 868 ---GGCCGTAGTGTCTGCTGCCAAGACGAGCTTACGACTTGGGGCGGGCCGACG 924
QY 340 SerSerAsnThrThr-----CysValAsnThrAsnGlnTyrTyrThrAsnCysSerAla 357
Db 925 GACCTCAATGCCAGCGGCTGTGTCTCACTGGAACCGTTACTACTCAATGTGTGCCGACG 984
QY 358 GlyGluHisAsnProPheLeysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTyrIle 377
Db 985 GGCAGCGCCAAACCCCAACAAGGGTGCATCACTTGACAACATCGGTTATGCTTGATT 1044
QY 378 AlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAsp 397
Db 1045 GTCATCTTCCAGGTGATTCATCTGAAAGCTGGGTGAGATCATGTACTACGTGATGAT 1104
QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
Db 1105 GCTCACTCCTTCTACAATTTCATCTACTTCATCCTGCTTATCATAGTGGCTCCTTCTTC 1164
QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1165 ATGATCAACCTGTGCTCTGTTGTATAGCGAACCCAGTTCTCGAAGCAACGAGGAG 1224
QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1225 CACCGGCTGATGCTGGAGCAGCGGAGCGCTAAGCTGTCC--TCCAGCAGGTTGCCAGC 1281
QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1282 TACGCCGAGCCTGGCACTGTACGAGAGATCTTCCAGTATGTCTGCCACATCCTGCGC 1341
QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1342 AAGGCCAAGCGCGCGCTGGCCTTACACAGCCCTGCAGAGCGGCGCCAGGCCCTG 1401
QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1402 ---GGCCCGAGGCGCGCGCCCGCCAAACCTGGGCCC----- 1437
QY 518 HisArgArgLeuSerValHisIleLeuValHisHisHisHis----- 533
Db 1438 -----CACGCCAAGGACCCCGGCACTACCATGGGAAGACTAAG 1476
QY 534 -----HisHisHisTyrHisIleGlyAsn-----GlyThrLeuArgValPro 547
Db 1477 GGTCAAGGAGATGAAGGAGACATCTCGAAGCCGGCATTTGCCAGACTTTGCATGGGCT 1536
QY 548 ArgAlaSerPro-GluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuPr 567
Db 1537 ---GCCTCCCTCGAATGATCACTCGGGAAGAGACTGTGCCCAACATA--GCCCC 1590
QY 567 oProProSerThrProThrPro-----SerGlyGlyProProArgGlyAlaGluSerVa 585
Db 1591 CTGGATGCGAGCGCCCAACCTGTGTGAGCCCATCCCGCCACGC----- 1636
QY 585 HisSerPheTyrHisAlaAspCysHisIleGluProValArgCysGlnAlaProProPr 605
Db 1637 -----TGGCTTCCGATCCC 1650

QY 605 oArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVa 625
Db 1651 GCCAGTGCCTTGTCTGCCAGATGAGACGCGCGCGCCTCGGCTGTG----- 1702
QY 625 HisThrSerProProProGluIleLeuLysAspLysAlaLeuValGluValAlaProSe 645
Db 1703 -----GCAGACCCGACTCGGGCCAGAGGAGCTCGGCT----- 1735
QY 645 rProGlyProProThrThrLeuThrSerPheAsnIleProProGlyProPheSerSerMetHi 665
Db 1736 -CCGGAGCTCCGCTGTGGCG----- 1756
QY 665 sLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLysIleSerSerPr 685
Db 1757 -----AGGACGAGCGGATGGG----- 1774
QY 685 oCysSerLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgTh 705
Db 1775 -----AC 1776
QY 705 rGlyAlaGlyGluProGluSerAlaAspHisValMetProAspSerAspSerGluAlaVa 725
Db 1777 GGGGCCCGAGCAGCAGG----- 1795
QY 725 lTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgAr 745
Db 1796 -----ACGGAGCCTCCTCAGAACTGGGAGAGAG-----AGAGAGAGAG 1836
QY 745 gGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuAlaPheThrPArgLeuIl 765
Db 1837 GAGCAGCGGATGGGCGGTCTGCTG-TGCCGGGATGTG-----TGGCGGAGAGAC 1886
QY 765 eCysAspThrPheArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAl 785
Db 1887 GCGAGCCAAAGCTCGCGGCATGTGGACAGCAAGTACTTCAACCGGGGCATCATGATGGC 1946
QY 785 aIleLeuValAsnThrLeuSerMetGlyIleGlyTyrHisGluGlnProGluGluLeuTh 805
Db 1947 CATCCTGTCAACACCGTCAAGATGGGCATGAGCACCAAGCAGCAGCCGAGAGAGCTGAC 2006
QY 805 rAsnAlaLeuGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLe 825
Db 2007 CAACATCCTGGAGATCTGCAATGTGTCTTCAACACGATGTTGCCCTGGAGATGATCCT 2066
QY 825 uLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGl 845
Db 2067 GAAGCTGGCTGCATTTGGGCTCTCGACTACCTGCGTAACCCCTACAACATCTTCAGACAG 2126
QY 845 yValIleValValIleSerValTyrGluIleValGlyGlnGlnGlyGlyLeuSerVa 865
Db 2127 CATCATTTGCATCATCAAGCATCTGGAGATCGTGGGCGAGCGGAGCGGTGGCTGTGGT 2186
QY 865 lLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGl 885
Db 2187 GCTGGGACTTCGGGCTGTGCGGTGCTGAAACTGGTGGCTTCATGCTGCTGCTGCG 2246
QY 885 nArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLe 905
Db 2247 GCGCCAGCTCGTGTGCTCATGAAGACCATGACAAACGTGGCCACCTTCGATGTGCT 2306
QY 905 uMetLeuPheIlePheIlePheSerIleLeuGlyMetHisIleuPheGlyCysLysPheAl 925
Db 2307 CATGCTTTCATCTTCATCTTCAGCATCCTTGGAGTGAATATTTTGGCTGCAAGTTGAG 2366
QY 925 aSerGluArgAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTr 944
Db 2367 CCTCCGACGAGCACTGGAACAACGCTGCCGACAGGAAGAACTTCGACTCCTGCTGTG 2426
QY 944 pAlaIleValThrValPheGlnIleLeuThrGlnGluAspTyrAsnLysValLeuTyrAs 964
Db 2427 GGCCATGTCATGTGTTCCAGATCCTCACCCAGAGGAGACTGGAACGTGCTTCTTACAA 2486
QY 964 nGlyMetAlaSerThrSerSerTyrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGl 984

Db	2487	TGGCATGGCCCTCCACTTCTCCCTGGGCCCTCCCTTACTTTGTGCGCCCTCATGACCTTCGG	2546
Qy	984	YASnTyValLeuPheAsnLeuValAlaIleLeuValGluGlyPheGlnAlaGluGly	1004
Db	2547	CAACTATGTGCTTCAACTGCTGTGGCCATCTGTGGAGGCTTCCAGCGGAGGG	2606
Qy	1004	YASpAlaThrLysSerGluSerGluProAspPheSerProSerVal-----	1020
Db	2607	TGACGCCAATCGCTCTACTCCGACGAGACCCAGACTCATCCAAACATAGAAGATTGA	2666
Qy	1021	-----ASpGlyAspGlyAspArgLysLysArgLeuAlaLeuValAla	1034
Db	2667	TAAGCTCCAGGAAGCGCTGGACAGACGCGAGATCCCAAG-----CTCTGCCCAATCCC	2720
Qy	1034	AlaGluGlyLHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThr--	1053
Db	2721	CATGACCCCAATGGGCACTGGACCCCACTC-----CCACTGGGTGGGCACCTAGG	2774
Qy	1054	-----AlaAlaThrPrometSerHisProLysSerSerSerThrGlyValGlyGly	1070
Db	2775	TCCTGCTGGGCTGGGGAAGCTTGC-----CCCGCACTCTCACTGCAGCCGGAACCCAT	2828
Qy	1070	uAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAl	1090
Db	2829	GCTGCTGGCCCTGGGCTCCCGAAGAAGCAGTGTCTCTCTA-----GGAGAGAT	2879
Qy	1090	ahHisGluMetLysCysProProSerAlaArgSerSerProHisSerProTyrSerAl	1110
Db	2880	GAGCTATGACCAAGCGCTCCCTGTCCAGCTCCCGAGCTCTACTACGGGCCATGGGGCCG	2939
Qy	1110	aAlaSerSerTyrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLe	1130
Db	2940	CAGCGCGGCTGGGCGCAGCGCTCGCTCCAGCTGGAAC-----AGCCT	2981
Qy	1130	uLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu--GlyGlnGly	1149
Db	2982	CAAGCACAAAGCCGCGCTCGCGGAGCATGAGTCCCTGCTCTGCGGAGCGCGCGCGCG	3041
Qy	1149	uSerGlnAspGluGluGluSerSerGlyGlu-----AspArgAlaSerProAlaGlySe	1167
Db	3042	CGCCCGGCTCTGAGGTTGCGCGGAGCGGAGCGGCGCGCGCGCGCACCCCTGCACAC	3101
Qy	1167	rAspHis-----ArgHisAr	1172
Db	3102	CCCAACAGCCCAACCATTCATCAAGGCGCCCATCTGGCGCAACGCCACGCCACCAACG	3161
Qy	1172	gGlySerLeuGluuArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValPr	1192
Db	3162	CCGGAACGCTGTCCCTCGACACACAGGACTCGGTGACCTGCCGCGAGCTGTGCCCGCGT	3221
Qy	1192	oGlyLeuHisArgThrAlaSerGlyArgSerSer-----AlaSerGluHisGlnAspCy	1210
Db	3222	GGGCGCCACCCCGGGCGCTGGAGGGCGGCGAGCCCGCGCCCGGCATGAGGACTG	3281
Qy	1210	sAsnGlyLysSerAlaSerGlyArgLeuAlaArgThrLeuArgThrAsp--AspProGly	1229
Db	3282	CAATGGCAGGATGCCACG-----ATCGCAAAAGACGTCTTCAACCAAGATGGCGCACCG	3335
Qy	1229	nLeuAspGlyAspAspAspAsnAspGluGlyAsnLeuSerLysGlyGluArgGlyLeuAl	1249
Db	3336	CGGGGATCGCGGGAGGATAGAGGAATCGACTACACCTGTGCTTCGCGTCCGCA	3395
Qy	1249	aTyrValArgSerArgLeuProAlaCysCysArgGlyuArgAspSerTyrSerAlaTyrI	1269
Db	3396	GATGATCGACGCTATAAGCCCGACTGCTGCGAGGTCCGCGAAGACTGTGTCTTACTT	3455
Qy	1269	ePheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPh	1289
Db	3456	CTTCTCTCCGAGAACAGGTTCCGGGTCTGTGTCAAGACCATTAATTGCCACAACACTCTT	3515
Qy	1289	eAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPr	1309

Db	3516	CGACTACGTGCTGCTGGCCCTTCATCTTTCTGCACTGCATCACCATCGCCCTGGAGCGGCC	3575
Qy	1309	oLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheTh	1329
Db	3576	TCAGATCGAGGCCGGCAGCACCGAACGCATCTTCTCACCGGTGCCAACTACATCTTCAC	3635
Qy	1329	rAlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGly	1349
Db	3636	GGCCATCTTCGTGGCGGAGATGACATTGAAGTAGTCTCGCTGGCGCTGTACTTCGGCGA	3695
Qy	1349	uGlnAlaTyrLeuArgSerSerTyrAsnValLeuAspGlyLeuLeuValLeuIleSerVa	1369
Db	3696	GCAGGCGTACCTAGCAGACAGCTGGAAAGTGGATGGCTTTCCTGTTCGTTCAT	3755
Qy	1369	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuAr	1389
Db	3756	CATGCACATCGTGTGTCTCCCTGGCCCTCAGCCGGGGAGCCAAGATCTTGGGGTCTCCG	3815
Qy	1389	gValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLe	1409
Db	3816	AGTCTTGGCGCTCTGCGCACCCCTACGCCCCCTGCGTGCATCAGCCGGCGCGCGGCT	3875
Qy	1409	uLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIle	1429
Db	3876	GAACTGTGTGGAGACACTCATCTCTCCCTCAAGCCCATCGGCACATCGTGTCTCAT	3935
Qy	1429	eCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPh	1449
Db	3936	CTGCTGTGCTTCTTCATCATCTTGGCATCCTGGAGTGACAGCTCTTCAAGGCAAGTT	3995
Qy	1449	ePheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAl	1469
Db	3996	CTACCACCTGTCTGGCGGTGGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCCG	4055
Qy	1469	aSerTyrArgTyrValAlaArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSe	1489
Db	4056	CAACTACCGCTGGGTGCATCAAAATACAACCTTGCACAACCTGGGCCAGGCTCTGATGTC	4115
Qy	1489	rLeuPheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAl	1509
Db	4116	CCTCTTGTGCTGGCATCCAAAGATGTTGGGTGAACATCATGTACATGAGACTGATGC	4175
Qy	1509	aValGlyValAspGlnGlnProIleMetAsnHisAsnProTyrMetLeuLeuTyrPheI	1529
Db	4176	TGTTGCTGTGACCAAGCAGCCTGTGACCAACCAACCCCTGGATGCTGTACTTCAT	4235
Qy	1529	eSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGly	1545
Db	4236	CTCCTTCTGCTCATCGTCAAGCTTCTTGTGTCAACATGTTGTGGGTGCTGTGTGGA	4295
Qy	1549	uAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGlyL	1565
Db	4296	GAACTTCCACAAGTGGCGGAGCACCAAGAGGCTGAAGAGGCACGGCGCGTGAGAGAA	4355
Qy	1569	sArgLeuArgArgLeuGlnLysLysArgArgSerLysGlnMetAlaGluAlaGly	1589
Db	4356	GGGCGCTGGCGCGCTGGAGAGAAGCGCGG-----AAGGCCCA	4394
Qy	1589	nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisIleLeuCysTh	1609
Db	4395	GGGCGTGCCTACTATGCCACTATTGTACACACCCGGCTGCTCATCCACTCATGTGCAC	4454
Qy	1609	rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLysAsnValValThrMetAl	1629
Db	4455	CAGCACTACCTGACATCTTCATCACCTTCATCATCTGCTTCAACGTGTCAACCATGTC	4514
Qy	1629	aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrI	1649
Db	4515	CTTGAGACACTACAATCAGCCCAAGTCCCTGAGACAGCCCTCAAGTACTGCAACTATAT	4574
Qy	1649	ePheThrValIlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgAr	1669
Db	4575	GTTCAACCACTGTCTTGTGTGTGTGAGAGCGCTGTGCTGAAGCTGTGTGCATTGTGCTGAGGCG	4634

QY	1669	gpPhepHeGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetG1	1689
Db	4635	CTTCTTCAAGAACCGATGGAACACGACTGACCTGGCCATTGTGCTACTGTCAATGATGGG	4694
QY	1689	YIleThrLeuGluGluIleGluValAsnLeuSerLeuProIleAsnProThrIleIleAr	1709
Db	4695	CATCAACCCCTGAGAGAGATCGAGATCATATGCGGCCCTGCCCATCATCCACCATCATCCG	4754
QY	1709	gIleMetArgValLeuArgIleAlaArgValLeuIlysLeuLeuIysMetAlaValGlyMe	1729
Db	4755	CATCATGAGGGTTCTGCCCATTTGCCAGTGTGAAGATGGGCCACAGGAAT	4814
QY	1729	lArgAlaLeuLeuHisThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe	1749
Db	4815	GCGGGCCCTGCTGGACACGGTGGTCCAAAGCTTTGCCAGGTGGCAACCTGGGCTTCCT	4874
QY	1749	uPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuG1	1769
Db	4875	CTTCATGCTGCTCTTCTTCACTATGCTGCTCGGGGTGGAGCTCTTTGGGAAGCTGGT	4934
QY	1769	uCyAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAspPheG1	1789
Db	4935	CTGCAACGACGAGAACCCGTCGAGGGCATGAGCCGGCATGCCACTTCGAGAATTCGG	4994
QY	1789	yMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLy	1809
Db	4995	CATGGCTTCTCACACTTCTCCAGGTCCTCCACGGGTGACAACTGGAACGGGATCATGAA	5054
QY	1809	sAspProSerArgAspCys--AspGlnGluSerThrCysTyrAsnThrVal-----Il	1826
Db	5055	GGACACGCTGCGGACTGCAACCCACGACGAGCGAGCTGCTGACAGCCTGCACTTGT	5114
QY	1826	eSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa	1846
Db	5115	GTCGCCGCTGACTTCGTGAGCTTCTGCTCACCGCGCAATTCTGCTCATCAACGTGT	5174
QY	1846	lIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaG1	1866
Db	5175	GGTGGCTGTGCTCATGAGCACTTGACGACACACAAAGAGCGCAGAGAGACGCCGA	5234
QY	1866	uLeuGluAlaGluLeuGluLeuGluMet--LysThrLeuSerProGlnProHisSerPr	1885
Db	5235	GATGATGCCGAGCTCGAGCTGGAATGAGATGCCATGCTGGGCCCTGGCCCGAGGCTGCC	5294
QY	1885	oLeuGlySerProPheLeuTrpPro-----GlyValGluGlyValAsnSe	1900
Db	5295	TACCGGCTCCCCGGGGCC--CCTGGCCGAGGGCCGGAGGGCGGGCGGGCGGA	5351
QY	1900	rThrAsp-----SerProLysProGlyAlaPro-----	1909
Db	5352	CACCGAGGGCGGCTTGTGCCGGCGCTGCTACTCGCCTGC-CCAGGAGAACCTGTGCTGG	5410
QY	1910	----HisThrThrAlaHisIleGlyAlaAlaLaserGlyPheSerLeuGluHisProThrMe	1928
Db	5411	ACAGCGTCTTAAATCATCAAGCACTCCTTGAGGG--GAGCTGACCAT-----	5459
QY	1928	tValProHisProGluGluValProValProLeuGlyProAspLeuLeuThrValArgLy	1948
Db	5460	-----CATCGACAACCTGTGCGGCTCCATCTTCCACCACTACTCCTCGCCTGCGGCT	5512
QY	1948	sSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySe	1968
Db	5513	GCAAGAAGTGCA-----CCACGACAA-----	5534
QY	1968	rThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySe	1988
Db	5535	----GCAAGAGGTGCAGCTGGCTGAGACGAGAGGCCCTTCTCCCTGAACACTCAGACAGTCT	5590
QY	1988	rIleLeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAs	2008
Db	5591	CGTCCATCTGCTGGGTGACGACCTGAGTCTCGAGA-----	5627

QY	2008	pvalhistrleuLeuGlnProHisglYalaProThrTrpGlyAlaIleProLysLeuPr	2028
Db	5628	-----CCCCACAGCCTGCCACCTGG-----CCGCAAGACA	5659
QY	2028	oPro-----ProGlyArgSerProle	2035
Db	5660	GCAAGGTGAGCTGACCCACCTGAGCCCATGCGTGTGGAGACCTGGCGGATGCTTCT	5719
QY	2035	uAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnI	2055
Db	5720	TCCCCTGTG-T-CCTCTACGGCCGTCTCGCCGGATCCAGAACTTCTGT--GTGAGATG	5775
QY	2055	ylLeuGlySerArgGluAspLeuLeuSerGluValSerGlyProSerCysProLeuThrAr	2075
Db	5776	GAGGAGATCCCAT-----TCAACCCCTGTCCGGTCTCTGGCTGAACATGACA--	5821
QY	2075	gSerSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSe	2095
Db	5821	-----	5821
QY	2095	rlYsValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAl	2115
Db	5822	---GCAGTCAAGCACCCCAAGTCCCTTCTCCC-----	5851
QY	2115	alYsAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSe	2135
Db	5852	-CGATGCTCCAGCC-----CTCTC	5871
QY	2135	rgLYAspLeuLeuProSerSerSerGlnGluGluProLeuPhePro-----ArgAspLeuLY	2153
Db	5872	CTGCCCATGCCAGCCGAGTTCTTCCACCCTGCAGTGTCTGCCAGCAGAAAGGCCAGAA	5931
QY	2153	sLYsCyTrYSerValGluThrGlnSerCysArgArgArgProGlyPheTrpLeuAspGl	2173
Db	5932	AAGGGACTGGCACTGGAAACCTTCCCAAGATTGGCTG-CAGGGCTCTGGGCATCT--	5988
QY	2173	uGlnArgArgHisSerIleAlaValSerCysLeu-----AspSerGlySerGl	2189
Db	5989	-----CTGCGGTCAACCAAGGTCAACTGTACCTCTCTCGGCAGGCCACCGGAGCGA	6041
QY	2189	nProArgLeuCySProSerProSerSerLeuGlyGlyGlnProLeuGlyGlyProGlySe	2209
Db	6042	CACGTGCTGAGACGCCAGCCCCAGCAG-CTCCGGCGGGCAGCCTGCAGACCAACGCTCAGG	6100
QY	2209	rArgProLYsLYsLYsLeuSerProProSerIleSerIleAspProProGluSerGlnI	2229
Db	6101	ACAGCCTGACCCCTGAGCGACAGCCCGCGCG-----TGCCCTGG	6139
QY	2229	ySerArgProProCysSer-----ProGlyValCysLeuArgArgAlaProAlaSe	2247
Db	6140	GGCCGCGCGCGCTGCTCCAGGACCCCGGGCGGCGCTGTCCCCCGCGCTCGCGCGCC	6199
QY	2247	raspSerLYsAspProSerValSerSerProLeuAspSerThrAlaIaIaSerProSerPr	2267
Db	6200	TGAGCCTGCGCGCGCGGCTTCTTACGCTTGGGGGGCTGCGGGCGCATCAGCGCAGCC	6259
QY	2267	oLYsLYsAspThrLeuSerLeuSerGlyLeu	2277
Db	6260	ACAGCAGCGGGGCTCCACCAAGCCCGGCTG	6290
RESULT 12			
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; APPLICANT: Dietrich, Paul S.			
; APPLICANT: McGivern, Joseph G.			
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FEATURE:
NAME/KEY: CDS
LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 0
Score: 5420.00
Percent Similarity: 61.74%
Best Local Similarity: 51.82%
Query Match: 45.06%
Length: 6816
Matches: 1223
Conservative: 234
Mismatches: 494
Indels: 413
Gaps: 60

US-09-611-257A-24 (1-2287) x US-09-935-541-1 (1-6816)

OY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
:::|||||:::|||||:::|||||:::|||||
DB 207 TCCCGCGCTCTCATCTGCAGACGCCAGCGCTGAGCCAGAGATCACCGAGCAG 266
OY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
|||||
DB 267 CCGGACCCCGG----- 278
OY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
|||||:::|||||:::|||||
DB 279 -----AGCCCCCATCTCCCGCCAGCGCTGAGAGCCTTGATGAGCT----- 326
OY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
|||||
DB 327 -----GATCT-----CATGTCCACAC 344
OY 86 ProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
|||||:::|||||:::|||||:::|||||
DB 345 CCAGACCTGGCGCTATTGCTTCTTCTGCTGCGACAGACCACAGCCCGGAACCTGG 404
OY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
|||||:::|||||:::|||||:::|||||
DB 405 TGCATCAAGATGGTGTGCAACCCGGTTTGAATGTGTCAAGCATGTGTGATCTCTGCTG 464
OY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
|||||:::|||||:::|||||:::|||||
DB 465 AACTGCGTGAACACTTGGCATGTACAGCCGTCGACGACATGGACTGCTGTCCGACCGC 524
OY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
|||||:::|||||:::|||||:::|||||
DB 525 TGCAGATCTTCAGAGTCTTGATGACTTATCTTATCTTCTTGCCATGAGATGCTG 584
OY 166 ValIysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
:::|||||:::|||||:::|||||:::|||||
DB 585 CTCAGATGGTGGCCCTGGGGAATTTGGCAAGAGTGTACTTCGGGACACATGGAAC 644
OY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
|||||:::|||||:::|||||:::|||||
DB 645 CGCCTGATTTCTCATCTGTCATGGCAGGAGATGTGAGTACTCCCTGACCTTCAAGAAC 704
OY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
:::|||||:::|||||:::|||||:::|||||
DB 705 ATCAACCTGTCAAGCCATCCGACCCGTGCGCTCTGAGGCCCCCTCAAGCCATCAACCGC 764
OY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
|||||:::|||||:::|||||:::|||||
DB 765 GTGCCCAGTATGCGGATCTGTGTAACCTGCTCTGACACACTGCCCATGTGGGGAAT 824
OY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
|||||:::|||||:::|||||:::|||||
DB 825 GTCTGTGCTGTCTTCTTGTGCTTCTTCTTGTGATCATAGGTGTGACAGCTCTGG 884

OY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
|||||:::|||||:::|||||:::|||||
DB 885 GCGGCGCTGTGCGTAACCGCTGCTTCTGAGAGAGAACTTCAACATACAAAGGGATGTG 944
OY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
|||||:::|||||:::|||||:::|||||
DB 945 GCCTTGCCCCCACTAACACAGCCGAGAGAGATGATGATGATGCTCATCTGCTCCCTG 1004
OY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGly 325
:::|||||:::|||||:::|||||:::|||||
DB 1005 TCGGGGACAAATGGATATATGGCTGCCATGAGATCCCCCGCTCAAGAGACG----- 1058
OY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
|||||:::|||||
DB 1059 ---GGCCGTAGTGTCTCTGTCCAAGACGACGTCTACGACTTGGGGCGGGCCGACG 1115
OY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
|||||:::|||||
DB 1116 GACCTCAATGCCAGCGGCTCTGTGTCACTGGAACCGTTACTTACAATGTGTGCCGACG 1175
OY 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
|||||
DB 1176 GGCAGCGCCAAACCCCAACAAGGTGCGCACTTGAACAACATCGGTATGCTTGATTT 1235
OY 378 AlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAsp 397
|||||
DB 1236 GTCATCTTCCAGGTATCACTGTGAAGCTGGGTGAGATCATTACTACGTGATGAT 1295
OY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
|||||
DB 1296 GTTCACTCTTTCACAACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTC 1355
OY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
|||||
DB 1356 ATGATCAACCTGTGCTGTGTGATAGCGAACCACTTCTCGGAGACCAAGCAACGGGAG 1415
OY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
:::|||||:::|||||:::|||||
DB 1416 CACCGCTGATGCTGGAGCAGCGGACGCTAAGCTGTC--TCCAGACGCTGGCCAGC 1472
OY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
:::|||||:::|||||:::|||||
DB 1473 TACGCCGAGCCTGGCGACTGTACGAGAGATCTTCCAGTATGTGTGCCACATCTGCGC 1532
OY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
|||||
DB 1533 AAGGCCAAGCGC-----CGCGCCCTGGGCTTCAAGGCCCTGCAG 1574
OY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
|||
DB 1575 AGC----- 1577
OY 518 HisArgArgLeuSerValHisIleuValHisHisHisHisHisHisIleTyr 537
|||||:::|||||
DB 1578 ---CGGCGCAGGCCCTG----- 1592
OY 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
|||||
DB 1593 -----GGCCCGGAG----- 1601
OY 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577
|||||
DB 1602 -----GCCCGGCCCCGCCAACCCTGGGCC----- 1628
OY 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
|||||
DB 1629 -----CACGCCAAG-----GAGCCC 1643
OY 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
|||||
DB 1644 CGGCACTACAGCTGTGCGGCAACATAGCCCCCTGATGCG----- 1685

QY 618 SerGlyLysValTyrProThrValHisThrSerProProGluIleLeuLysAspLys 637
Db 1686 -----ACGCCCCACACC----- 1697
QY 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
Db 1698 ---CTGGTGACG-----CCCATCCCGCCACCGCTGCTCC----- 1730
QY 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCCGCCACGCTGCCCTTGCTGCCAG 1757
QY 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1758 CATGAGACGCGCGCGCCCTCGGGCTGGGCAGCACCGACTCGGGCCAGAGGGCTCG 1817
QY 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGAGCTCCGCTGTGGCGAGACGAGGCG----- 1853
QY 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -----GATGGGACGGGGCC-----CGAGACAGCGAGACGAGCCCTCCTCAGAA 1898
QY 737 LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGGAGAGAGAGAGAGAGAGAGAGAG-----GCCGATGGGGCG 1940
QY 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
Db 1941 GTCTGGCTGTGCGGGGATGTGTGGCGGAGACCGGAGCCAAGCTCGCGCATCGTGAC 2000
QY 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGCATCATGATGACCATCTGTGTAACAACCGTCAGCATGGCC 2060
QY 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlnIleSerAsnIleVal 814
Db 2061 ATCGAGCACACGACGACCGCGAGAGCTGACCAACATCTCGAGATCTGCAATGTGATC 2120
QY 815 PheThrSerLeuPheAlaLeuGluMetLeuLysLeuLeuValTyrGlyProPheGly 834
Db 2121 TTCACCAAGCATGTTCCTCCCTGGAGATGATCTGGAAGCTGGCTGCATTTGGGCTCTTCGAC 2180
QY 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTyrGlu 854
Db 2181 TACCTGCGTAACCCCTACAACATCTTCGACAGCATCATTTGTATCATCAGCATCTGGGAG 2240
QY 855 IleValGlyGlnGlnGlyGlyLysSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCGTGGGGCAGCGCGGACGGTGGCTGTGCTGCGGACCTTCGGCTGTGCGCGTG 2300
QY 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAAACTGTGCGCTTCATGCTCCCTGCGCGCCGACGCTCGTGTGCTCATGAAGACC 2360
QY 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle 914
Db 2361 ATGGACAACGTGGCACCTTCTGCATGCTGCTCATGCTCTTCATCTTCAGCATC 2420
QY 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933
Db 2421 CTTGGGATGCATATTTTGGCTGCAGAGTTCAGCCTCCGCACGGACACTGGAGACACGGTG 2480
QY 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db 2481 CCCGACAGGAAGAACTTCACTCCCTGCTGTGGGCCATCGTCACTGTGTCCAGATCTTC 2540
QY 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973
Db 2541 ACCCAGGAGGACTGGAACGTGCTTCTTACAATGGCATGGCCTCCACTTCTCCCTGGGCC 2600
QY 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal 993

Db 2601 TCCCTTACTTTGTGCGCCCTCATGACCTTCGGCACTATGTGCTTTCACCTGCTGTG 2660
QY 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013
Db 2661 GCCATCTGTGTGAGGGCTTCCAGGGCGAGGGTGACGCCAATCGCTCTTACTTCGACGAG 2720
QY 1014 AspPheSerProSerVal-----AspGlyAsp 1023
Db 2721 GACCAGACCTCATCCAACATAGAAGATTGATAGCTCCAGAAAGCCTCGACACGACG 2780
QY 1024 GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLys 1043
Db 2781 GGAGATCCCAAG-----CTCGCCCAATCCCATGACCCCCAATGGCACCTGGACCCC 2834
QY 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrPrometSer 1059
Db 2835 AGTCTC-----CCACTGGGTGGGACCTAGGTCCTGTGGGCTGCGGGACCTGCC--- 2885
QY 1060 HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
Db 2886 ---CCCCACTCTCACTGCAGCGGACCCCATGCTGTGGCCCTGGGCTCCGAAAGAGC 2942
QY 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisGluMetLysCysProProSer 1099
Db 2943 AGTGTCATGTCTCTA-----GGAGAGATGAGCTATGACACGAGCTCTGTCTCAGC 2993
QY 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119
Db 2994 TCCCGAGCTCTTACTACGGGCGCATGGGGCCGACGCGGCTGGGCCACCGCTGCTCC 3053
QY 1120 SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyLysArg 1139
Db 3054 AGCTGGAC-----AGCCTCAAGCACAAGCCGCGCTGGCGGAGCAT 3095
QY 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluSerSerGlu 1158
Db 3096 GAGTCCCTGCTCTTGCAGAGCGCGGCGGCGCGCGCGCTGCGAGGTGCCCGGAC 3155
QY 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3156 GAGGGCGCGCGGCGCGCACCTTGACACACCCACACGCCACCATTCATCAGCGG 3215
QY 1170 -----ArgHisArgLysSerLeuGluArgGluAlaLysSer 1181
Db 3216 CCCCATGTGGCGCACCGCCACCGCCACCGCGGACGCTGTCCCTGCACACAGGGAC 3275
QY 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201
Db 3276 TCGGTGACCTGGCCGAGCTGGTGCCCGGCTGGCGCCCAACCCCGGCGCGCTGGAAG 3335
QY 1202 SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db 3336 GCGGACGCGCGCGCGCGCGGCGATGAGACTGCAATGGCAGAGATGCCACG-----ATC 3389
QY 1220 AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAspAsnAspGlu 1238
Db 3390 GCCAAAGACGTCTTCACCAAGATGGCGGACCGCGGGGATCCGGGAGGATGAGAGGAA 3449
QY 1239 GlyAsnLeuSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCys 1258
Db 3450 ATGACTACACCCCTGTGCTTCGCGCTCCGCAAGATGATCGACTATAAGCCGCACTGG 3509
QY 1259 CysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeu 1278
Db 3510 TGGAGGTCCGGAAGACTGTGTCTTACCTCTTCTCCGAGAACAGGTTCCGGGTC 3569
QY 1279 LeuCysHisArgIleIleThrHisLysMetPheAspHisValLeuValIleIlePhe 1298
Db 3570 CTGTGTCAACCATATATTGCCCAAACTCTTGACCTAGCGTCCCTGCGCTTCATCTTT 3629
QY 1299 LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318

D	b	3630	CTCAACTGCATCACCATCGCCCTGGAGCGGCTCAGATCGAGGCCGGCAGCAACCGAACGC	3689
O	y	1319	ILEPHELEUTHrLeuSerAsnTyrILEPHEThrAlaValPheLeuAlaGluMetThrVal	1338
D	b	3690	ATCTTCTCACCGGTGTCCAATCAATCTTCACGCGCCATCTTCGTGGCGAGATGACATTG	3749
O	y	1339	LYSValAlaAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn	1358
D	b	3750	AAGTAGTCTCGCTGGGCTGTACTTCGGCGAGCAGCGGTACCTACGACAGCTGGAAAC	3809
O	y	1359	ValLeuAspGlyLeuLeuValLeuLeuSerValILEAspILELeuValSerMetValSer	1378
D	b	3810	GTGCTGGATGGCTTCTTGTCTTCGTCCATCATCGACATCGTGTTCCCTGGECTCA	3869
O	y	1379	AspSerGlyThrLySILELeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
D	b	3870	GCGGGGGGAGCCAAAGATCTTGGGGGTCTCCGAGTCTTGCGGCTCTGCGCACTTACGC	3929
O	y	1399	ProLeuArgValILESerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1418
D	b	3930	CCCTGCGTGCATCAGCCGGCGCCGGGCTGAACTGTGTGTGGAACACTCATCTCC	3989
O	y	1419	SerLeuLysProILEGlyAsnILEValValILECysCysAlaPhePheILEIlePheGly	1438
D	b	3990	TCCCTCAAGCCCATCGGCAACATCGTCTCATCTGCTGTGCTTCTTCATCATCTTTGGC	4049
O	y	1439	ILELeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1458
D	b	4050	ATCCTGGAGAGTGACAGCTCTTCAAGGCAAGTCTTACCACACTGTCTGGCGTGAGACCCGC	4109
O	y	1459	AsnILEThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr	1478
D	b	4110	AACATCAACCAACCGCTCGGACTGCATGCGCCGCAACTACCGCTGGTCCATCACAATAC	4169
O	y	1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
D	b	4170	AACTTGCACAACCTGGGCCAGGCTCTGATGTCCCTTTGTCCTGGCATCCAAAGATGCT	4229
O	y	1499	TrpValAspILEMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProILEMet	1518
D	b	4230	TGGGTGAACATCATGTACAAATGGAATGGATGCTGTGTGTGGACCAAGCCTGTGACC	4289
O	y	1519	AsnHisAsnProTrpMetLeuLeuTyrPheILESerPheLeuILEValAlaPhePhe	1538
D	b	4290	AACCAACAACCCCTGGATGCTGCTAATTCATCTCTTCCGTCTCATCGTCAAGCTTCTT	4349
O	y	1539	ValLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGln	1558
D	b	4350	GTGCTCAACATGTTTGTGGGTGTCTGTGTGAGAACTTCCACAAGTGCCGGCAGCAACAG	4409
O	y	1559	GluGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArg	1578
D	b	4410	GAGGCTGAAGAGGCAACGGCGCGTGAAGAGAAGCGGCTGCGGCGCTGGAGAAGAGCGC	4469
O	y	1579	ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer	1598
D	b	4470	CGG-----AAGGCCAGCGGCTGCCCTAATATGACCACTATTGT	4508
O	y	1599	ArgPheArgLeuLeuValHisILEuCysThrSerHisTyrLeuAspLeuPheILEThr	1618
D	b	4509	CACACCGGCTGCTCATCCACTCCATGTGCACACCAGCCACTACTGGAACATCTTCATCAC	4568
O	y	1619	GlyValILEGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnILE	1638
D	b	4569	TTTCATCATCTGCCTCAACGTTGTCACCATGTCCCTGGAGCACAATCAGCCACGTC	4628
O	y	1639	LeuAspGluAlaLeuLysILECysAsnTyrILEPheThrValILEPheValPheGluSer	1658
D	b	4629	CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCACCACTGTCTTGTGTGAGAGCT	4688
O	y	1659	ValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeu	1678
D	b	4689	GTGCTGAAGCTGTGTCATTGTGTCTGAAGGCGCTTCTTCAAGAGACCGATGAAACCACTG	4748

Qy	1679	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1698
Db	4749	GACCTGGCCATTGTGCTACTGTCACTGATGGGATCAACCTGGAGAGATCGAGATCAAT	4808
Qy	1699	LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1718
Db	4809	GCGGCCCTGCCCATCATCCCAACCATCATCCGCATCATGAGGGTCTCGCCGATTGCCGA	4868
Qy	1719	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln	1738
Db	4869	GTGCTGAAGCTGTGAAGATGGCCACAGGAATCGGGCCCTGTGACACAGGTGTGCAA	4928
Db	1739	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla	1758
Db	4929	GCTTGCCCGAGGTGGGCAACCTGGGCCCTCTCTTCACTGTGCTCTTTCATCTATGCT	4988
Qy	1759	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1778
Db	4989	GCTCTCGGGGTGAGCTCTTTGGGAAGCTGTGTCGAACGACGAAACCCGTGCGAGGGC	5048
Qy	1779	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1798
Db	5049	ATGAGCCCGCATGCCACCTTCAGAACTTCGCATGGCTTCTCACACTCTTCCAGGTC	5108
Qy	1799	SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys---AspGln	1817
Db	5109	TCCACGGGTGACAACTGGAACGGGATCATGAAGACACGCTGCGGACTGCACCCACGAC	5168
Qy	1818	GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal	1835
Db	5169	GAGCGAGCTGCCTGAGCAGCCTGAGTTGTGTGCGCGCTGTACTTCGTGACTTCGTG	5228
Qy	1836	LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu	1855
Db	5229	CTCACCGCGAGTTCGTGCTCATCAACGTGTGTGTGCTGTGCTCATGAAGCACTTGAC	5288
Qy	1856	GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMet	1875
Db	5289	GACAGCAACAGAGAGCGCAGAGACGCCGAGATGATGCCGAGCTCGAGCTGAGATG	5348
Qy	1876	---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGly	1894
Db	5349	GCCCATGGCTGGGCCCTGGCCCGAGGCTGCCTACCGGCTCC-----	5390
Qy	1895	ValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThrAlaHis	1914
Db	5391	-----CCGGCGCCCTGGCCGAGGCGCG---	5414
Qy	1915	IleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValPro-----	1930
Db	5415	---GGAGGGGCGGGCGGGG- GGGGACACCGAGGCGGCTGTGCGGCGCTGACTC	5470
Qy	1931	-----HisProGluGluValProValPro	1938
Db	5471	GCCTGCCAGAGCTCTTGAGGGGAGCTGACCATCATGACAACTGTGGGCTCCAT	5530
Qy	1939	LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro	1958
Db	5531	CTTCCACCACACTACTCTCGCCTGCGGCTGCAAGAAGTGTCA-----CCA	5575
Qy	1959	AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly	1978
Db	5576	CGACAA-----GCAAGAGGTGACGCTGGCTGACACGGA	5608
Qy	1979	TrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp	1998
Db	5609	GGCCTTCTCCCTGAACACTCAGACAGAGTCTGTCCATCTGTGCTGGTGACGACCTGAGTCT	5668
Qy	1999	ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla	2018
Db	5669	CGAGGA-----CCCAACAGCCTG	5686


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QY 2019 ProThrTrpGlyAlaIleProLys----- 2026
Db 5687 CCCACCTGG-----CCGCAAGACAGCAAGGCTGAGCTGGACCCACCTGAGCCCAT 5737
QY 2027 ---LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAla 2045
Db 5738 GCGTGTGGAGACCTGGGGCAATGCTTCTTCCCTTGT-CCTCTACGGCCGTTCGCCGG 5796
QY 2046 ILeArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGlu 2065
Db 5797 ATCCAGAGAACTTCTGT---GTGAGATGAGAGAGATCCCAT-----TCAACC 5841
QY 2066 ValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSerIle 2085
Db 5842 CTGTCCGCTCCTGGCTGAACATGACA----- 5868
QY 2086 GlnValGlnGlnArgSerGlyIleGlnSerIleValSerIleArgLeuProAla 2105
Db 5869 -----GCAGTCAAGCACCCCAAGTCCCTTCT 5895
QY 2106 ProCysProGlyLeuGluProSerTrpAlaIleAspProProGluThrArgSerSerIleu 2125
Db 5896 CCC-----CGATGCTTCCAGCC----- 5913
QY 2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2145
Db 5914 -----CTCTCCTGCCATGCCAGCCGAGTTCTTCCACCTG 5949
QY 2146 ProLeuPhePro-----ArgAspLeuIleCysTyrservalGluThrGlnSerCys 2163
Db 5950 CAGTGTCTGCCAGCCAGAAAGCCAGAAAAGGCACTGGCACTGGAACCTCCCAAGA 6009
QY 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys 2183
Db 6010 TTGCGCTG-CAGGGCTCTGGGCATCT-----CTGCGGTACCAAGGTTCACTGT 6059
QY 2184 Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu 2199
Db 6060 ACCCTCCTCCGGCAGGCCACCGGAGCAGACACGTGCTGAGCGCCAGCCACAGCAG-CTC 6118
QY 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProSer 2219
Db 6119 CGCGGGCAGCCTGCAGACCACGCTCGAGACAGCCTGACCTGAGCGACAGCCCGGCG 6178
QY 2220 IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly 2237
Db 6179 -----TGCCTTGGGGCGCCCGCCTGCTCCAGAGACCCGGGCG 6217
QY 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257
Db 6218 CGGCCTGTCCCCCGCGCTGCCCGCCTGAGCCTGCGCGCGCGGCGCTTTCAGCCT 6277
QY 2258 LeuAspSerThrAlaAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
Db 6278 GCGGGGCTGCCGGCGCATCAGCGCAGCCACAGCAGCGGGGCTCCACCAAGCCGGGCTG 6337

RESULT 13
US-10-425-800-1
; Sequence 1, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

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; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-10-425-800-1

Alignment Scores:
Pred. No.: 0
Score: 5420.00
Percent Similarity: 61.74%
Best Local Similarity: 51.82%
Query Match: 45.06%
DB: 16

US-09-611-257A-24 (1-2287) x US-10-425-800-1 (1-6816)

QY 12 ThrProProleuAArgGlySerAlaArgProSerSerAspPro----- 25
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Db 207 TCCCCCGCCCTCTCATCTGCAGCAGCCGCCAGCCCTGAGCCAGAGTACCAACGAGCAG 266
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 267 CCCGGACCCCGG----- 278
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 279 -----AGCCCCCATCTCTCCCGCCAGGCGCTGAGAGACCTCTTGATGAGCT----- 326
QY 66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 327 -----GATCCT-----CATGTCCACAC 344
QY 86 ProAlaLeuAlaProValValPhePheTyrLeuSerGluAspSerArgProArgSerTrp 105
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 345 CCAGACCTGGCGCCTATGCTCTTCTGCTCGCAGACAGACCACAGCCCGGAACTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 405 TGCATCAAGATGGTGTGCAACCCGCTGTTGAATGTGTCAGCATGCTGTGATCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 465 AACTGCGTAGCACTTGCGATGATACAGCCGTCGAGCAGCATGAGACTGCTTCGACCGC 524
QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 525 TGCAAGATCCTGCAGGCTTTGTGATGACTTCATTATCTTCTTGCCATGAGATGGTG 584
QY 166 ValLysMetValAlaLeuGlyIlePheGlyLysCysTyrLeuGlyAspThrTrpAsn 185
   ::::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 585 CTCAGATGGTGGCCCTGGGATTTTGGCAAGAAGTCTACCTCGGGGACATGGAAC 644
QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
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Db 645 CGCCTGATTTCTTCATCGTCATGGCAGGAGTGTGAGTACTCCCTGGACCTTCAGAAC 704
QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
   :::::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 705 ATCAACCTGTACGCATCCGACCCGTGCGCTCTGAGGCCCTCAAAAGCATCAACCGC 764
QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 765 GTGCCAGATATGGGATCCTGTGAACCTGCTCCTGACACACTGCCCATGTGGGGAAT 824
QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 825 GTCTGCTGTCTCTCTTCTTGTCTTCTTCATCTTTGGCATCATAGGTGTGACTCTGG 884
QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 885 GCGGGCCTGCTGCGTAAACCGCTGCTTCTTGAGAGAGAACTTACCATCAACGAGGATGTG 944

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Oy		286	AspleuGluproTyrTyrglnThrGluasnGluaspGluSerProphelIeCysSergln	305
Dd		945	GCCTTGCCCCCATACTACCAAGCCGGAGAGATGATGATGCCCTTCATCTGCTCCCTG	1004
Oy		306	ProArgGluasnGlyMetArgSerCysArgServalProThrLeuArgglyglgly	325
Dd		1005	TCCGGCGACAATGGGATATAGGGCTGCCATGAGATCCCCGCTCAAGAGCAG-----	1058
Oy		326	GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer	339
Dd		1059	---GGCCGTAGTGTCTGCTCTGCCAAGACGACGCTTACGACTTTGGGGCGGCCAG	1115
Oy		340	SerSerAsnthrthr----CysValasntPrasngIntYrtyrThrAsnCysSeraIa	357
Dd		1116	GACCTCAATGCCAGCGGCTGTGTGTCAACTGGAACCGTTACTACAATGTGTGCCGACG	1175
Oy		358	GlyGluHisAsnProPhelysglyAlaIleasnPhaspsnllleglYtYralaTrpile	377
Dd		1176	GCGAGCGCCAACCCCAAGAGGTGCCATCACTTGTGAACAATCGGTTATGCTTGATT	1235
Oy		378	AlaIlepheglnValIlethrLeuglnglyTyrvalAsprIleMetTyrpheValmetAsp	397
Dd		1236	GTCATCTTCCAGGTGATCATCTGGAAGGCTGGGTGAGATCATGTACTACGTATGGAT	1295
Oy		398	AlahisSerpheTyrAsnphelIeTyrpheIleLeuleuIlelleValglySerphe	417
Dd		1296	GCTCACTCCTTACAACTTCATCTACTTCATCTGCTTATCATAGTGGGCTCTTCTTC	1355
Oy		418	MetIleasnLeuCysLeuValValIlealathrglnPheSerglutThrylglnArgglu	437
Dd		1356	ATGATCAACCTGTGCTGCTGTTCATAGCAGACCAGTTCGGAAGACCAAGCAAGCGGAG	1415
Oy		438	SerGlnLeuMetArggluGlnArgValArgpheLeuSerAsnaIaserThrLeualaSer	457
Dd		1416	CACCGCTGATGCTGGAGCAGCGGACGCTACTGTCC--TCCAGCACGGTGGCCAGC	1472
Oy		458	PheSergluProglySerCysTyrGlnGluLeuleuLyleuTyrrleuValTyrIleuArg	477
Dd		1473	TACGCCGAGCCTGGCGACTGCTACGAGAGATCTTCCAGTATGTCTGCCACATCTCGGC	1532
Oy		478	LysAlaalargArgLeualaglnValSerArgalaIeglyValArgAlaglyLeu	497
Dd		1533	AAGGCCAAGCGC-----CGCGCCTGGGCTTACCAGGCGCTTGcAg	1574
Oy		498	SerSerProValAlaArgSerglynglnuProGlnProserGlySerCystHrArgSer	517
Dd		1575	AGC-----	1577
Oy		518	HlsArgArgLeuServalHisIleuValHisHisHisHisHisHisHisIeTyr	537
Dd		1578	---CGCGCCAGGCCCTG-----	1592
Oy		538	HisLeuGlyasnGlyThrLeuArgValProArgAlaserProglutIleglnAspArgAsp	557
Dd		1593	-----GGCCCGAG-----	1601
Oy		558	AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly	577
Dd		1602	-----GCCCGCGCCCCGCCMAACCTGGGCCC-----	1628
Oy		578	ProProArgGlyAlagluServalHisSerPheTyrHisAlaAspCysHisLeuGluPro	597
Dd		1629	-----CACGCCAAG-----GAGCCC	1643
Oy		598	ValArgCysGlnAlaProProProArgCysProSerglnAlaserGlyArgThrValgly	617
Dd		1644	CGGCACTACCACTGTGCCCCGAACAATAAGCCCCCTGATGCG-----	1685
Oy		618	SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys	637
Dd		1686	-----ACGCCCCACAGC-----	1697

QY	638	AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro	657
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Db	1698	---CTGGTCAG-----CCCATCCCGCCACGCTGGCTTCC-----	1730
QY	658	ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys---	676
Db	1731	-----:::	
QY	677	HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro	696
		:::	
Db	1758	CATGAGACGGCGCGCGCCCTCGGGCCTGGGACGACCACTCGGGCCAGAGGGCTCG	1817
QY	697	AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal	716
		:::	
Db	1818	GGCTCC-----GGAGCTCCGCTGTGGCGAGGACGAGCG-----	1853
QY	717	MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp	736
		:::	
Db	1854	-----GATGGGAGCGGGCC-----CGAGCAGCGAGACGAGCCTCTCAGAA	1898
QY	737	LeuArgAspProHisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSer	756
		:::	
Db	1899	CTGGGAGAGGAGGAGGAGGAGGAGCAG-----GCCGATGGGGCG	1940
QY	757	SerValLeuAla-----PheTyrArgLeuIleCysAspThrPheArgLysIleValAsp	774
		:::	
Db	1941	GTCTGCTGTGCGGGGATGTGTGGCGGGAGACGCGAGCCAAAGCTGCGCGCATCTGGAC	2000
QY	775	SerLysTyrPheGlyArgGlyIleMetIleAlaIleValAsnThrLeuSerMetGly	794
		:::	
Db	2001	AGCAAGTACTTCAACCGGGCATCATGATGCCATCTCGGTCAACACCGTCAGCATGGGC	2060
QY	795	IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal	814
		:::	
Db	2061	ATCAGACACCAAGAGCAGACCGGAGAGCTGACCAACATCTGGAGATCTGCATGTGTC	2120
QY	815	PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGly	834
		:::	
Db	2121	TTCACCAGCATGTTCCTCGGAGATGATCCTGAAGCTGGCTGCATTTGGGCTTTCGAC	2180
QY	835	TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyrGlu	854
		:::	
Db	2181	TACCTGCGTAACCCCTACAACATCTTCGACAGCATCATGTGCATCATCAGCATCGGAG	2240
QY	855	IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal	874
		:::	
Db	2241	ATCGTGGGCGAGCGGACGCTGGCTGTGCTGCGGACCTTCGGCTGTCGCGTG	2300
QY	875	LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr	894
		:::	
Db	2301	CTGAAACTGTGCGCTTCATGCTCGCTCGCGCGCAGCTGTGTGCTCATGAAGACC	2360
QY	895	MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle	914
		:::	
Db	2361	ATGACACACGTGCGCACCTTCGCACTGCTCATGCTCTTCATCTTCATCTTCAGCATC	2420
QY	915	LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp--GlyAspThrLeu	933
		:::	
Db	2421	CTTGGATGCATATTTTGGCTGCAATTCAGCCTCCGACGAGCACTGGAGACACGGTG	2480
QY	934	ProAspArgLysAsnPheAspSerLeuLeuTyrPalaIleValThrValPheGlnIleLeu	953
		:::	
Db	2481	CCCGACAGGAAGAACTTGCACCTCGCTGTGGGCCATGTCATCTGTTCACATCTTC	2540
QY	954	ThrGlnGluAspTyrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrPala	973
		:::	
Db	2541	ACCCAGAGAGACTGGAACGTGTTCTCTACAATGCGATGGCTCCACTTCTCCCTGGGCC	2600
QY	974	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal	993
		:::	
Db	2601	TCCCTTACTTTGTGCGCCTCATGACCTTCGGCACTATGTGCTTCAACCTGTGTG	2660
QY	994	AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro	1013

Db	2661	GCCATCCTGGTGAGGCGCTCCAGCGGAGGCTGACGCCAATCGCTCTACTCGACGAG	2720
QY	1014	AspPhePheSerProSerVal-----AspGlyAsp	1023
Db	2721	GACCAGAGCTCATCCACATGAGAAGATTGTATAAGCTCCAGGAAGCCCTGGACACGACG	2780
QY	1024	GlyAspArgLysLysArgLeuAlaLeuValAlaLeuGlyLysAlaGluLeuArgLys	1043
Db	2781	GGAGATCCCAAG-----CTGTGCCAATCCCATGACCCCCCAATGGGCACCTGACCC	2834
QY	1044	SerLeuLeuProProLeuIleIleHisThr-----AlaIleThrProMetSer	1059
Db	2835	AGTCTC-----CCACTGGGTGGGCACCTAGTCTGTGGGGCTGCGGACCTGCC---	2885
QY	1060	HisProLysSerSerSerThrGlyValGlyLysAlaLeuGlySerGlySerArgArgThr	1079
Db	2886	---CCCCGACTCTCACTGCAGCCGAGCCCATGCTGTGGTCCCTGGGCTCCGGAAGAGC	2942
QY	1080	SerSerSerGlySerAlaGluProGlyAlaAlaHisIleGluMetLysCysProProSer	1099
Db	2943	AGTGCATGTCCTA-----GGAGGATGAGCTATGACCAGCGCTCCCTGTCCAGC	2993
QY	1100	AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer	1119
Db	2994	TCCCGAGCTCTACTACGGGCCATGGGGCCGACGGCGGCTGGGCCAGCCGCTCGCTCC	3053
QY	1120	SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyLysArg	1139
Db	3054	AGCTGGAAC-----AGCCTCAAGCAAGCCGCGTGGCGGAGCAT	3095
QY	1140	ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu	1158
Db	3096	GAGTCCCTGCTCTTGGGAGCGCGGCGGCGGCGGCGGCTGCGAGTTGCGCGAC	3155
QY	1159	Glu-----AspArgAlaSerProAlaGlySerAspHis-----	1169
Db	3156	GAGGGCGCGCGCGCGCGCACCCCTGCACACCCCAAGCCCAACACATTATCAACGGG	3215
QY	1170	-----ArgHisArgGlySerLeuGluArgGluAlaLysSer	1181
Db	3216	CCCCATCTGGCGCACCGCCACCGCCACACCGCCGAGCGCTGCCCTCGACAACAGGAC	3275
QY	1182	SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg	1201
Db	3276	TGGGTGACCTGGCCGAGCTGTGTCGCCGGTGCGGCCCAACCCCGGCGCTTGAGG	3335
QY	1202	SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu	1219
Db	3336	GCGGACGCGCGCGCCCGCGGCATGAGACTGCAATGGCAGATGCCAGC-----ATC	3389
QY	1220	AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAsnAspGlu	1238
Db	3390	GCCAAAGACGTCTTACACAGATGGCGACCGCGGGATCGCGGAGATGAGAGGAA	3449
QY	1239	GlyAsnLeuSerLysGlyLysArgGlnGlnAlaTrpValArgSerArgLeuProAlaCys	1258
Db	3450	ATCGACTACACCCCTGTGCTCCGCGCTCCGCAAGATGATGCACTATTAAGCCGACTGG	3509
QY	1259	CysArgGluArgAspSerTrpSerAlaTyrllePheProProGlnSerArgPheArgLeu	1278
Db	3510	TGCGAGGTCCGCGAAGACTGTGTCTACCTCTTCTCCGAGAACAAGTTCCGGGTTC	3569
QY	1279	LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe	1298
Db	3570	CTGTGTCAAGACCATTAATGCCCACAACTCTTCGACTAGTGTCTTGCCCTTCATCTTT	3629
QY	1299	LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg	1318
Db	3630	CTCAACTGCATCACCATCGCCCTGAGCGGCTCAGATCAGAGCCGGCAGACCGAAGC	3689
QY	1319	IlePheLeuThrLeuSerAsnTyrllePheThrAlaValPheLeuAlaGluMetThrVal	1338

Db	3690	ATCTTTCTCACCGGTGTCCAACTACATCTTCACGGCCATCTTCGTGGCGCAGATGACATTG	3749
Qy	1339	LysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn	1358
Db	3750	AAGTAGTCTCGCTGGCGCTGTACTTCGGCGAGCAGCGGTACTACGACAGCTGGAAC	3809
Qy	1359	ValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSer	1378
Db	3810	GTGTGATGAGCTTCTTGTCTTCGTGTCATCATCGACATCGTGTGTCTTCCTGACCTCA	3869
Qy	1379	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
Db	3870	GCCGGGGAGCCAGATCTTGGGGGTCTCCGAGTCTTGCGGCTCCGCGCACCTTAGC	3929
Qy	1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGlyThrLeuMetSer	1418
Db	3930	CCCCGCGTGTATCAGCCGGCGCCGGGCTGAAGCTGTGTGTGAGACACTCATCTCC	3989
Qy	1419	SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly	1438
Db	3990	TCCCTCAAGCCCATCGGCAACATCGTGTCTATCTGCTGTGCTTCTTCATCATCTTTGGC	4049
Qy	1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1458
Db	4050	ATCCTGGAGTGCAGCTCTTCAGGGGCAAGTTCTACCACTGTCTGGGCGTGACACCCGC	4109
Qy	1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr	1478
Db	4110	AACATCACCAACCGCTCGACTGCATGCGCGCAACTACCGCTGGTCCATCACAATAC	4169
Qy	1479	AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
Db	4170	AACTTCGACCACTGGGGCCAGGCTGTGATGTCCCTTTGTCTTGCGCATCCAAGATGT	4229
Qy	1499	TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet	1518
Db	4230	TGGGTGAACATCATGTACAATGAGACTGGATGCTGTGCTGTGAGACCAGCCTGTGACC	4289
Qy	1519	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe	1538
Db	4290	AACACAAACCCCTGGATGCTGTACTTCACTCTTCCTGCTCATCGTCACTTCTTT	4349
Qy	1539	ValLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGln	1558
Db	4350	GTGCTCAACATGTTTGTGGGTGTCGTGTGAGAACTTCACAAGTGC CGGACACACAG	4409
Qy	1559	GluGluGluGluAlaArgArgArgGluLysArgLeuArgArgLeuGluLysLysArg	1578
Db	4410	GAGGCTGAAGAGGACGGCGGCTGAGGAGAAGCGGCTGCGGCTGGAGAAGAAGCGC	4469
Qy	1579	ArgSerLysGluLysGlnMetalaglAlaGlnCysLysProTyrTyrSerAspTyrSer	1598
Db	4470	CGG-----AAGGCCAGCGGCTGCCCTACTATGCCACTATTGT	4508
Qy	1599	ArgPheArgLeuLeuValHisIleLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1618
Db	4509	CACACCGGCTGTCTATCCACTCCATGTGCACCAACCACCTAGACATCTTCATCAC	4568
Qy	1619	GlyValIleGlyLeuAsnValValThrMetalMetGluHisTyrGlnGlnProGlnIle	1638
Db	4569	TTCATCATCTGCTCAACGTGTGCACCATGTCCCTGGAAGCACTACAATCAGCCACGTCC	4628
Qy	1639	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer	1658
Db	4629	CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCACCACTGTCTTGTGTGAGGGCT	4688
Qy	1659	ValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeu	1678
Db	4689	GTGCTGAAGCTGTGGCATTTGTGTCTGAGCGGCTTCTTCAAGAACCGATGGAACAGCTG	4748
Qy	1679	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1698
Db	4749	GACCTGGCCATTGTCTACTGTCAGTCAATGGGCATCACCTGGAGGAGATCGACATCAAT	4808

QY 1699 LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1718
DB 4809 GCGGCCCTGGCCCATCAATCCACCATCATCCGATCATGAGGTTCTGCGATTGCCCGA 4868
QY 1719 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738
DB 4869 GTGTGAAGCTGTTGAAGATGGCCACAGGAATGGCGGCCCTGTGTGACACGGTGTGCAA 4928
QY 1739 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1758
DB 4929 GCTTTGCCCCAGGTGGGCAACCTGGGCTCCTTCATGTGTCTCTTCATCTATGCT 4988
QY 1759 AlaLeuGlyValGlyLeuPheGlyAspLeuGlyCysAspGlyThrHisProCysGlyGly 1778
DB 4989 GCTCTCGGGGTGAGCTCTTTGGGAAGCTGTGTGCAACGACGAGAACCCGTGCGAGGGC 5048
QY 1779 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1798
DB 5049 ATGAGCCGGCATGCCACCTTGAGAACTTCGGCATGGCTTCTCCACACTCTTCAGGTC 5108
QY 1799 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys--AspGln 1817
DB 5109 TCACGCGGTGACAACCTGGAACGGGATCATGAAGACACGCTGCGGACTGCACCCACGAC 5168
QY 1818 GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal 1835
DB 5169 GAGCGCAGCTGCCTGAGCAGCTGCAGTTGTGTGCGCGCTGACTTCGTGAGCTTCGTG 5228
QY 1836 LeuThrAlaGlnPheValLeuValAsnValAlaValIleAlaValLeuMetLysHisLeuGlu 1855
DB 5229 CTCACCGCGCAGTTCGTGTCTCATCAACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5288
QY 1856 GluSerAsnLysGlyAlaLysGlyGlyAlaGlyLeuGlyAlaGlyLeuGlyLeuMet 1875
DB 5289 GACAGCAACAAGAGAGCGCGCAGAGACGCGGAGATGATCCGAGCTCGAGCTGAGATG 5348
QY 1876 ---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpGly 1894
DB 5349 GCCCATGGCTGGCGCTGGCCCGAGGCTGCCTACCGGCTCC----- 5390
QY 1895 ValGluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrThraHis 1914
DB 5391 -----CCGGCGCGCCCTGGCCGAGGGCGG--- 5414
QY 1915 IleGlyAlaAlaSerGlyPheSerLeuGluHisProThrMetValPro----- 1930
DB 5415 ---GGAAGGGCGGGCGGGCGG--GGGCGACACCGAGGGCGGCTGTGTGCGCGGCTGTACTC 5470
QY 1931 -----HisProGluGlyValProValPro 1938
DB 5471 GCCTGCCCAGAGCTCTTGAGAGGGGAGCTGACCATCATCGAACACCTGTGGGCTCCAT 5530
QY 1939 LeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1958
DB 5531 CTTCACCACTACTCCTCGCTGGCTGGCTGCAAGAGTGTCA-----CCA 5575
QY 1959 AsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGly 1978
DB 5576 CGAACA-----GCAAGAGGTGACAGTGGGTGAGACGGA 5608
QY 1979 TrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAsp 1998
DB 5609 GGCCTTCTCCCTGAACCTCAGACAGGTCCTGCTCCATCTGTGTGGGTGACGACCTGAGTCT 5668
QY 1999 ThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAla 2018
DB 5669 CGAGGA-----CCCAACAGCCTG 5686
QY 2019 ProThrTrpGlyAlaIleProLys----- 2026
DB 5687 CCCACCTGG-----CCGCAAGGACAGCAAGGTTGAGCTGAGCCACCTGAGCCCAT 5737

QY 2027 ---LeuProProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaAla 2045
DB 5738 GCGTGTGAGAGACTGGCGGAATGCTTCTTCCCTTGT-CTCTCAAGCGCGCTTCGCGG 5796
QY 2046 IleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGlu 2065
DB 5797 ATCCAGAGAACTTCTGT---GTGAGATGAGAGATCCCAT-----TCAAACC 5841
QY 2066 ValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSerIle 2085
DB 5842 CTGTCCGGTCTGTGCTGAACATGACA----- 5868
QY 2086 GlnValGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAla 2105
DB 5869 -----GCAGTCAAGCACCCCAAGTCCCTTCT 5895
QY 2106 ProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSerLeu 2125
DB 5896 CCC-----CGGATGCTCCAGCC----- 5913
QY 2126 GluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2145
DB 5914 -----CTCTCCTGCCCATGCGACCGGAGTTCTTCCACCTG 5949
QY 2146 ProLeuPhePro-----ArgAspLeuLysLysCysTyrSerValGluThrGlnSerCys 2163
DB 5950 CAGTGTCTGCCAGCCAGAAAGGCCAGAAAGGACACTGGCACTGGAACCTCCCCACAGA 6009
QY 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCys 2183
DB 6010 TTGCGCTG-CAGGCTCTCTGGGCATCT-----CTGCGGTCAACCAAGGTTCAACTGT 6059
QY 2184 Leu-----AspSerGlySerGlnProArgLeuCysProSerProSerSerLeu 2199
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QY 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSer 2219
DB 6119 CGCGGGCAGCCTGCAGACCAACGCTCGCGGCTGAGCCTGACCTGAGCGACAGCCCGGCG 6178
QY 2220 IleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----ProGly 2237
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QY 2238 ValCysLeuArgArgAlaProAlaSerAspSerLysAspProSerValSerSerPro 2257
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QY 2258 LeuAspSerThrAlaSerProSerProLysLysAspThrLeuSerLeuSerGlyLeu 2277
DB 6278 GCGGGGCTGCGGGCGCATCAGCGCAGCACAGCAGCGGGGCTCCACAGCCCGGCTG 6337

RESULT 14
US-09-935-541-3
; Sequence 3, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

! NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-935-541-3

Alignment Scores:

Pred. No.:	0	Length:	6855
Score:	5420.00	Matches:	1228
Percent Similarity:	61.97%	Conservative:	235
Best Local Similarity:	52.01%	Mismatches:	500
Query Match:	45.06%	Indels:	402
DB:	9	Gaps:	63

US-09-611-257A-24 (1-2287) x US-09-935-541-3 (1-6855)

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QY      26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArgSer 45
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Db      267 CCGGACCCCG----- 278
QY      46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
      |||||
Db      279 -----AGCCCCCATCTCCCGCCAGGCGCTGAGAGAGCCTTGATGAGCT----- 326
QY      66 AlaGlySerThrGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
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Db      327 -----GATCCT-----CATGTCCACAC 344
QY      86 ProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
      |||||
Db      345 CCAGACCTGGCGCTATTGCTCTTCTGTGCTGCAGACAGACCACGCCCGGAACTGG 404
QY      106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
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QY      126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
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Db      465 AACTGCGTGACACTTGCGCATGTACACAGCCGTGCAGACATGACTGCTGTCCGACCGC 524
QY      146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
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Db      525 TGCAAGATCCTGAGGCTTTGTGATGACTTCATCTTATCTTTGGCCATGAGATGTG 584
QY      166 ValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsn 185
      ::::::|
Db      585 CTCAGATGTGGCCCTGGGATTTTGGCAAGAAGTGTACTCTGGGGAACATGGAAC 644
QY      186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
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Db      645 CGCTGATTCTTCATCTGTCATGTGAGGAGTGTGAGTACTCTTGACCTTGACGAAC 704
QY      206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
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QY      226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
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Db      765 GTGCCAGATATGCGGATCCTGTGAACCTGCTCTGACACACTGCCCATGTGGGGAAT 824
QY      246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
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Db      825 GTCTGTGCTGTCTCTTCTTTGTCTTCTTCATCTTTGGCATATAGTGTGACGCTGTG 884
QY      266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
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Db      885 GCGGGCCTGTGCTGAACCGCTGCTTCTTGAGAGAGAACTTACCATATCAAGGGGATGTG 944
QY      286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
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Db      945 GCCTTGCCCCCATACTACACAGCCGGAGAGATGATGAGATGCCCTTCATCTGTCTCTG 1004
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QY      306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGluGly 325
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Db      1005 TCGGGCCGACATGGGATATGGGCTGCCATGAGATCCCCCGCTCAAGAGACAG----- 1058
QY      326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
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Db      1059 --GGCCGTGAGTGTGCTCTGTCTCAAGAGACGACGCTTACGACTTTGGGGCGGCGCCAG 1115
QY      340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
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Db      1116 GACCTCAATGCCAGCGGCTCTGTGTCAACTGGAACCGTTACTACAATGTGTGCCGACG 1175
QY      358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIle 377
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Db      1176 GGCAGCGCCAAACCCACACAGGGTGCATCAACTTGACAACATCGGTTATGCTTGATT 1235
QY      378 AlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAsp 397
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Db      1236 GTCATCTTCCAGGTGATCATCTGGAAGCTGGTGAGATCATGTACTACGTGATGAT 1295
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Db      1296 GCTCACTCTTCTTACAACCTTACTTACTTCACTTCACTTATCATATAGTGGCTCTTCTTC 1355
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QY      458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
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QY      478 LysAlaIlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
      |||||
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QY      498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
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QY      538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
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QY      558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577
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QY      578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
      |||||
Db      1629 -----CACGCCAAG-----GAGCCC 1643
QY      598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
      |||||
Db      1644 CGGACTACCAAGCTGTGCCGCAACATAGCCCCCTGATGCG----- 1685
QY      618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
      |||||
Db      1686 -----ACGCCCACACC----- 1697
QY      638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
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QY 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCCGCCAGCTGCCCTTGCTGCCAG 1757
QY 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1758 CATGAGGACGCGCGGCCCTCGGGCTGGGAGCACCAGCTCGGGCCAGAGGGCTCG 1817
QY 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGGAGCTCCGCTGGTGGGAGAGCAGGCG----- 1853
QY 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -----GATGGGACGGGGCC-----CGGAGCAGCGAGGACCGGACCTCTCAGAA 1898
QY 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGGAGAGGAGGAGGAGGAGGAGCAG-----GCCGATGGGGCG 1940
QY 757 SerValLeuAla-----PheTyrArgLeuIleCysAspThrPheArgLysIleValAsp 774
Db 1941 GTTCGCTGTGCGGGGATGTGTGGCGGAGACGCGAACCTGCGCGGCATCTGGAC 2000
QY 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleuValAsnThrLysSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGGCATCATGATGCATCTGTCAACACCGTCAGCATGGGC 2060
QY 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
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Db 2121 TTCACGACATGTTTGGCCCTGGAGATGATCTGAACTGGCTGCATTTGGGCTCTTCGAC 2180
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QY 994 AlaIleLeuValGlyGlyPheGlnAlaGlyLysAspAlaThrLysSerGluSerGluPro 1013
Db 2661 GCCATCTCTGTGGAGGGCTTCAGGGGAGGGGTGACGCCAATCGCTCTACTCGGAAGAG 2720
QY 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023

Db 2721 GACCAGAGCTCATCCAAACATAGAAGATTGTGATAGCTCCAGGAAGCCTGGACAGCAGC 2780
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Db 2781 GGAGATCCCAAG-----CTGTGCCCAATCCCATGACCCCCCAATGGGCACCTGAGCCCC 2834
QY 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrProMetSer 1059
Db 2835 AGTCTC-----CCACTGGGTGGACCTAAGTCTGTGGGGCTGGCGGACCTGCC--- 2885
QY 1060 HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
Db 2886 ---CCCGACTCTCACTGCAGCCGAGCCCATGCTGTGGGCTGGGCTCCCGAAAGAGC 2942
QY 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099
Db 2943 AGTGTCATGTCTTA-----GGAGAGATGAGCTATGACCAAGCCTCCTGTCCAGC 2993
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Db 2994 TCCCGAGCTCTTAACGCGGCATGGGGCGGACGCGCGCTGGGCCAAGCCGTGCTCC 3053
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QY 1140 ArgSerLeuLeuSerGlyGlu--GlyGlnGluSerGlnAspGluGluGluSerSerGlu 1158
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QY 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3156 GAGGGGCGCGCGGGCGGACCCCTGCACACCCACACGCGCCACCATTCATCACGGG 3215
QY 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
Db 3216 CCCCATCTGGCGACCGGCCACCGCCACCGCGGAGCGTGTCCCTGCACAACAGGGAGC 3275
QY 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201
Db 3276 TCGGTGACCTCGGCCAGCTGTGCCCCGCGGTGGCGGCCACCCCGGGCGCCTGGAGG 3335
QY 1202 SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
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Db 3570 CTGTGTCAAGACCATTAATGCCCAACAACCTTCGACTACGTGCTGCTGCTCATCTTT 3629
QY 1299 LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318
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Db 3690 ATCTTCTCACCGTGTCACAACTACATCTTCACGGCCATCTTCGTGGGAGATGACATTG 3749
QY 1339 LysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn 1358

Db	3750	AAGGTAGTCTCGCTGGGCTGTACTTCGGCGAGCAGGCCGTACTTACGACAGACTGGAAAC	3809
QY	1359	ValLeuAspGlyLeuLeuValleuIleSerValIleAspIleLeuValSerMetValSer	1378
Db	3810	GTGCTGGATGCTTTCTTGTCTTCGTGTCCATCATGACATCGTGGTGTCCCTGGCTCA	3869
QY	1379	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1398
Db	3870	GCCGGGGAGCCAAAGATCTTGGGGGTCTCCGAGTCTTGGCGCTCTGCGCACCTTAAGC	3929
QY	1399	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1418
Db	3930	CCCCGTGCTGTATCAGCCGGGGCGCCGGCTGAAGCTGGTGGTGAGACACTCATCTCC	3989
QY	1419	SerLeuLysProIleGlyAsnIleValIleCysCysAlaPhePheIleIlePheGly	1438
Db	3990	TCCCTCAAGCCCATCGGCACATCGTCTCATCTGTGTGCTTCTTCATCATCTTTGGC	4049
QY	1439	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg	1458
Db	4050	ATCTGGAGTGCAGCTCTTCAAGGGCAAGTTCTACCACTGTCTGGCGTGACACCCGC	4109
QY	1459	AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr	1478
Db	4110	AACATCACCAACCGCTCGGACTGCATGGCCGCCAACTAACCGCTGGTCATCAAAATAC	4169
QY	1479	AsnPheAspAsnLeuGlyClnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly	1498
Db	4170	AACTTCGACACACTGGGCCAGGCTGTGATGTCCCTCTTGTCTGCGATCCAGATGGT	4229
QY	1499	TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet	1518
Db	4230	TGGGTGAACATCATGTACATGGACTGGATGCTGTGTGTGGACCAAGACCTGTGACC	4289
QY	1519	AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe	1538
Db	4290	AACCACAAACCCCTGGATGCTGTACTTCACTCTCTCTGCTCATCGTCAGCTTCTTT	4349
QY	1539	ValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHisGln	1558
Db	4350	GTGCTCAACATGTTGTGGGTGTCTGTGTGAGAACTTCCACAAGTGGCGGACAGCAG	4409
QY	1559	GluGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArg	1578
Db	4410	GAGGCTGAAGAGCAGCGGCGGTGAGGAGAAGCGGCTGGCGCTGAGAGAAGACGC	4469
QY	1579	ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer	1598
Db	4470	CGG-----AAGGCCAGCGGCTGCCCTACTATGCCACCATTTGT	4508
QY	1599	ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1618
Db	4509	CACACCCGGCTGTCTCATCCACTCCATGTGCACCAAGCCACTAACCCTGGACATCTTCAC	4568
QY	1619	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1638
Db	4569	TTCATCATCTGCTCAACGTGGTCAACCATGTCCCTGGAGACCTACAATCAGCCACGTCC	4628
QY	1639	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer	1658
Db	4629	CTGGAGACAGCCCTCAAGTACTGCAACTATATATGTTCACCACTGCTTTGTGTGGAGCT	4688
QY	1659	ValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeu	1678
Db	4689	GTGCTGAAGCTGTGGCATTTGGTCTGAGGCGCTTCTTCAAGAACCGATGAACAGCTG	4748
QY	1679	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1698
Db	4749	GACCTGGCCATTGTCTACTGTACGTATGGGCATCACCTGGAGAGATCGAGATCAAT	4808
QY	1699	LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1718
Db	4809	GCGGCCCTGCCCCATCAATCCACCATCATCCGCATCATGAGGGTTCTGCGCATTTGCCGA	4868

OY	1719	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln	1738
Db	4869	GTCGTGAAGCTGTGAAGAATGGCCACAGAAATGCCGGCCCTGTGCACACCGTGTGC	4928
OY	1739	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla	1758
Db	4929	GCTTTGCCCCAGGTGGGGCAACCTGGGCTCCTCATGTGCTCTTCTTCATCTATGCT	4988
OY	1759	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1778
Db	4989	GCTCTCGGGGTGAGCTCTTTGGGAGCTGGTCTGCAACGACGAGAACCCGTGGAGGC	5048
OY	1779	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1798
Db	5049	ATGAGCCCGGCATGCCACTTCGAGAACTTGCGCATGCGCTTCCTCACACTTCCAGGTC	5108
OY	1799	SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys--AspGln	1817
Db	5109	TCCACGGGTGACAATTGGAACGGATCATGAAGACACGCTGCGGACTGCACCACGAC	5168
OY	1818	GluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVal	1835
Db	5169	GAGCGACAGCTGCCTGAGCAGCAGCTGCAGTTGTTGTGCGCGCTGACTTGAGCTTCGTG	5228
OY	1836	LeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlu	1855
Db	5229	CTCACCGCGCAGTTCTGCTCATCAACGTGTGTGGTGTGCTGTCTCATGAACACCTGGAC	5288
OY	1856	GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMet	1875
Db	5289	GACAGCAACAAGAGGCGCAGAGAGACCGCAGATGATGCCAGCTCGAGCTGGAGATG	5348
OY	1876	--LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro--	1893
Db	5349	GCCCATGACCTGGGCCCCGGCCGAGGCTGCTACCGGCTCCC GGCGCC--CCTGGC	5405
OY	1894	-----GlyValGluGlyValAsnSerThrAsp-----	1902
Db	5406	CGAGGGCCGGAGGGCGGGCGGGCCGACACCGAGGGCGGCTGTGCCGGCGCTGC	5465
OY	1903	--SerProLysProGlyAlaPro-----HisThrThrAlaHisIleGlyAla	1917
Db	5466	TACTCGCCTGC-CCAGGAGAACCTGTGGCTGGACAGCGTCTTTAATCATCAAGGACTC	5524
OY	1918	AlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValProVal	1937
Db	5525	CTTGAGGG--GAGCTGACCAT-----CATGCACAACCTGTCCGGGCTC	5566
OY	1938	ProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu	1957
Db	5567	CATCTTCCACCACACTCTCTCGCCTGCGGCTGCAAGAAGTGTA-----	5611
OY	1958	ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGluHisArg	1977
Db	5612	CCACGACAA-----GCAAGAGGTGCACTGGGCTGAGAC	5644
OY	1978	GlyTyrGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla	1997
Db	5645	GGAAGCCTTCTCCCTGAACCTACAGACAGGTCTCTCCATCCTGCTGGGTGACGACCTGAG	5704
OY	1998	AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly	2017
Db	5705	TCTCGAGGA-----CCCCACAGC	5722
OY	2018	AlaProThrTrpGlyAlaIleProLysLeuProPro-----	2029
Db	5723	CTGCCACCTGG-----CCGCAAGAACAAGGTGAGCTGACCCACCTGAGCC	5773
OY	2030	-----ProGlyArgSerProLeuAlaGlnArgProLeuAlaArgGlnAla	2044
Db	5774	CATGCGTGTGGAGACCTTGGGCGAATGCTTCTTCCCTTGT-CCTTACAGGCGGCTTCGC	5832

QY 2045 AlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSer 2064
|||::: |||::: |||::: |||
Db 5833 CGGATCCAGAGAACTTCTGT--GTGAGATGAGAGATCCCAT-----TCA 5877
QY 2065 GluValSerGlyProSerCysProLeuThrArgSerSerPheTrpGlyGlySerSer 2084
:::||||| |||::: |||
Db 5878 ACCGTGTCGGTCTGCTGCAACATGACA----- 5907
QY 2085 IleGlnValGlnGlnArgSerGlyIleGlnSerIleValSerIleHisIleArgLeuPro 2104
5908 -----GCAGTCAAGCACCCCAAGTCCCT 5931
QY 2105 AlaProCysProGlyLeuGluProSerTrpAlaIleAspProProGluThrArgSerSer 2124
:::||||| |||::: |||
Db 5932 TCTTCC-----CGGATGCCCTCCAGCC----- 5952
QY 2125 LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2144
5953 -----CTCTCTGCCCATGCCAGCCGAGTTCTTCCACC 5985
QY 2145 GluProLeuPhePro-----ArgAspLeuIleCysIleCysTyrrSerValGluThrGlnSer 2162
|||::: |||::: |||::: |||
Db 5986 CTGCACTGTCTGCCAGCCAGAAAGGCCAGAAAGGCCACTGGCACTGGAACCTCCCA 6045
QY 2163 CysArgArgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleAlaValSer 2182
|||::: |||::: |||::: |||
Db 6046 AGATTGGCTG-CAGGGCTCTGGGCATCT-----CTGGGTCAACCAAGGTCAAC 6095
QY 2183 CysLeu-----AspSerGlySerGlnProArgLeuCysProSerProSerSer 2198
|||::: |||::: |||::: |||
Db 6096 TGTACCTCTCTCCGAGCGCCACCGGAGCGACACGTGCTGAGCGCCAGCCCAAGCAG- 6154
QY 2199 LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProIleValSerProPro 2218
|||::: |||::: |||::: |||
Db 6155 CTCCGGGGCAGCCTGCAGACCAAGCTCGAGGACAGCCTGAGCCGACAGCCCGG 6214
QY 2219 SerIleSerIleAspProProGluSerGlnGlySerArgProProCysSer-----Pro 2236
::: |||::: |||::: |||
Db 6215 GCG-----TGCCCTGGGGCGCGCGCGCTGCTCCAGGACCCCG 6253
QY 2237 GlyValCysLeuArgArgAlaProAlaSerAspSerIleAspProSerValSerSer 2256
|||::: |||::: |||::: |||
Db 6254 GGCCTGCTGTCCCGCGCTGCGCGCGCTGAGCTGCGCGCGCGCTTTCAG 6313
QY 2257 ProLeuAspSerThrAlaAlaSerProSerProIleValSerProIleSerLeuSerGly 2276
|||::: |||::: |||::: |||
Db 6314 CCTGGGGGGCTGCGGGCGCATCAGCGCAGCAGCAGCGGGGGCTCCACCGCCCGG 6373
QY 2277 Leu 2277
|||
Db 6374 CTG 6376

NAME/KEY: CDS
LOCATION: (192)..(6755)
US-10-425-800-3
Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5420.00 Matches: 1228
Percent Similarity: 61.97% Conservative: 235
Best Local Similarity: 52.01% Mismatches: 500
Query Match: 45.06% Indels: 402
DB: 16 Gaps: 63
US-09-611-257A-24 (1-2287) x US-10-425-800-3 (1-6855)
QY 12 ThrProProLeuArgGlySerAlaArgProSerSerAspPro----- 25
:::||||| |||::: |||::: |||
Db 207 TCCCGGCCCTCCTCATCTGCAGCAGCCCGCAGCGCTGAGCCAGAGTCAACCGAGCAG 266
QY 26 ProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAlaProArgSer 45
|||::: |||::: |||
Db 267 CCGGACCCCGG----- 278
QY 46 ArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAlaGly 65
|||::: |||::: |||
Db 279 -----AGCCCCCATCTCTCCCGCCAGGCTGAGGAGCCTTGGATGAGCT----- 326
QY 66 AlaGlySerThrGluAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyr 85
|||::: |||::: |||
Db 327 -----GATCCT-----CATGTCCACAC 344
QY 86 ProAlaLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTrp 105
|||::: |||::: |||
Db 345 CCAGACCTGGCGCTATGCTTCTTCTGCTGCGACAGACACACCGCCCGGAAGTGG 404
QY 106 CysLeuArgThrValCysAsnProTrpPheGluArgValSerMetLeuValIleLeuLeu 125
|||::: |||::: |||
Db 405 TGCATCAAGATGATGTGCAACCGGTGTGATATGTGTCAAGATGCTGTGATCCTGCTG 464
QY 126 AsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArg 145
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Db 465 AACTGCGTGACACTTGGCATGTACCAAGCCGTGCGACGACATGAGTGCCTCGACCCG 524
QY 146 CysArgIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetVal 165
|||::: |||::: |||
Db 525 TGCAGATCCTGCAAGTCTTGTGATGACTTCACTTATCTTCTTGGCATGAGATGCTG 584
QY 166 ValIleMetValAlaLeuGlyIlePheGlyIleCysTyrIleGlyAspThrTrpAsn 185
|||::: |||::: |||
Db 585 CTCAGATGTGTGCGCTGGGATTTTGGCAAGAGTCTACCTCGGGGACACATGGAAC 644
QY 186 ArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsn 205
|||::: |||::: |||
Db 645 CGCTGATTTCTTCATGTCATGTGAGGAGATGTCAGTACTCCCTGACCTTCAGAAC 704
QY 206 ValSerPheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArg 225
|||::: |||::: |||
Db 705 ATCAACTGTCAAGCCATCGCACCGTGGCGCTGAGGCCCTCAAGCCATCAACCGC 764
QY 226 ValProSerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsn 245
|||::: |||::: |||
Db 765 GTGCCAGTATGCGATCTGTGAACCTGTCTGACACACTGCCATGCTGGGAAT 824
QY 246 ValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrp 265
|||::: |||::: |||
Db 825 GTCTGTGCTGTGCTTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 884
QY 266 AlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSerLeuProLeuSerVal 285
|||::: |||::: |||
Db 885 GCGGCGCTGTGCTAAGCGCTGCTTCTGAGAGAGAACTTCAACCATCAAGCGGATGTG 944
QY 286 AspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGln 305
|||::: |||::: |||
Db 945 GCCTTGGCCCATCTACTACGACCGGAGAGAGATGAGATGCCCCCTTCTGCTCCCTG 1004

QY 306 ProArgGluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyGlyGly 325
Db 1005 TCGGGCGACAATGGATATATGGCTGCATGAGATCCCCCGCTCAAGAGCAG----- 1058
QY 326 GlyGlyProProCysSerLeu-----AspTyrGluThrTyrAsnSer 339
Db 1059 ---GGCCGTAGTGTGCTGCTGCCAAGACGACGTCTACGACTTTGGGCGGGCGCAG 1115
QY 340 SerSerAsnThrThr-----CysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAla 357
Db 1116 GACCTCAATGCCAGCGGCTCTGTGTCAACTGGAAACCGTTACTACAATGTGCGCCGACG 1175
QY 358 GlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrrIle 377
Db 1176 GGCAGCGCCAAACCCCAACAAGGCTGCCATCACTTGACAACAATCGGTATGTGGAATT 1235
QY 378 AlaIlePheGlnValIleThrLeuGlyTyrPValAspIleMetTyrPheValMetAsp 397
Db 1236 GTCATCTTCCAGGTGATCACTCTGGAAGCTGGGTGGAGATCATGTACTAATGATGAT 1295
QY 398 AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePhe 417
Db 1296 GCTCACTCCTTCAACACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCTTC 1355
QY 418 MetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGlu 437
Db 1356 ATGATCAACCTGTGCTCGTTGTATAGCGACCCAGTTCTCGGAGACCAAGCAACGGGAG 1415
QY 438 SerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSer 457
Db 1416 CACCGGCTGATGCTGGAGCAGCGGACGCTACCTGTCC--TCCAGCACGGTGCGCAGC 1472
QY 458 PheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArg 477
Db 1473 TACGCCGAGCCTGGCGACTGTCTACGAGAGATCTTCCAGTATGTCTGCCACATCCTGCGC 1532
QY 478 LysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeu 497
Db 1533 AAGGCCAAGCGC-----CGCGCCCTGGGCTTCTACCAAGGCCCTGCGAG 1574
QY 498 SerSerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSer 517
Db 1575 AGC----- 1577
QY 518 HisArgArgLeuSerValHisIleLeuValHisHisHisHisHisHisHisIstYr 537
Db 1578 ---CGGCGCCAGGCCCTG----- 1592
QY 538 HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp 557
Db 1593 -----GGCCCGGAG----- 1601
QY 558 AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly 577
Db 1602 -----GCCCGGGCCCCGCCAAACCTGGGCC----- 1628
QY 578 ProProArgGlyAlaGluSerValHisSerPheTyrHisAlaAspCysHisLeuGluPro 597
Db 1629 -----CACGCCAAG-----GAGCCC 1643
QY 598 ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly 617
Db 1644 CGGCACTACCACTGTGCCGCAACATAGCCCCCTGGATGCG----- 1685
QY 618 SerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLys 637
Db 1686 -----ACGCCCCACACAC----- 1697
QY 638 AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro 657
Db 1698 ---CTGGTGACG-----CCCATCCCCGCCACGCTGGCTTCC----- 1730

QY 658 ProGlyProPheSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCys--- 676
Db 1731 -----GATCCCGCCAGCTGCTGCTGCCAG 1757
QY 677 HisSerSerCysLysIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro 696
Db 1758 CATGAGAGACGGCCGCGGCTCGGGCTGGCGACGACCGACTCGGGCCAGAGGGCTCG 1817
QY 697 AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisVal 716
Db 1818 GGCTCC-----GGAGCTCCGCTGCTGGCGAGACGAGCG----- 1853
QY 717 MetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAsp 736
Db 1854 -----GATGGGGACGGGGCC-----CGAGCAGCGAGGACGAGCCTCCTCAGAA 1898
QY 737 LeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSer 756
Db 1899 CTGGGGAAGAGAGAGAGAGAGAGCAG-----GCCGATGGGGCG 1940
QY 757 SerValLeuAla-----PheTrpArgLeuIleCysAspThrPheArgLysIleValAsp 774
Db 1941 GTCTGGCTGTCCGGGATGTGTGGCGGAGACGCGAACCAAGCTCGCGGCAATGTGGAC 2000
QY 775 SerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGly 794
Db 2001 AGCAAGTACTTCAACCGGGCATCATGATGGCCATCTGGTCAACACCGTCAGCATGGGC 2060
QY 795 IleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleVal 814
Db 2061 ATGAGCACCAAGAGACGCGGAGAGCTGACCAACATCCTGGAGATCTGCATGTGGTC 2120
QY 815 PheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGly 834
Db 2121 TTCACCAAGATGTTTGGCTGGAGATGATCCTGAAGCTGGCTGCATTTGGGCTTTCCGAC 2180
QY 835 TyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGlu 854
Db 2181 TACCTGCGTAACCCCTACAAACATCTTGACAGACATATGTTCATCATCAGCATGTGGAG 2240
QY 855 IleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgVal 874
Db 2241 ATCGTGGGCGAGCGGACGGTGGCTGTGCTGTCGCGACCTTCGGCTGTCGCGCTG 2300
QY 875 LeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThr 894
Db 2301 CTGAACCTGTGCGCTTCATGCTGCCCCCTGCGCGCGCACTCGTGTGCTCATGAAGACC 2360
QY 895 MetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIle 914
Db 2361 ATGACACACGTGGCCACCTTCTGCATGCTGCTCATGCTCTTTCATCTTCATCAGCATC 2420
QY 915 LeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeu 933
Db 2421 CTTGGGATGATATTTTGGCTGCAAGTTCAAGCTCCGACGGAACACTGGAGACAGGTG 2480
QY 934 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 953
Db 2481 CCCGACAGGAAGAACTTGACTCCTGCTGGCGCATGCTCACTGTGTCCAGATCTC 2540
QY 954 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 973
Db 2541 ACCCAGAGGACTGGAACGTGTTCTTACAATGGCATGGCTTCACTTCCCTGGGCC 2600
QY 974 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 993
Db 2601 TCCCTTACTTTGTGCGCCCTCATGACCTTGGCACTATGTGCTTCAACCTGTGTTG 2660
QY 994 AlaIleLeuValGluGlyPheGlnAlaGluGlyAspAlaThrLysSerGluSerGluPro 1013
Db 2661 GCCATCTGTGTGAGGGCTTCCAGGCGGAGGGTGACGCCAAATCGCTCCTACTCGGACGAG 2720
QY 1014 AspPhePheSerProSerVal-----AspGlyAsp 1023

Db 2721 GACCAGAGCTCATCCAAACATAGAAGATTGTGATTAAGCTCCAGAAAGCGCTGACAGCAGC 2780
QY 1024 GLYAspArgLysLysArgLeuAlaLeuValAlaLeuGlyLuhIbAlaGluLeuArgLys 1043
Db 2781 GGAGATCCCAAG-----CTGTGCCCAATCCCAATGACCCCAATGGGCACTTGACCCC 2834
QY 1044 SerLeuLeuProProLeuIleIleHisThr-----AlaAlaThrPrometSer 1059
Db 2835 AGTCTC-----CCACTGGGTGGGCACCTAGGTCCTGGGGCTGCCGGGACCTGCC--- 2885
QY 1060 HisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThr 1079
Db 2886 ----CCCCGACTCTCACTGCAGCCGAGCCCAATGCTGGTGGCCCTGGGCTCCGAAAGAGC 2942
QY 1080 SerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSer 1099
Db 2943 AGTGTCAATGCTCTA-----GGGAGGATGAGCTATGACCAAGCGCTCCCTGTCCAGC 2993
QY 1100 AlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSer 1119
Db 2994 TCCCGGAGCTCTACTACGGGCCATGGGGCCGAGCCGGCCCTGGGCCAGCGCTCGCTCC 3053
QY 1120 SerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyLysArg 1139
Db 3054 AGCTGGAAC-----AGCCTCAAGCACAAGCCGCCCTCGCGGAGCAT 3095
QY 1140 ArgSerLeuLeuSerGlyGlu---GlyGlnGluSerGlnAspGluGluGluSerSerGlu 1158
Db 3096 GAGTCCCTGTCTCTGCGGAGCGCGCGCGCGCGCGCGGTCTGCGAGGTTCGCGCGGAC 3155
QY 1159 Glu-----AspArgAlaSerProAlaGlySerAspHis----- 1169
Db 3156 GAGGGGCGG 3215
QY 1170 -----ArgHisArgGlySerLeuGluArgGluAlaLysSer 1181
Db 3216 CCCCATCTGGCGCACCGGCCAACCGGCCAGCGCTGTCCCTGCACAAACAGGAGC 3275
QY 1182 SerPheAspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArg 1201
Db 3276 TCGGTGGAACCTGGCCGAGCTGGTGGCCCGGGTGGGCCGCCACCCCGGGCGCTTGAGG 3335
QY 1202 SerSer-----AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeu 1219
Db 3336 GCGGAGCGG 3389
QY 1220 AlaArgThrLeuArgThrAsp---AspProGlnLeuAspGlyAspAspAspAsnAspGlu 1238
Db 3390 GCCAAAGACGTCTTCACCAAGATGGCGCAGCCGCGGGAATCGCGGAGATGAGAGAA 3449
QY 1239 GlyAsnLeuSerLysGlyLysArgIleGlnAlaTrpValArgSerArgLeuProAlaCys 1258
Db 3450 ATCGACTACACCTGTGCTTCCGCGCTCCGCAAGATGATGACGTCTATAAGCCGACTGG 3509
QY 1259 CysArgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeu 1278
Db 3510 TGGGAGGTCCGCGAAGACTGGTGTGTCTAACCCTTCTCCCGAAGAACAGGTTCCGGGTC 3569
QY 1279 LeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePhe 1298
Db 3570 CTGTGTCAAGCAATTATTGCCACAACCTCTTCGACTAGTGTCTCTGGCCTTCACTTT 3629
QY 1299 LeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArg 1318
Db 3630 CTCAACTGCATCACCATCGCCCTTGAGCGGCGCTCAGATCGAGCGCGGACCGCAACGCC 3689
QY 1319 IlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrVal 1338
Db 3690 ATCTTCTCAACGTTGCCAACTACTTCAACGCCATCTTCGTGGCGAGATGACATTG 3749
QY 1339 LysValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn 1358
|||||

Db 3750 AAGTAGTCTCGGTGGGCGCTGTACTTCGGCGAGCAGCGGCTACTACGACAGCTGGAAC 3809
QY 1359 ValLeuAspGlyLeuLeuValIleuIleSerValIleAspIleLeuValSerMetValSer 1378
Db 3810 GTGCTGATGGCTTTCTTGTCTTCGTCCATCATCATGACATCGTGGTGTCCCTGGCGCTCA 3869
QY 1379 AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1398
Db 3870 GCCGGGGAGCCAGATCTTGGGGGTCTCCGAGTCTTGGCGCTCTGCGCACCCCTACGC 3929
QY 1399 ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer 1418
Db 3930 CCCCTGCGTCAATCAGCCGCGCGCGCGCGCTGAAGCTGGTGGAGACACTCATCTCC 3989
QY 1419 SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly 1438
Db 3990 TCCCTCAAGCCCATCGGCAACATCGTCTCATCTGTGCTTCTTCATCATCTTGGC 4049
QY 1439 IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArg 1458
Db 4050 ATCTTGGAAGTGCAGCTCTTCAAGGCGCAAGTTCTACCACTGTCTGGCGGTGACACCCGC 4109
QY 1459 AsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyr 1478
Db 4110 AACATCACCAACCGCTTCGACTGCATGCGCCCAACTACCGCTGGCTCATCAACAATAC 4169
QY 1479 AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGly 1498
Db 4170 AACTTGACAACCTGGGCCAGGCTGTGATGTCCCTTGTGTCTTGCGCATCCAAAGATTGGT 4229
QY 1499 TrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMet 1518
Db 4230 TGGGTGAACATCATGTACAATGAGACTGATGCTGTGTGTGAGACAGCAGCTGTGACC 4289
QY 1519 AsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePhe 1538
Db 4290 AACCAACACCCCTGATGTGCTGTACTTCACTCTCTCTGCTCAATGTCTGAGCTTCTT 4349
QY 1539 ValLeuAsnMetPheValGlyValValGluAsnPheHisLysCysArgGlnHisGln 1558
Db 4350 GTGCTCAACATGTTGTGGGTGTCTGTGTGAGAACTTCCACAAGTCCGGCAGCACAG 4409
QY 1559 GluGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArg 1578
Db 4410 GAGGCTGAAGAGGACGCGCGCGGTGAGGAGAACCGGCTGCGCGCGCTGAGAGAAAGCGC 4469
QY 1579 ArgSerLysGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSer 1598
Db 4470 CGG-----AAGGCCACGCGCTGCCCTACTATGCCACTATTGT 4508
QY 1599 ArgPheArgLeuLeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleThr 1618
Db 4509 CACACCCGGCTGCTCATTCACCTCCATGTGCACAGCAGCACTACCTGACATCTTCATCAC 4568
QY 1619 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1638
Db 4569 TTCAATCATCTGCTCAACGCTGTCTACCACTGTCCCTGGAGCACTACATGACCCACGTCC 4628
QY 1639 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSer 1658
Db 4629 CTGGAGACAGCCCTCAAGTACTGCAACTATATGTTCACCACTGTCTTGTGCTGAGGCT 4688
QY 1659 ValPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGlnLeu 1678
Db 4689 GTGTGAAGCTGTGTCATTGTGTGTAGGCGCTTCTTCAAGAACCGATGGAACCAAGCTG 4748
QY 1679 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1698
Db 4749 GACCTGGCCATTGTGCTACTGTAGTCATGGGATCACCTGAGAGATCGAGATCAAT 4808
QY 1699 LeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1718
Db 4809 GCGGCCCTGCCCATCAATCCACCATCATCCGCAATGAGGTTCTGCGCAATTGCCCGA 4868
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QY 1719 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGln 1738
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Db 4869 GTGCTGAAGCTGTTGAAGATGCGCACAGAAATGCGGCCCTGTGACACAGGTGTGAA 4928
QY 1739 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1758
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Db 4929 GCTTTGCCCCAGGTGGGCAACCTGGGCTCTCTTCATGCTGCTCTTCTTCATCTATGCT 4988
QY 1759 AlaLeuGlyValGlyLeuPheGlyAspLeuGluCysAspGluThrHisProCysGlyGly 1778
|||||
Db 4989 GCTCTCGGGGTGGAGCTCTTTGGGAAGCTGCTGCAACGACGAGAAACCGTGGAGGGC 5048
QY 1779 LeuGlyArgHisAlaThrPheArgAsnGlyMetAlaPheLeuThrLeuPheArgVal 1798
:::
Db 5049 ATGAGCCGGCATGCCACTTGAGAACTTCGGCATGGCTTCTTCACACTCTTCAGGTC 5108
QY 1799 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCys--AspGln 1817
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Db 5109 TCCACGGGTGACAACTGGAACGGATCATGAAGACACGCTCGGGACTGCACCCACGAC 5168
QY 1818 GluSerThrCysTrpAsnThrVal-----IleSerProIleTyrPheValSerPheVal 1835
|||||
Db 5169 GAGCGCAGCTGCTGAGCAGACCTGACGTTGTGTGCGCGCTGTACTTCGTGAGCTTCGTG 5228
QY 1836 LeuThrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGlu 1855
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Db 5229 CTCACCGCGCAGTTCGTGCTCATCAACGTGTGTGTGTGCTCATGAAGACCTGGAC 5288
QY 1856 GluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuMet 1875
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Db 5289 GACAGCAACAAGAGGCGCAGAGAGACCGCCAGATGATGCCGAGCTCGAGCTGGAGATG 5348
QY 1876 ---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpPro--- 1893
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Db 5349 GCCCATGGCTGGGCTGGCCCGAGGCTGCTACCGGCTCCCGGGCGCC--CTTGGC 5405
QY 1894 -----GlyValGluGlyValAsnSerThrAsp----- 1902
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Db 5406 CGAGGGCCGGAGGGCGGGCGGGCGGCGACACCGAGGGCGGCTGTGCGCGCGCTGC 5465
QY 1903 ---SerProLysProGlyAlaPro-----HisThrThrAlaHisIleGlyAla 1917
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Db 5466 TACTCGCCTGC-CCAGAGAACTGTGCTGACACAGCGTCTTTAATCATCAAGACTC 5524
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Db 5525 CTTGGAGGG--GAGCTGACCAT-----CATGACAACTGTGCGGCTC 5566
QY 1938 ProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 1957
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Db 5567 CATCTTCACCACTACTCTCGCTGCGCGCTGCAGAGAGTGTCA----- 5611
QY 1958 ProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArg 1977
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QY 1978 GlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAla 1997
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Db 5645 GGAGGCCTTCTCCCTGAATCAGACAGTCTCTCATCTGTGCGGTGACGACCTGAG 5704
QY 1998 AspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGly 2017
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Db 5705 TCTCGAGGA-----CCCCACAGC 5722
QY 2018 AlaProThrTrpGlyAlaIleProLysLeuProPro----- 2029
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QY 2030 -----ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAla 2044
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Db 5774 CATGCGTGTGGAGACTGGGCGAATGCTTCTTCCCTTGT-CTCTACGGCGCTCTCGC 5832

QY 2045 AlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSer 2064
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QY 2065 GluValSerGlyProSerCysProLeuThrArgSerSerSerPheTrpGlyGlySerSer 2084
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QY 2085 IleGlnValGlnGlnArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuPro 2104
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Db 5908 -----GCAGTCAAGACCCCCCAAGTCCCT 5931
QY 2105 AlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSerSer 2124
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Db 5932 TCTCCC-----CGATGCTTCCAGCC----- 5952
QY 2125 LeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGlnGlu 2144
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Search completed: September 19, 2005, 17:19:14
Job time : 3522.34 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2005, 17:44:07 ; Search time 14386.6 Seconds
(without alignments)
6050.997 Million cell updates/sec

Title: US-09-611-257A-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVRTPPLRGSAR.....KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO.spool/US09611257/runat_15092005_134301_25185/app_query.fasta_1.4878
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bl0sum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09611257 @CCN 1 1_23209 @runat_15092005_134301_25185 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
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2: gb_est2: *
3: gb_htc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gsa81: *
9: gb_gsa82: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1719.5	14.3	6636	3	BC043482	BC043482 Mus muscu
2	1698	14.1	6035	3	BC051413	BC051413 Mus muscu
3	1406	11.7	990	4	BI905383	BI905383 603167426
4	1385.5	11.5	939	4	BI736618	BI736618 603361089
5	1343	11.2	1076	4	BM479323	BM479323 AGENCOURT
6	1300	10.8	1064	4	BM451648	BM451648 AGENCOURT
7	1293.5	10.8	5666	9	AY416501	AY416501 Mus muscu
8	1275	10.6	879	7	CF548698	CF548698 AGENCOURT
9	1256.5	10.4	793	6	CA319705	CA319705 UI-M-FW0-

10	1230.5	10.2	5943	9	AY416499	AY416499 Homo sapi
11	1198	10.0	715	7	CF745071	CF745071 UI-M-GV0-
12	1197	10.0	810	5	BU709095	BU709095 UI-M-EW0-
13	1195.5	9.9	952	7	CF584866	CF584866 AGENCOURT
14	1190.5	9.9	4675	3	AK083220	AK083220 Mus muscu
15	1187.5	9.9	771	5	BU058818	BU058818 UI-M-FR0-
16	1185	9.9	736	4	BI160856	BI160856 602864778
17	1182	9.8	711	5	BM950154	BM950154 UI-M-EH0P
18	1172	9.7	777	5	BU708898	BU708898 UI-M-F10-
19	1163.5	9.7	957	4	BG298038	BG298038 602396253
20	1162.5	9.7	777	6	CA945335	CA945335 UI-M-FD0-
21	1141	9.5	973	2	BF783704	BF783704 602109506
22	1140.5	9.5	828	2	BF606929	BF606929 MY2_00012
23	1136.5	9.4	784	7	CF742232	CF742232 UI-M-HB0-
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26	1111	9.2	6813	9	AY406056	AY406056 Homo sapi
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28	1102.5	9.2	773	4	BI249987	BI249987 602995228
29	1096	9.1	676	4	BI917129	BI917129 603181539
30	1088.5	9.0	727	5	BQ443110	BQ443110 UI-M-EV0-
31	1088	9.0	710	7	CR576255	CR576255 CR576255
32	1079.5	8.9	647	6	CB518482	CB518482 UI-M-GH0-
33	1075	8.9	667	7	CF531859	CF531859 UI-M-GH0-
34	1074.5	8.9	731	7	CN534628	CN534628 UI-M-HS0-
35	1067	8.9	707	7	CN216936	CN216936 RJAO02G02
36	1061.5	8.8	708	5	BQ179746	BQ179746 UI-M-EW0-
37	1059	8.8	693	5	BM949227	BM949227 UI-M-EG0P
38	1055.5	8.8	803	6	CB245297	CB245297 UI-M-FY0-
39	1034	8.6	843	5	BQ180375	BQ180375 UI-M-EX0-
40	1032.5	8.6	710	5	BU704267	BU704267 UI-M-FY0-
41	1018.5	8.5	684	5	BU262763	BU262763 603374462
42	1012	8.4	772	6	CB524438	CB524438 UI-M-FY0-
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44	1009	8.4	640	6	CB056097	CB056097 NISC_J112
45	997.5	8.3	658	5	BQ109588	BQ109588 imageqc_7

ALIGNMENTS

RESULT 1
BC043482
LOCUS
DEFINITION
BC043482 6636 bp mRNA linear HTC 19-NOV-2003
Mus musculus calcium channel, voltage-dependent, alpha 1f subunit,
mRNA (CDNA clone IMAGE:5369391), containing frame-shift errors.

ACCESSION
BC043482
VERSION
BC043482.1
KEYWORDS
GI:28175783

SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
AUTHORS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 6636)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uedlin, T.B., Toshlyuk, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.B.,
Scherer, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26),	16899-16903	(2002)
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2	(bases 1 to 6636)			
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-JAN-2003)	National Institutes of Health, Mammalian			

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Natassja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAK Plate: 86 Row: 0 Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972
This clone has the following problem: frame shifted.

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FEATURES
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location/Qualifiers
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/note="Vector: pCMV-SPORT6"

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ORIGIN

Alignment Scores:	
Pred. No.:	1.32e-107
Score:	1719.50
Percent Similarity:	40.38%
Best Local Similarity:	26.28%
Query Match:	14.30%
DB:	3
	Gaps: 95
	Length: 6636
	Matches: 658
	Conservative: 353
	Mismatches: 810
	Indels: 691
	Gaps: 95

US-09-611-257A-24 (1-2287) x BC043482 (1-6636)

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Oy	70	GluLysaspProGlySeralaspSerglualaglIyleuProTyrrProAlaleuAla		89
		: : :	: : :	:
Dd	147	AGAAGAGAGAACCCAGCACACAACAACAAGACTGTGGCGGTGCCAGTGCTCAGAGATCA		206
Oy	90	ProValValPhePheTyrlLeuSerglnaspSeraArgProargSerTrpCysleuArgThr		109
		:		:
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Oy	110	ValCysasnProTrp-----PhegluArgValSerMetIeuValIleleuLeuasCys		127
		:		:
Dd	267	GTA-----GAGTGAAGCCTTTTGATATTTCTCATCTCCTGACCAATCTTTGCCAAGCTGC		320
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QY	139	-----IleAla	140
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QY	146	-----Cys--ArgIle-Le	149
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QY	149	ucGlnAlpheAsp-----AspPheIlePhe--	157
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QY	381	nValIleThrLeuGlyTYrTPrValAspIleMetTYrPheValMetAspAlaHisSerPh	401
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Qy	770	rglValIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnT	790
Db	2012	GCCGGCGCCTCAAGTCACCAACGCCTGTACTGGGCTGTACTGTTGCTCGCTTCTCAACA	2071
Qy	790	hrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluI	810
Db	2072	CgTTGACCATTAGCTTCAGAGCACCATGGGACGCCCTTGCTGCTCACCCAGACCAAGAGT	2131
Qy	810	IeSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValT	830
Db	2132	ATGCCAACAAAGTCTGCTCTGCTCTTCACTGTGAAGATGCTCTCAAAGTGTACGGCC	2191
Qy	830	yrgLYProPheGLYTyriLeLysAsnProTYraeniLePheASP-----G	845
Db	2192	TGGGCCCTCTGTCTACGTGCTCTTTTTCACCGCTTGACTGCTTCGTGCTCTGTG	2251
Qy	845	lyValIleValIleValIleSerValTrpGluIleValGlGlngInglyGlyLeuServ	865
Db	2252	GGGGCATCTAGAACCACACTTGGTGAGGTGGGGCCATGACGCTCTTGSCATCTCAG	2311
Qy	865	alleuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeug	885
Db	2312	TGCTCCGATGTGTACGTCTCTCAGGATCTTCAGGATCACAGGCATGGGCATCCCTGA	2371
Qy	885	InArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCyMetLeuL	905
Db	2372	GCAATCTGGTGGCATCTTGTCTCAATTCATGAAAGTCCATCGCTCTTGCTGCTCTCC	2431
Qy	905	eumetLeuPheIlePheIlePheSerileuenglyMetHisleuPheGlyCylsYPhea	925
Db	2432	TCTTCTCTCATCATCATCTCTCCCTGCTGGCATGCAGCTGTTGGGGCAAGTTCA	2491
Qy	925	lasergluArgaspGlyasprThrLeuProaspArgLysAsnPheaspSerleuLeuTrpa	945
Db	2492	ACTTtgaccag-----acccacaaccaagagcacccttgataacctcccccaag	2542
Qy	945	IaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsng	965
Db	2543	CCCTCCTCACTGTCTTCAgATCCTGACTGtGAgAATTGGAACGTTGTCAgtATgATG	2602
Qy	965	lyMetalaser-----ThrSerSerTrpAlaIaleuTyrPheIlea	979
Db	2603	GTATCATGGCCTACGtGGCCCTTCTCCAGGATGCTGtGCgTtTAITTCATCA	2662
Qy	979	IalEumetThrPheGlyAsnTYrValleuPheAsnleuLeuValAlaIleLeuValGluG	999
Db	2663	TCCTCTTCATCTGTGGCACTACATCCTGTGAACGTGTCTTGCCATTGCCGTGATA	2722
Qy	999	lyPheGlnIaGluGlyAspAlaThrLysSerGluSerGluProaspPhePheSerPros	1019
Db	2723	ACCTA--GCCAGCGGGATGCAGGCACTGCCAA-----	2754
Qy	1019	erValaspGlyaspGlyAsparGlysLysargLeuAlaLeuValAlaLeuGlyGluHisa	1039
Db	2755	-----GACAAGGGCAGAGAGAAG-----	2772
Qy	1039	IaGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaIaIaThrPromets	1059
Db	2773	-----AGCAGTGAAAGAA	2785
Qy	1059	erHisProLysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgT	1079
Db	2786	ACCCTCCAAGAGAGACAAGATATGTG-----	2814
Qy	1079	hrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCyBProPros	1099
Db	2815	-----CCTGCTGAGAGAGATGAGACGCAAG-----G	2842
Qy	1099	erAlaArgSerSerProHisSerProTrpSerAlaIalaSerSerTrpThrSerArgArGs	1119
Db	2843	GTGCAAGAGAGTGAA-----	2856

QY 1119 erSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgSerProSerGlyGluA 1139
Db 2857 -----GGAGCAGCACCGCATG----- 2874
QY 1139 rgArgSerLeuLeuSerGlyGluGlyGlnLuserGlnAspGluGluLuserSerGluG 1159
Db 2875 -----GAG 2914
QY 1159 luAspArgAlaSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluA 1179
Db 2915 AGGAAGAGAGAAATGGTGCAGGA-----CATGTGAACTCTTGACAGGAAGTA- 2961
QY 1179 laLysSerSerPheAspLeuProAspThrLeuGlnVal-ProGlyLeuHisArgThrAla 1198
Db 2962 -----GTACCCAGAGAGAAAGGTGTGTAACCATCCCTGAAGGCAGTGCCCT 3004
QY 1199 SerGlyArgSerSerAlaSerGluHisGlnAspCys-AsnGlyLysSerAlaSerGlyAr 1218
Db 3005 TCTTCT---GCCTTAGCCAAACCAACCCGTGAGTGTGGGAATGCCAGTAGGCGAGGCCA 3061
QY 1218 gLeuAlaArgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAspG1 1238
Db 3062 ACAGCGCGGAGCCCTAGACTACCCAGAGGAGCATG----- 3098
QY 1238 uGlyAsnLeuSerLysGlyGlyArg-1IeGlnAlaTyrValArgSerArgLeuProAlaC 1258
Db 3099 -----GGCCACAGATGTATCCCTTGATCTCCAGAAACACCAATCC 3142
QY 1258 ysCysArgGluArgAspSerTrpSerAlaTyr-1IephProProGlnSerArgPheArg 1277
Db 3143 TGGTT-----TCTACTCACTGCCCTTTCTCCACTCCCGAGGCTTCGG 3184
QY 1278 LeuLeuCysHisArg1IeIleThrHisLysMetPheAspHisValValLeuValIleIle 1297
Db 3185 AAGCCTGCCACACACTCATACATCACATATCTTCACCAGTCTCATCTAGTGTTCATC 3244
QY 1298 PheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGlu 1317
Db 3245 ATCTCTAGTAGTGTCTCCCTGCTGCTGAGGACCCC--ATCCGAGCTCACTCTTCGGA 3301
QY 1318 ArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThr 1337
Db 3302 AACCATATCTGGGATATTTGATATGCTTCACCTCCAAATATCACTGTGAGATTTCTA 3361
QY 1338 ValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTrp 1357
Db 3362 CTCAAGATGACAGTGTGGGGCCCTTCCTGCACCGAGGCTTTCTGCCGTAGCTGTTC 3421
QY 1358 AsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetVal 1377
Db 3422 AATCTGTGATCTCTTGTGTGTCAGTGTCTCCCTCATCTCTTCGGCATCCAC----- 3475
QY 1378 SerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeu 1397
Db 3476 -----TCCAGTGCCATCTCAGTTGTGAAGATTCTCCGAGTCCCTCCGAGTCCTG 3523
QY 1398 ArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMet 1417
Db 3524 CGGCCTCTCCGAGCCATCAACAGAGCAAGGAGCTCAAGCATGTGGTGCAGTGTGTTC 3583
QY 1418 SerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePhe 1437
Db 3584 GTGGCCATCCGAGCCATCGGAACATCATGATTGTCAACCACTCTTGACATTCAATGTC 3643
QY 1438 GlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThr 1457
Db 3644 GCCTGCATTTGGTGTTCAGCTGTTCAGGGGAAATTTCTACAGTTGCACGTAGAGGCCAAA 3703
QY 1458 ArgAsnIleThrAsn-----LysSerAspCysAlaGlu 1468
Db 3704 CACACCCCTGAAGAATGCAAGGGCTCCTTCCTCATCTACCTGATGAGATGTGTCAAGA 3763
QY 1469 AlaSerTyrArg-----TrpValArgHisLysTyrAsnPheAspAsnLeuGlyGln 1485

Db 3764 CCTTGGTCCGGGAGCGGCTCTGGGTCAACAGTGAATTTTAACCTTTGACAACGTCCTTTCA 3823
QY 1486 AlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAsp 1505
Db 3824 GCCATGATGGCCCTGTTCACGTCTCTACCTTGAAGGCTGGCCCTGCTATATACAAG 3883
QY 1506 GlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeu 1525
Db 3884 GCCATGATGCAAAACGACAGAGATGAGGGCCCTTACTACAATTACCATGTGAGATATCA 3943
QY 1526 LeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGly 1545
Db 3944 GTATTCTTCATTGTCTACATCATCATCGCCTTCTTCATGATGAACAATCTTTGTGGGC 4003
QY 1546 ValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArg 1565
Db 4004 TTGTATATCATCATTC-----CGTGCCAGGAGAGACAGAGATACCAAAAC 4051
QY 1566 ArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgSerLysGluLysGlnMet 1585
Db 4052 TGTGAA-----CTGACAAAGAACCAAGCCAGTGCTGTGAATATGCC 4093
QY 1586 AlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHis 1605
Db 4094 CTCAAGCTCAGCCACTCCGCCGATACATCCCTAAGAATCCTCATCAGTACCGCGTGTGG 4153
QY 1606 HisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnVal 1625
Db 4154 GCCACTGTGAACCTGTGCTGCTTGTGAGTACCTCATGTCTGTCTCATCTGCTCAACACG 4213
QY 1626 ValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIle 1645
Db 4214 GTGCCCTTAGCCATGACAGCACTATGAACAGACTGCTCCCTTAACTATGCAATGACATC 4273
QY 1646 CysAsnTyrIlePheThrValIlePheValPheGluSerValPheLysLeuValAlaPhe 1665
Db 4274 CTCAACATGCTCTTCACTGGCCTTTCACCATGTAGATGTGCTCAAAATCATCGCCTTT 4333
QY 1666 AlaPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeu 1685
Db 4334 AAACCCAGCATTACTTTGCGAGATGCCCTGGAATACGTTTGATGCTCTCATTTGAGTGGC 4393
QY 1686 SerIleMetGlyIleThrLeuGluGluIle-----GluVal 1697
Db 4394 AGTGTAGTCACATCGCCGCTCACAGAAATACGAAGCCAGGCACTTGCGGAGAGTTCA 4453
QY 1698 AsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAla 1717
Db 4454 GAGACAGCTCCCGCATATATCACGTTCTTTCGCTCTTCGAGTCAAGAGGCTG--- 4510
QY 1718 ArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMet 1737
Db 4511 -----GTCAAGTCTGTGAGTAAGGTGAGGGGATCCGCACACTGTGACATTCATC 4564
QY 1738 -----GlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhe 1754
Db 4565 AAGTCTTTCAGGCGCTTGCCCTATGTG-----GCACTTCTCATAGCAATGATATTC 4615
QY 1755 PheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCys---AspGluThr 1773
Db 4616 TTCAATATGCAATGTCATTTGGCATGCAAGATGTTGGCAAGGTGGCTTTCAGAGACGGCACG 4675
QY 1774 HisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeu 1793
Db 4676 CAG-----ATAAATCGAAACAACAATTTCCAGACCTTTCCGAGGCTGTGCTG 4723
QY 1794 ThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMet-----LysAspPro 1811
Db 4724 CTTCTGTTCAGGTGTGCCACTGCTGAGGCGCTGCAAGAGATTAATGTCAGCACCTTCCA 4783
QY 1812 SerArgAspCysAspGlnLuser-----ThrCysTyrAsn 1823

Db 4784 GGAATCGATGACCTGAGTCTGACTTTGGCCCGAGGAGGAATTACCTGT---GGT 4840

QY 1824 ThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuVal 1843

Db 4841 AGCAGTTTGGCAGTCGCTACTTCATCATGCTCTTATGCTCTGCTCCCTTGATTTATA 4900

QY 1844 AsnValValIleAlaValLeuMet----- 1851

Db 4901 AATCTCTTGTGCTGTATCATGATTAACCTTGTATTACCTAACCAAGAGATTGTTCTATC 4960

QY 1852 -----LysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGlu 1868

Db 4961 CTGGGACCCCAACCACCTTGATGAATTC---AAGAGATCTGCTGTGAATATGACCCCGGA 5017

QY 1869 AlaGluLeuGluLeuGlu-----MetLysThrLeuSerProGln 1881

Db 5018 GCCAAGGGCCGCATCAAGCACTTGATGTGTTGCCCTGCTGAGAGCATCCAGCCCCCA 5077

QY 1882 -----ProHisSer----- 1884

Db 5078 TTGGGATTTGAAAGCTATGCCACACCGAGTGGCTGCAGAGACTCGTGCAATGAAT 5137

QY 1885 ---ProLeuGlySerProPhe-----LeuTrpProGlyVal 1895

Db 5138 GTGCCCCCTCAACTCAGA-TGGAACAGTACATTCACGCTACACTCTTGCCCTGTGCG 5196

QY 1896 GluGlyValAsnSerThrAspSerProLysProGlyAlaProHisThrAlaHisIle 1915

Db 5197 GACATCCCTGAAGATCAGACAGAAAGGGAACCTGGATCAAGCCAACGAGAGCTTCGGAT 5256

QY 1916 GlyAlaAlaSerGlyPheSerLeuGluHisProThrmecVal-----ProHisProGlu 1933

Db 5257 GGTTCATCAAAAAGATCTGGAAGCGGATAAAGCAGAAATTTGTTGGATAGAGTCAATCCCTCC 5316

QY 1934 -----GluValProValPro---Leu 1939

Db 5317 TCCCGATGAGAGAGAGTCACTGTGGAAATTTCTATGCCACATTCCTGATCCAAAGATTTA 5376

QY 1940 GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsn 1959

Db 5377 TTTCGAAAATTCGCGAAGAAAGAAAGAGGGCTACTAGGAAGAGAGGC---CCCAAC 5433

QY 1960 AspSerTyrMetCysArgAsnGlySerThrAlaGluArgSer----- 1973

Db 5434 AAGCACATCCTCTGCTCCCTCAGGCTGTCTAAGAGCCTGCAGAGACTGGGTCTGAGAT 5493

QY 1974 -----LeuGlyHisArgGlyTrpGlyLeuProLysAlaGln 1985

Db 5494 CCGTCAAGCCCTCACTATGACACTGAGGAAGAAAGAGAGAGAGGAGGAGTGGTCA 5553

QY 1986 SerGly-----SerIleLeuSerValHisSerGln 1995

Db 5554 GGAGGCTGAGGAAGAGAGAGCTGAGAACCAACCAGAACCATACAAAGACTCCATAGACTC 5613

QY 1996 ProAla-----AspThrSerCysIleLeuGlnLeuProLysAsp 2008

Db 5614 CCAGCCCCCAATCTCGATGGAATCTAGATTT-CGGTGTCTCTACCTGTTAAGAGAAAC 5672

QY 2009 ValHisTyrLeuLeuGlnProHisGlyAlaProThrTrpGlyAlaIleProLysLeuPro 2028

Db 5673 TTCCAGATTCTCTCTCAACTGGCGCCGAGTGATGATGGGC-----TGGCTCCCA 5723

QY 2029 ProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIleArgThr 2048

Db 5724 ACTCCAGGC---AGCCAGTGTGATACAGGCTGGCTCCCAACACACA----- 5768

QY 2049 AspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuSerGluValSerGly 2068

Db 5769 -----GGAGAAAGCTCTGGGG 5783

QY 2069 ProSerCysProLeuThrArg-----SerSerSerPheTrpGlyGlySer 2083

Db 5784 TTTTCATGTTCATCTATCCCGAAGAGAGAGTATTACGCTCAAGGGAAGTCAAGGGCAGG 5843

QY 2084 SerIleGlnValGlnLysArgSerGlyIleGlnSerLysValSerLysHisIleArgLeu 2103

Db 5844 ACAATCAGATGAGGAACAGAGAGTCCCTGACTGACTCTGACCTGATGAGCAGG--- 5900

QY 2104 ProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProGluThrArgSer 2123

Db 5901 -----CCGGGACTC-----CTTGAACCCAGTCC 5924

QY 2124 SerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProSerSerGln 2143

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QY 2144 GluGluProLeuPheProArgAspLeuLysLysCysTyrSerValGluThrGlnSerCys 2163

Db 5984 TTGCTGCCCCCAAGCCTGCAGGTGGAAAGCCCTCCTTCAACCATCCAG-----TGT 6034

QY 2164 ArgArgArgProGlyPheTrpLeuAspGluGlnArgHisSerIleAlaValSerCys 2183

Db 6035 CTGCAACGCCAGGAGC-----AGTTGT 6055

QY 2184 LeuAspSerGlySerGlnProArgLeuCysProSerProSerSerLeu----- 2199

Db 6056 GAAGATT---ACCTATCCCAAGCACTTACCATCGTGACGAGACCTCAGACCAAGCAG 6111

QY 2200 GlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro--- 2218

Db 6112 GGCTCAGGGTTCTGGGAGACCCCTCCTCAGAAGGGTGCAGCTGCTATATGCCCCCTGTT 6171

QY 2218 ----- 2218

Db 6172 GTTGTGAGAGAAATCTACAGTGGGTGAAGATACCTTGGCAAACTTGGCGGCCACTGCG 6231

QY 2219 -----SerIleSerIleAspProProGluSerGlnGlySerArgProPro----- 2233

Db 6232 TACCTTCACCTGTCTGCAAGTGCTGAGCTCATCCGAATCCAGCCACCGCAAGAGGGG 6291

QY 2234 ---Cys-----SerProGlyValCysLeuArgArgAlaProAlaSerAspSerLys 2250

Db 6292 CAGTGTGACAGTTTGTGTGAGAGGCTGTCTCATCTCCGAAGGCTTAGGTCTTTGCCCA 6351

QY 2251 AspProSerValSerSerPro-----LeuAspSerThrAlaAlaSerProSerPro 2267

Db 6352 AGACCCACGATTTGTGGCCCTGGCCCAAGCAGAGATTGCAGATGCATGTCACTGACCTT 6411

RESULT 2

BC051413 6035 bp mRNA linear HTC 19-NOV-2003

LOCUS

DEFINITION

Mus musculus calcium channel, voltage-dependent, alpha 1F subunit, mRNA (cDNA clone IMAGE:6493332), containing frame-shift errors.

ACCESSION

BC051413

VERSION

BC051413.1 GI:30802106

KEYWORDS

HTC.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 6035)

1. Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Woley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 6035)
Strausberg,R.
Direct Submission
Submitted (25-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT

NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hgrl.nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghghi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantiripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgoun,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAK Plate: 108 Row: o Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9624972
This clone has the following problem: frame shifted.

FEATUES

Location/Qualifiers
1. 6035
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6493332"
/tissue_type="Eye, retina, mouse strain C57Bl\6"
/clone_id="NIH_MGC_94"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
Pred. No.: 3.53e-106 Length: 6035
Score: 1698.00 Matches: 615
Percent Similarity: 38.96% Conservative: 338
Best Local Similarity: 25.14% Mismatches: 767
Query Match: 14.12% Indels: 730
DB: 3 Gaps: 83

US-09-611-257A-24 (1-2287) x BC051413 (1-6035)

OY 37 ArgArgMetGluArgAlaProArgSerArgASP---SerProValAlaSerArgSerSer 55
Db 12 AGGAGATGTGGAATCTGAAGTCGGAAAGATACAAACCCAGAGCCAGTCCAGCCAAT 71
OY 56 ThrThr-----CysProGlyPro----- 61
Db 72 GGGACTGGCCCTGGCCCTGAATGGGGCTGTCTGGCCCTCCAACCTGTGGGACTGAT 131
OY 62 -----GlyAlaGlyAlaGlySerThrGluLysAspProGlySerAlaAspSerGlu 79

Db 132 ACCAGCGGGCGCTCAGGCTGGGGACCCCAAGAGAAGACCAGACACAACAACAAG 191
OY 80 AlaGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAsp 99
Db 192 ACTGTGGCGGTGGCAGTGTCTCAGAGATCACCTCGACGCGCTCTTGCTCCACCTTACT 251
OY 100 SerArgProArgSerTyrCysLeuArgThrValCysAsnProTyr-----PheGluArg 117
Db 252 AATCCCATTCGTGCGTCCCTGCATCAGCATTTGTA-----GAGTGAAGCCTTTGATATT 305
OY 118 ValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGlu 137
Db 306 CTGATCTCTCTGACAATCTTTGCCAACTGCGTGCAATTGGGGTATATATCCCTTCCCT 365
OY 138 AspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePhe 157
Db 366 GAGAGCACTCCAAACACTGCTTAACCACTTGGAACAGTA-----GAATACGTGTTTC 419
OY 158 ---AlaPhePheAlaValGluMetValValLysMetValAlaLeuGly---IlePheGly 175
Db 420 CTGTGATTTTCAACCGTGAGACAGTGTCTCAAGATCTGAGCCTATGGCTGTGCTCCAT 479
OY 176 LysLysCysTyrLeuGlyAspThrTyrPAsnArgLeuAspPhePheIleValIleAlaGly 195
Db 480 CCCAGCGCTATATTCGCAATGCGCTGGAACCTGTGCACTTCATCATCTGTGTGCGG 539
OY 196 MetLeuGluTyrSerLeuAspLeu----- 203
Db 540 CTGTTCAGCGTGTCTGTGAACAAGACCTGGCGGCCAGAGATGCCCGCATACTGA 599
OY 204 -----GlnAsnValSerPheSerAlaValAlaArgThrValArgValLeuArgProLeu 220
Db 600 GGAAGCCAGAGAGGCTTCGATGTAAGGCACTGCGGCGCATTTAGGGTGTCTACGACCTCTA 659
OY 221 ArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAspThrLeu 240
Db 660 AGGCTAGTGTGGGGTCCGAGTCTGCACATAGTCTCAATTCCATCATGAAGCGGCTT 719
OY 241 PrometLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleVal 260
Db 720 GTGCCGTGCTGCACATGTGCCCTGTGTGTCTCTTCATTCATTCATTAAGCCATCATC 779
OY 261 GlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsnPheSer 280
Db 780 GGACTGAGCTATTCTCGACGAATGCACAAGACATGCTACTTC----- 824
OY 281 LeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerPro 300
Db 825 -----CTGGATCTGATATGAA-----GCAGAGAGAGACCATCACCT 863
OY 301 PheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValProThrLeu 320
Db 864 -----TGTCATCT----- 872
OY 321 ArgGlyGluGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSerSer 340
Db 873 -----TCTGGCTTGGCGGCTTCATGCACACTGAAC----- 902
OY 341 SerAsnThrThrCysValAsnTyrAsnGlnTyrTyrThrAsnCysSerAlaGlyGluHis 360
Db 903 -----CATACGAGTGCCGCGGCGCTGGCCA 929
OY 361 AsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTyrIleAlaIlePhe 380
Db 930 GGACCCGAACGGTGCATCAGCAACTTCGACAATTTTCTTTGCCATGCACTGTGTTTC 989
OY 381 GlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheValMetAspAlaHisSer 400
Db 990 CAGTGATTAATCATGGAAGCTGACAGACGTCCTCTACTGATGCAGAGATGCCATGGGG 1049
OY 401 Phe---TyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIle 419
Db 1050 TATGAGCTGCTTGGTGTACTTTGTGAGCCTTGTCATCTTTGGGTCTTCTTGTCTCTC 1109

OY		420	AsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGln	439
Db	1110	AACCTTGCTTGGAGTCCTTAAGCGGGAGATTCTCCAAAGAAAGAAAAGCAAAAGCA	1169	
OY		440	LeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSer	459
Db	1170	CGAGGTGACTTTCAAGAAGCTTCGG-----	1193	
OY		460	GluProGlySerCysTyrlGluGluLeuLeuLysTyrlLeuValTyrlLeuArgLysAla	479
Db	1194	GAGAAGCAGCAGATGGAAGAAGACCCTTCGGGGCTACCTGGATGCATCACAGGCTGAG	1253	
OY		480	AlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSer--	498
Db	1254	GAGTTAGACCTTCATGACCCCTCA-----	1301	
OY		499	SerProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHis	518
	:::			
Db	1302	GCTGAAGAAGAGACGGGGGCCCATCGGCCACAACSTGTCAAGCTGACCAATAGAGGGCGC	1361	
OY		519	ArgArgLeuSer---ValHisHisLeuValHisHisHisHisHisHisHisTyrl	537
Db	1362	GGACGGCTGCGATGTTGACGCCACTTACTCGCTCCACACACTCCACAGCAGCCAGCCC	1421	
OY		538	HisLeuGlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAsp	557
Db	1422	AGCCTC-----	1427	
OY		558	AlaAsnGlySerArgArgLeuMetLeuProProProSerThrProThrProSerGlyGly	577
Db	1428	-----	1454	
OY		578	ProProArgGlyAlaGluSerValHisSerPheTyrlHisAlaAspCysHisLeuGluPro	597
Db	1455	GACACCCCTTGAGATGAGATGAAGAAGAGGGGACCACTGGCTAGCTGT-----	1502	
OY		598	ValArgCysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGly	617
Db	1503	ACACGCTGC-----	1511	
OY		618	SerGlyLysValTyrlProThrValHisThrSerProProProGluIleLeuLysAspLys	637
Db	1511	-----	1511	
OY		638	AlaLeuValGluValAlaProSerProGlyProProThrLeuThrSerPheAsnIlePro	657
Db	1511	-----	1511	
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Db	1512	-----	1535	
OY		678	SerSerCysLysIleSerSerProCysSerLysValaAspSerGlyAlaCysGlyProAsp	697
Db	1536	--ATCTGCCGC-----	1544	
OY		698	SerCysProTyrlCysAlaArgThrGlyAlaGlyGluProGluSerAlaAspHisValMet	717
Db	1544	-----	1544	
OY		718	ProAspSerAspSerGluAlaValTyrlGluPheThrGlnAspAlaGlnHisSerAspLeu	737
Db	1544	-----	1544	
OY		738	ArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSer	757
Db	1545	-----	1571	
OY		758	ValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValaAspSerLysTyrl	777
Db	1572	-----	1607	

Qy		778	pheGIYArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetCglyIleGluTyr	797
Dd		1608	TGCTACTGGCGGTGTAAGTTGGCTTCCTCCACCAACGTTGACCATTGCTCAGAGCAC	1667
Qy		798	HISgluGlnProgluGluLeuThrAsnAlaleuGlulileSerAsnIleValPheThrSer	817
Dd		1668	CATGGGCAGCCCTTGTTGGCTCACCCAGACCAGAAGTATGCCAACAAAGTCTGCTCGC	1727
Qy		818	LeuPheAlaleuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys	837
Dd		1728	CTCTTCACTGTGAAGATGCTCTCAAACGTATACGGCCCTGGCCCCCTGTCTAAGTTGCC	1787
Qy		838	AsnProTyrAsnIlePheasp-----GlyValIleValIleSerVal	852
Dd		1788	TCCTTTTTC AACCGCTTTGACTGCTTCGTGTTGTGGGGGCATCCTAGAAAACCACTTGG	1847
Qy		853	TyrGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet	872
Dd		1848	GTCGAGGTGGGGGCCCATGCAGCCCTTTGGCATCTCAGTGTCCGATGTGTACGTCTCCTC	1907
Qy		873	ArgValLeuLysLeuValArgPheLeuProAlaleuGlnArgGlnLeuValValLeuMet	892
Dd		1908	AGGATCTTCAGAGGTACACCAAGCACTGGGCATCCCTGAGCAATCTGTGGCATCTTGGCTC	1967
Qy		893	LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe	912
Dd		1968	AATTCATGAGTAGTCCATCGCCTCCTTGCTGCTCTTCTCTTCTTCATCATCATCTTC	2027
Qy		913	SerIleLeuGlnMethisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr	932
Dd		2028	TCCCTGCTTGGCATGCAGCTGTGGGGGCAAGTTCACTTTGACCAG-----ACC	2078
Qy		933	LeuProAspArgLysAsnPheAspSerLeuLeuTPrAlaIleValThrValPheGlnIle	952
Dd		2079	CACACCAGAGGAGCACCTTTGATACCTTCCCACAGCCCTCCTCACGTCTTTCAGATC	2138
Qy		953	LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSer-----	968
Dd		2139	CTGACTGTTGAGGATTGGAACGTTGTCATGTATGATGATCATGCGCTACGGTGGGCC	2198
Qy		969	-----ThreSerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyr	986
Dd		2199	TTCTTCCAGGAGTGTGTTGTTTATTTTCATCATCTTTCATCTGTGGCAACTAC	2258
Qy		987	ValLeuPheAsnLeuLeuValAlaIleLeuValGlnGlyPheGlnAlaGlnGlyAspAla	1006
Dd		2259	ATCCTGCTGAACGTGTTCTTCCATTGCGCGTGATACCTA--GCCAGCGGGGATGCA	2315
Qy		1007	ThrLysSerGluSerGluProAspPhePheSerProSerValAspGlyAspGlyAspArg	1026
Dd		2316	GGCACTGCCAAA-----GACAAGGGCAGA	2339
Qy		1027	LysLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeu	1046
Dd		2340	GAGAAG-----	2345
Qy		1047	ProProLeuIleIleHisThrAlaAlaThrPrometSerHisProLysSerSerSerThr	1066
Dd		2346	-----AGCAGTGAGGAACCCCTCCAAAGGAGACAAAGTA	2381
Qy		1067	GlyValGlyGluAlaLeuGlySerGlySerArgArgThrSerSerSerGlySerAlaGlu	1086
Dd		2382	TTGGTG-----	2387
Qy		1087	ProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgSerSerProHisSer	1106
Dd		2388	CCTGGTGAAGATGAGACGCAAG-----GGTGCAAGAGTGA	2429
Qy		1107	ProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArg	1126
Dd		2430	-----GAGACA	2435
Qy		1127	AlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu	1146

Db 2436 GCACCAAGGCATG-----GAG 2450
QY 1147 GYGInGIuSerGIuAspGIuGIuSerSerGIuGIuAspArgAlaSerProAlaGIy 1166
Db 2451 GAGGAGGAGGAGGAGGAAGAGAGAGGAGGAGGAGGAAGAAAATGTCGACGA 2510
QY 1167 SerAspHisArgHisArgGIySerLeuGIuArgGIuAlaIySerSerPheAspLeuPro 1186
Db 2511 -----CATGTGAACTCTTGCAAGAAAGTAGTACCAGGAGGAGGTGTACCC 2558
QY 1187 AspThrLeuGIuValProGIyLeuHisArgThrAlaSerGIyArgSerSerAlaSerGIu 1206
Db 2559 -----ATCCCT----- 2564
QY 1207 HisGIuAspCysAsnGIyLyssSerAlaSerGIyArgLeuAlaArgThrLeuArgThrAsp 1226
Db 2564 ----- 2564
QY 1227 AspProGIuLeuAspGIyAspAspAsnAspGIuGIuAsnLeuSerLySGIyGIuArg 1246
Db 2565 -----GAAGGC----- 2570
QY 1247 ILeGIuAlaTrpValArgSerArgLeuProAlaCysCysArgGIuArgAspSerTrpSer 1266
Db 2571 -----AGT 2573
QY 1267 AlaTyrIlePheProGIuSerArg---PheArgLeuLeuCysHisArgIleIleThr 1285
Db 2574 GCCTTCTTGCCTTAGCCAAACCAACCCGCTTCGGAAGCCCTGCACACACTCATACAT 2633
QY 1286 HisLySmetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAla 1305
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QY 1306 MetGIuArgProIySIIeAspProHisSerAlaGIuArgIlePheLeuThrLeuSerAsn 1325
Db 2694 GCTGAGGAGACCC---ATCCGAGCTCACTCTTCCGAACCATATTCTGGGATATTTGAT 2750
QY 1326 TyrIlePheThrAlaValPheLeuAlaGIuMetThrValIySValValAlaLeuGIyTrp 1345
Db 2751 TATGCTTCACTCCATATTCTACTGTGAGATTTCTACTCAAGATGACAGTGTGGGGCC 2810
QY 1346 CysPheGIyGIuGIuAlaTyrLeuArgSerSerTrpAsnValLeuAspGIyLeuLeuVal 1365
Db 2811 TTCCTGCACCGAGGCTCTTCTGCGGAGCTGTGTTCAATCTGTGGATCTCTTGTC 2870
QY 1366 LeuIleSerValIleAspIleLeuValSerMetValSerAspSerGIyThrLySIIeLeu 1385
Db 2871 AGTGTCTCCCTCATCTCTTCGCGATCCAC-----TCCAGTGGCATC 2912
QY 1386 GIyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArg 1405
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QY 1406 AlaGIuGIyLeuLySIIeValGIuThrLeuMetSerSerLeuLySProIIeGIyAsn 1425
Db 2973 GCCAAGGAGCTCAAGCATGTGTGTCAGTGTGTTCGTGGCCATCCGGACATCGGAAC 3032
QY 1426 ILeValValIleCysCysAlaPhePheIleIlePheGIyIleLeuGIyValGIuLeuPhe 1445
Db 3033 ATCATGATTGTCAACCACTTTCAGTTTCATGTTGCGCTGCATTGTGTTCAGCTGTTC 3092
QY 1446 LySGIyLySPhetheValCysGIuGIyGIuAspThrArgAsnIleThrAsn----- 1462
Db 3093 AAGGAAAATTCTACAGTTGCACGTGAGGCCAAACACACACCTGAAGAATGCAAGGC 3152
QY 1463 -----LysSerAspCysAlaGIuAlaSerTyrArg-----Trp 1473
Db 3153 TCCTTCTCATCTAACCTGATGAGATGTGTACGACCTTTGGTCCGGAGCGGCTGTGG 3212
QY 1474 ValArgHisLySIIeTyrAsnPheAspAsnLeuGIyGIuAlaLeuMetSerLeuPheValLeu 1493

Db 3213 GTCAACAGTGATTTTAACTTTGACAACGTCCTTTCAGCCATGATGGCCCTGTCACTGTC 3272
QY 1494 AlaSerLySAspGIyTrpValaAspIleMetTyrAspGIyLeuAspAlaValGIyValaAsp 1513
Db 3273 TCTACCTTTGAAGGCTGGCTCGCTGCTACTATACAGGCCATGATGACAAACGACGAAGAT 3332
QY 1514 GIuGIuProIIeMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeu 1533
Db 3333 GAGGCCCTTACTACAATTAACCATGTGAGATATCAGTATTCTTCATGTCTCATCATC 3392
QY 1534 ILeValAlaPhePheValLeuAsnMetPheValGIyValValaGIuAsnPheHisLyS 1553
Db 3393 ATCATGCGCTTCTTCATGATGAACATCTTGTGGGCTTTGTATCATCATCATTC----- 3446
QY 1554 CysArgGIuHisGIuGIuGIuGIuGIuAlaArgArgArgGIuLySArgLeuArgArg 1573
Db 3447 -----CGTGCCAGGAGGAGCAGAGTAGTACCAAACTGTAA----- 3482
QY 1574 LeuGIuLySArgArgSerLySGIuLySGIuMetAlaGIuAlaGIuCysLySProTyr 1593
Db 3483 CTGACAAAGAACACAGCGCAGTGTGTGAATATGCGCTCAAGCTCAGCACTCCGCCGA 3542
QY 1594 TyrSerAspTyrSerArgPheArgLeuLeuValHisIleuCysThrSerHisTyrLeu 1613
Db 3543 TACATCCCTAAGAATCCTCATCAGTACCGCGTGTGGGCCACTGTGAACSTGTGCTCTT 3602
QY 1614 AspLeuPheIleThrGIyValIleGIyLeuAsnValValThrMetAlaMetGIuHisTyr 1633
Db 3603 GAGTACTCATGTCTTGTGTCATCCTGCTCAACACGGTGGCCCTAGCCATGCAGACTAT 3662
QY 1634 GIuGIuProGIuIleLeuAspGIuAlaLeuLySIIeCysAsnTyrIlePheThrValIle 1653
Db 3663 GAACAGACTGCTCCCTTTAACTATGCCATGGACATCTCAACATGSGTCTCACTGGCCTC 3722
QY 1654 PheValPheGIuSerValPheLySIIeValAlaPheAlaPheArgArgPhePheGIuAsp 1673
Db 3723 TTCACCATTTGAGATGTGTCTCAAAATCATCGCCTTTAAACCCCAAGCATTTACTTGCAGAT 3782
QY 1674 ArgTrpAsnGIuLeuAspLeuAlaIleValLeuLeuSerIleMetGIyIleThrLeuGIu 1693
Db 3783 GCCTGGAATACGTTTGATGCTCTCATTTAGTGGCAGTGTAGTCGACATCGCCGTC-- 3839
QY 1694 GIuIleGIuValAsnLeuSerLeuPro--IleAsnProThrIleIleArgIleMetArgV 1713
Db 3840 ---ACAGAAGTCAATAGACAGCTCCGCATATGTATCACGTTCTTTCGCTCTTCCGAG 3896
QY 1713 allLeuArgIleAlaArgValLeuLySIIeLeuLySIIeMetAlaValGIyMetArgAlaLeu 1733
Db 3897 TCATGAGGCTG-----GTCAAGCTTCTGAGTAAGGGTGAGGGGATCCGACACTGC 3947
QY 1733 euHisThrValMet-----GIuAlaLeuProGIuValGIyAsnLeuGIyLeuLeuP 1750
Db 3948 TCTGACATTTCAACAAGTCTTTCAGGCTTGCCCTATGTG-----GCACTTCTCA 3998
QY 1750 heMetLeuLeuPhePheIlePheAlaIleLeuGIyValGIuLeuPheGIyAspLeuGIu 1770
Db 3999 TAGCAATGATATTCTTCATCTATGCAGTCAATTGGCATGCAGATGTTGGCAAGGTGGCTC 4058
QY 1770 ys---AspGIuThrHisProCysGIuGIyLeuGIyArgHisAlaThrPheArgAsnPheG 1789
Db 4059 TTCAGAGCGGCACGCAG-----ATMAATCGAAACAACAATTTCCAGACCTTTTC 4106
QY 1789 IyMetAlaPheLeuThrLeuPheArgValSerThrGIyAspAsnTrpAsnGIyIleMet- 1808
Db 4107 CGCAGGCTGTGCTGTTCTGTTCAGGTGTGCCACTGGTGAAGCCTGGCAAGAGATAATGC 4166
QY 1809 -----LysAspProSerArgAspCysAspGIuGIuSer----- 1819
Db 4167 TAGCCAGCCTTCCAGGAATGCATGTGACCCCTGAGTCTGACTTTGGCCCGAGGAGGAAT 4226
QY 1820 --ThiCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaG 1839
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		/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCCCTGTGTTTTTTTTTTT 3'] . Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN		
Alignment Scores:	3.84e-87	Length: 990
Pred. No.:	1406.00	Matches: 293
Score:	90.77%	Conservative: 2
Percent Similarity:	90.15%	Mismatches: 22
Best Local Similarity:	11.69%	Indels: 9
Query Match:		Gaps: 2
DB:	4	
US-09-611-257A-24 (1-2287) x BI905383 (1-990)		
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Db	1	AACACCGTCATCTCACCCCATCGTACTGTGTCCTTCGTGTCAGCGCCACGTTGTGCT 60
QY	1842	UValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaly 1862
Db	61	GGTCAACGTGGTCTATAGCCGCTGCTGATGAACACCTGGAAGACGACAAAGAGGCCAA 120
QY	1862	SGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerProGlnPr 1882
Db	121	GGAGGAGCGGAGTTGGAGGCGGAGCTGAGCTAGAGATGAAGACACTCAGCCCGCAGCC 180
QY	1882	OHissSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsnSerThrAs 1902
Db	181	CCACTCCCCCGCTGGGACAGCCCTTCTCTGGCTGGGTGGAAGGTGTCATATAGCCCTGA 240
QY	1902	PSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAla---SerGlyPh 1921
Db	241	CAGCCCTAAGCCTGGGGCTCCACACACACGCGCCACATTGAGACGCTTTCAGGCTT 300
QY	1921	eSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyPr 1941
Db	301	CTCCCTTGAGCACCCCAAGATGGTACTCACACTGAGGAGGGGCCAGTCCCCCTAGGACC 360
QY	1941	oAspLeuLeuThrValAlaArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSe 1961
Db	361	AGACCTGCTGACTGTGAGGAAGTCTGTGTTCAGCCGGAACACTCTCTGCCCAATGACAG 420
QY	1961	rTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpGlyLe 1981
Db	421	CTACATGTGCCGCAATGGAGCACCTGCCAGAGATCCCTAGGACACAGGGGCTGGGGCT 480
QY	1981	uProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrSerCy 2001
Db	481	CCCCAAAGCCCAGTCAAGCTCCATCTTGTCTGTTCACCTCCCAACCAAGACACACGCTG 540
QY	2001	sIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProThrTr 2021
Db	541	CATCCTACAGCTTCCCAAGATGCACACTATCTGCTCCAGCCTCATGGGGCTCCCACTG 600
QY	2021	pGlyAlaIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuAr 2041

Db	601	GGGCGCCATCCCTAAACTACCCCCACCTGGCGGCTCCCTCTGTGCTCAGAGGCTCTCAG 660
QY	2041	gArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAs 2061
Db	661	GCGCCAGGACGACATAGAAGTGAAGTCCCTGAGCTGACAGGCTGTGGTTAGCCGGAAGA 720
QY	2061	pLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerSerPheTrp-G 2081
Db	721	CTGTGTTGACAGAGGTGAGTGGGCCCTCTGCTGCCCTTGACCCGTC-CATCTTCTGGGG 779
QY	2081	lyGlySerSerIleGlnValGlnGlnArgSer---GlyIleGlnSerLysValSerLys- 2099
Db	780	GCGGGTCAGCATCCATGTGCCCAGCAGCGGCTCCGGCGGAGCCAGACGAAGTCTCCAAG 839
QY	2100	HisIleArgLeuPro-AlaProCysPro-GlyLeuGlu-ProSerTrpAlaLysAspPro 2118
Db	840	CACATCCGCTGCCAGGCGCCCTTGCCAGGGCCTGGAAACAGGCTGGGCCAAGGACCTC 899
QY	2119	ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2138
Db	900	AAGAGAACCAAGAACGATTAAACTTGACCGGAGCTGAAGCTGGATCAGGGGAATC 959
QY	2139	Leu 2139
Db	960	TTG 962
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BI736618		
LOCUS		
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ACCESSION	BI736618	
VERSION	BI736618.1 GI:15713631	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE		
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLML1936 row: b column: 23 High quality sequence stop: 853.	
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ORIGIN		
Alignment Scores:	9.39e-86	Length: 939
Pred. No.:	1385.50	Matches: 282
Score:	92.48%	Conservative: 1
Percent Similarity:		

Best Local Similarity: 92.16% Mismatches: 18
Query Match: 11.52% Indels: 8
DB: 4 Gaps: 2

US-09-611-257A-24 (1-2287) x B1736618 (1-939)

QY	1950	GIYValSerArgThHisSerLeuProAsnAspSerTyrMetCysArgAsnGlySerThr	1969
DB	3	GGTGTACGCCGACACTCTCTGCCCCAATGACACTATCATGTGCCCAATGGAGCACT	62
QY	1970	AlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerIle	1989
DB	63	GCCGAGAGATCCCTAGACACAGGGGCTGGGGCTCCCAAGCCCACTCAGGCTCCATC	122
QY	1990	LeuSerValHisSerGlnProAlaAspThrSerCysIleLeuGlnLeuProLysAspVal	2009
DB	123	TTGTCTGTCTACTCCCAACACAGACACCAGCTGCATCTTACAGCTTCCCAAGATGCA	182
QY	2010	HisTyrLeuLeuGlnProHisGlyAlaProThrTyrGlyAlaIleProLysLeuProPro	2029
DB	183	CACTATCTGCTCCAGCCTCATGGGGCTCCCACTGGGGCGCCATCCTTAACTACCCCA	242
QY	2030	ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAsp	2049
DB	243	CTGGCCGCTCCCTCTGGCTCAGAGGCTCTCAGCGCCAGCAGCAATAAGACTGAC	302
QY	2050	SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuSerGluValSerGlyPro	2069
DB	303	TCCCTGGACGTGACAGGGCTGGGTAGCCGGAGAAGCCTGTGTGACAGGTGAGTGGCCC	362
QY	2070	SerCysProLeuThrArgSerSerSerPheTyrGlySerSerIleGlnValGlnGln	2089
DB	363	TCCTGCCCTCTGACCCGCTCTCATCTTCTGGGGGGGTGAGCATTCAGGTGACGACG	422
QY	2090	ArgSerGlyIleGlnSerLysValSerLysHisIleArgLeuProAlaProCysProGly	2109
DB	423	CGCTCCGGCAGCCAGACAAGTCTCCAAGCACATCCGCTGCCAGCCCTTGGCCAGGC	482
QY	2110	LeuGluProSerTyrAlaLysAspProProGluThrArgSerSerLeuGluLeuAspThr	2129
DB	483	CTGGAACCCAGCTGGGCCAAGAGACCTCAAGAGACCAGAAGCAGCTTAGAGCTGACACG	542
QY	2130	GluLeuSerTyrIleSerGlyAspLeuLeuProSerSerGlnGluProLeuPhePro	2149
DB	543	GAGCTGAGCTGATTTCAAGAGACCTCTGCCCCAGACTCAGGAAGAACCCCTGTCCCCA	602
QY	2150	ArgAspLeuLysCysTyrSerValGluThrGlnSerCysArgArgArgProGlyPhe	2169
DB	603	CGGACTTGAAAAAATGCTACAGTGTAGAGGCCACAGACTGCCGGCGGCGCTGGGTCC	662
QY	2170	TyrPLeuAspGluGlnArgArgHisSerIleAla-ValSerCysLeuAspSerGlySerG1	2189
DB	663	TGGCTAGACGAACAGAGAGACACTCCATCGTTGTCAAGCTGTGACAGCGGCTCCCA	722
QY	2189	nProArgLeuCysProSerProSerSerLeu-GlyGlyGlnProLeuGlyGlyProGlyS	2209
DB	723	GCCCCGCTATGTCCAAGCCCCCTCAAGCTCGGGGGGCCCAACCTTGGGGGCCCTGGGGA	782
QY	2209	erArgProLysLysLeuSerProProSerIleSerIleAspProProGluSerGlnG	2229
DB	783	GCCGGCCTTAAGAAAAACTCAG-CCACCCAGTATCTTATAGACCCCGGAGAGACA---G	838
QY	2229	LysSerArgProProCysSerProGlyValCysLeuArgArgAlaPro-AlaSerAsp	2248
DB	839	GAACCTCGGGCCCATGCACT-GGCGTGTGCC-AGGAGAGG---CCGGCGCAAGAGAC	893
QY	2249	SerLysAspPro 2252	
DB	894	TCGAAGGATCCT 905	

RESULT 5
BM479323
LOCUS BM479323 1076 bp mRNA linear EST 05-FEB-2002

DEFINITION AGENCOURT_6418725 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502230
5', mRNA sequence.
ACCESSION BM479323
VERSION BM479323.1 GI:18528365
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1076)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM12140 row: a column: 15
High quality sequence stop: 692.
Location/Qualifiers
1. 1076
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5502230"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 1.06e-82 Length: 1076
Score: 1343.00 Matches: 281
Percent Similarity: 87.23% Conservative: 6
Best Local Similarity: 85.41% Mismatches: 19
Query Match: 11.17% Indels: 23
DB: 4 Gaps: 4

US-09-611-257A-24 (1-2287) x BM479323 (1-1076)

QY	1458	ArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrArgTyrValArgHisLys	1477
DB	3	AGGAACATCACCAATAATCGAGCTGCGCAGGCCAGTTACGGTGGTCCGACACAAG	62
QY	1478	TyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAsp	1497
DB	63	TACAACCTTGACAACCTTGGCCAGGCTGATGTCCCTGTTGCTTGGCTCCAAGAT	122
QY	1498	GlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIle	1517
DB	123	GGTTGGGTGACATCATGTAGATGGGCTGGATGCTGTGGGGTGGAGCACAGCCCATC	182
QY	1518	MetAsnHisAsnProTyrMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhe	1537
DB	183	ATGAACCAACAACCCCTGATGCTGCTGTACTTCATCTCGTTCCTCATTTGTGGCTTC	242
QY	1538	PheValLeuAsnMetPheValGlyValValValGluAsnPheHisLysCysArgGlnHis	1557
DB	243	TTGTCTGAACATGTTTGTGGGTGTGTGTGGAGAACTTCCACAAGTGTCCGCGACAC	302
QY	1558	GlnGluGluGluGluAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLys	1577
DB	303	CAGAGGAAGAGAGGCCCGCGCGGAGGAGGAAGCGCCTAAGAACTGAGAAAAAG	362

QY 1578 ArGArGSeRlySGlulysGlnMeCAlaGluAlaGlnCyAlsProTyrTyrSeRAspTyr 1597
Db 363 AGAAG-----AAAGCCAGTGCAACCTTACTACTCCGACTAC 401			
QY 1598 SeRArgPheArgLeuLeuValHisHisLeuCySthrSerHisTyrLeuAspLeuPheIle 1617			
Db 402 TCCCGCTTCCGGCTCCTCGTCCACCACTGTGCACCAAGCACTAACCCTTCTTCATC 461			
QY 1618 ThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGln 1637			
Db 462 ACAGGTGTCACTGGGCTGAACGTGTCAACCATGGCCATGGAGACACTACCAGCAGCCCCAG 521			
QY 1638 IleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGlu 1657			
Db 522 ATTCTGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTTGTGGAG 581			
QY 1658 SerValPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsnGln 1677			
Db 582 TCAGTTTCAACTGTGTGGCTTTGGTTCCGTGTTCTTCCAGGACAGGTGGAACAG 641			
QY 1678 LeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluVal 1697			
Db 642 CTGACCTGGCCATTGTGTCTGTTCATCATGGCATCAAGTGAAGAAATCGAGTTC 701			
QY 1698 AsnLeuSerLeuProIleAsnProThrIleIleArgIle-MetArgValLeuArgIleAl 1717			
Db 702 AACGCTCGCTGCCCATCAACCCCAACCATCATCCGATCATTGAAGGTGCTGCCATTGC 761			
QY 1717 aArgValLeuLysLeuLeu-LysMetAlaValGlyMet-ArgAlaLeuLeuHisThrVal 1736			
Db 762 CCGAGTGTGAAGCTGTGAAAAATGCGTGTGGCATGCCGCCGCTGTGCACACCGTGT 821			
QY 1737 MetGlnAla--LeuProGlnValGlyAsnLeuGlyLeuLeuPheMet-----LeuLeuP 1754			
Db 822 ATGCACGCCCTGTCCCGGTGGGAAACCTGGGACTTTTCTCTCCAGGCCGTTGTTT 881			
QY 1754 hePheIlePheAlaIleLeuGlyVal-----GluLeuPheGlyAspLeuGluCysAspG 1772			
Db 882 TTCATCCCTCGCCGCTCCTGCGCGGTGCAGCCTCTTTTGGAGAA----- 928			
QY 1772 luThrHisProCysGlu 1777			
Db 929 -----CCTTGCAAG 937

RESULT 6
BM451648 1064 bp mRNA linear EST 05-FEB-2002
LOCUS BM451648 1064 bp mRNA linear EST 05-FEB-2002
DEFINITION AGENCOURT_6394764 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5493169
5', mRNA sequence.
ACCESSION BM451648
VERSION BM451648.1 GI:18500688
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1064)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LHAM2116 row: h column: 02
High quality sequence stop: 657.
FEATURES
source 1..1064
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5493169"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_1db="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

Alignment Scores:
Pred. No.: 1.02e-79 Length: 1064
Score: 1300.00 Matches: 275
Percent Similarity: 78.89% Conservative: 9
Best Local Similarity: 76.39% Mismatches: 20
Query Match: 10.81% Indels: 56
DB: 4 Gaps: 6

US-09-611-257A-24 (1-2287) x BM451648 (1-1064)

QY 1475 ArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAla 1494
Db 1 CGGCAACAAGTACAACTTGAACAACCTTGGCCAGCCCTGATGTCCCTGTTGGCC 60			
QY 1495 SerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGln 1514			
Db 61 TCCAGGATGTTGGGTGACATCATGTACGATGGGCTGATGCTGTGGGCGTGAGACCAG 120			
QY 1515 GlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuIle 1534			
Db 121 CAGCCATCATGAACCAACACCCCTGATGCTGTACTTCATCTCGTCTCATTT 180			
QY 1535 ValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPheHisLysCys 1554			
Db 181 GTGGCTTCTTGTCTCTGAACATGTTGTGGGTGTGTGTGAGAGACTTCCACAAGTGT 240			
QY 1555 ArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLeuArgArgLeu 1574			
Db 241 CGGCAGACCAAGAGAGAGAGAGAGCCCGCGCGGAGAGAGAGCGCTTACGAAGACTG 300			
QY 1575 GluLysLysArgArgSerLysGluLysGlnMeCAla----- 1586			
Db 301 GAGAAAAAGAGAGAGTAAGAGAGAGAGATGGCTGATCTAATGCTGAGCATGTAATT 360			
QY 1587 -----GluAlaGlnCysLysProTyrTyrSerAsp 1596			
Db 361 GCTTCGGCAGCTCAGCCAGCGCTGCTCAGAGCCCAAGTGAACCTTACTCCGAC 420			
QY 1597 TyrSerArgPheArgLeuLeuValHisHisLeuCySthrSerHisTyrLeuAspLeuPhe 1616			
Db 421 TACTCCGCTTCCGGCTCTCTGTCACCACTTGTGCACCAAGCACTAAGACTCTTTC 480			
QY 1617 IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro 1636			
Db 481 ATCACAGGTGTCACTCGGGCTGAACGTGTACCACTGGCCATGGAGCACTACCAAGACCC 540			
QY 1637 GlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPhe 1656			
Db 541 CAGATTCTGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTTGTCTTG 600			
QY 1657 GluSerValPheLysLeuValAlaPheAlaPheArgArgPheGlnAspArgTrpAsn 1676			
Db 601 GAGTCAGTTTCAAACTTGTGGCTTGTTCCTTCAGAGCAAGTGAAC 660			
QY 1677 GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGlu 1696			
Db 661 CAGCTGACCTGNCATGTGTGTCTCATTCATGGGCATCACGCTGGAAGAAATCGAG 720			
QY 1697 ValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle 1716			

Db 721 GTCACGCGCTCGCTGCCCATCAACCCACCATCATCCGCATCATGAGGGTGCTGCCCAT 780

QY 1717 AlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHis-ThrVal 1736

Db 781 GCCCGAATGCTGAAGCTGCTGCAAAATGCTGTGGCATGCGGCGCTGTGCACAAACCGG 840

QY 1736 lMet-GlnAlaLeuProGlnValGlyAsnLeuGly--LeuLeuPheMetLeuLeuPheP 1755

Db 841 GATGCCAGGCGCTGCCAGAGTGGGAAACCTGGAACTTCCCTTCACAGTGTGGGTT 900

QY 1755 he---lIlePheAlaAlaLeuGlyValGlyLeuPheGlyAspLeuGlyCysAspGlyuThrH 1774

Db 901 TTCACACTTGGCCAGCTCTGGGGCC-----GGGGAACCTCCTTGT----- 941

QY 1774 lSProCysGlyGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuT 1794

Db 941 ----- 941

QY 1794 hrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspProSer 1812

Db 942 -----GGAGAACCGTGGATGGG--GACAAAGAACCCACC 974

RESULT 7

AY416501 5666 bp DNA linear GSS 17-DEC-2003

LOCUS Mus musculus SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence,

DEFINITION genomic survey sequence.

ACCESSION AY416501

VERSION AY416501.1 GI:39772461

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 5666)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 5666)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source

1..5666

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

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/gene="SCN8A"

/locus_tag="HCM5911"

ORIGIN

Alignment Scores:

Pred. No.: 4.33e-78 Length: 5666

Score: 1293.50 Matches: 533

Percent Similarity: 36.60% Conservative: 338

Best Local Similarity: 22.39% Mismatches: 757

Query Match: 10.75% Indels: 755

DB: 9 Gaps: 83

US-09-611-257A-24 (1-2287) X AY416501 (1-5666)

QY 25 ProProGlyProArgLeuAlaArgGlyTrpThrArgArgMetGluArgAlaProArg 44

Db 22 CCACGAGGCCCGACAGATTTCAGCCTTTCACC-----CCCGAG 60

QY 45 SerArgAspSerProValAlaSerArgSerSerThrThrCysProGlyProGlyAlaAla 64

Db 61 TCGCTGGCAACATCGAGAGCGCGCATCCCGAGAGCAAGCTCAAGAAACCAACCCAGGCG 120

QY 65 GlyAlaGlySerThrGlyLysAspProGlySer-----AlaAspSerGly 79

Db 121 GATGCAGCCACCGGAGAGCATGAAGACAGCAAGCCCAAGCCAAACAGTGAACCTGGAG 180

QY 80 Ala-----GluGlyLeu----- 83

Db 181 GCGGGGAAGTTTGCTTTCATCTACGGGACATCCCGAAGGCTGTGGCTTCCC 240

QY 84 -----ProTyr----- 85

Db 241 CTGAGAGCTTGAACCCGCTACTATTGACGACGAAAACTTTGTAGTATTAACAGAGG 300

QY 86 -----ProAlaLeuAlaProValValPhePheTyrLeu 96

Db 301 AAAACTCTCTTCAGATTTAGCGCCACTCTGCCTTG-----TACATTCTA 345

QY 97 SerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGly 116

Db 346 AGTCCTTTTAACCTGATAGAAGAAATAGCTATTAAATTGTGATTACATTCTTTCAGC 405

QY 117 ArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCys 136

Db 406 ATGATCATCATGTGCACCATCTTGACCAACTGTGATTTCATGACTTTTGTAAACCTGCC 465

QY 137 GluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIle 156

Db 466 GAA-----TGGTCCAAGAATGTGAGTAGACA 492

QY 157 Phe---AlaPhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGly 175

Db 493 TTCACAGGAGATTACACATTGTAATCACTGTTGAAATCATCGCAGAGGTTTC----- 546

QY 176 LysLysCys-----TyrLeuGlyAspThrTrpAsnArgLeuAspPhePhe 190

Db 547 -----TGCATAGACGGCTTCACTTCTTTCAGAGACCCCGTGAACCTGTTAGACTTCAGT 600

QY 191 lIleValIleAlaGlyMetLeuGlyuTyrSerLeuAspLeuGlnAsnValSerPheSerAla 210

Db 601 GTCATCATGATGGCGTATATATAACAGAGTTGTAAACCTAGGCAATGTT-----TCAGCT 654

QY 211 ValArgThrValArgValLeuArgProLeuArgAlaAlaIleAsnArgValProSerMetArg 230

Db 655 CTACGACACTTTCAGGGTACTGAGGGCTTGAAGAACTATTTCGTTAATCCAGGCGCTGAG 714

QY 231 lIleLeuValThrLeuLeuLeuAspThrLeuPrometLeuGlyAsnValLeuLeuLeuCys 250

Db 715 ACAATCGTGGCGCCCTCATCCAGTCTGTGAAGAGCTGTCAAGCGTATGATCCTGACG 774

QY 251 PhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArg 270

Db 775 GTGTTCTGCCTGAGTGTCTTCGCCCTGATTGGCCTGCAGGCTTTCATGGGGAACCTTGA 834

QY 271 AsnArgCysPheLeu---ProGluAsnPheSerLeuProLeuSerValAspLeuGluPro 289

Db 835 AACAAAGTGTGTGTGTGGCCCATTAACCTTCAAC-----GAGAGC 873

QY 290 TyrTyrGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsn 309

Db 874 TATCTG-----GAGAAC 885

QY 310 GlyMetArgSerCysArgSerValProThrLeuArgGlyGluGlyGlyGlyProPro 329

Db 886 GGCACACAGA----- 894

QY 330 CysSerLeuAspTyrGluThrTyr----- 337

Db 895 ---GGCTTCGACTGGGAGGAGTATATCAACAATAAAACAACTTTTACATGTCCTCCG 951
QY 338 -----AsnSerSerAsnThrThrCysValAsnTrpAsn 349
Db 952 ATGCTAGAACCTTGCTCTGCGGAAACAGCTCTGACGCCGGGCAATGCCAGAGGGGTTTC 1011
QY 350 GlnTyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPhe 369
Db 1012 CAG-----TGCATGAAGAAGCAGAAAGAAATCCCACTACGGCTTACACCACTTC 1059
QY 370 AspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlyTrpVal 389
Db 1060 GACACCTTGACCTGGCCTTCCTGCGACCTGTCGCTCATGACTCAGACTACTGGGAG 1119
QY 390 AspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeu 409
Db 1120 AACTTATACCACTGACCTTACGAGCGGCTGGGAAACGTAATGATCTCTTGTCTTG 1179
QY 410 LeuIleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGln 429
Db 1180 GTGATCTTCGTGGGTTCTTCTATTGTGTGAACCTTGATCTTGGCTGTGGGCCATGGCT 1239
QY 430 PheSerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeu 449
Db 1240 TACGAAGAG----- 1248
QY 450 SerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeu 469
Db 1249 CAGAACCAAGCAACACTGAGAGAGCAGACAGAAAGAGCAGATTCAAGCGCATGCTG 1308
QY 470 LysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAla 489
Db 1309 GAGCAGCTC-----AAGAAGCAGCAGAGAGCGCATCAGAAAGATGCC 1353
QY 490 IleGlyValArgAlaGlyLeuLeuSerSerProValAlaArgSerGlyGlnGlu----- 507
Db 1354 ATT-----GAAGAAGAGGGAAGATGGGCTA 1380
QY 508 -----ProGlnProSerGly-SerCysThrArgSerHisArgArgLeuSerValHisHis 525
Db 1381 GGCTCTCCGAGAGCTCATCTGAGCTGTCTAAACTCA----- 1417
QY 525 sLeuValHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 545
Db 1417 ----- 1417
QY 545 gValProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMe 565
Db 1418 -GTTCCAAAGAGCGCGAAGAGCGCTCGGAACCGACGGAAGAGAGAAAGCAGAGGAGCTC 1476
QY 565 tLeuProProProSerThrProThrProSerGlyGlyProProArgGlyAlaGluSerVa 585
Db 1477 TCTGAAG-----GGAGAGAAAGGGGAGCC----- 1501
QY 585 lHisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPr 605
Db 1502 -----CCGAG 1506
QY 605 oArgCysProSerGluAla-----SerGly--ArgTh 615
Db 1507 AAGGTGTTTAAGTCAGAGTCGGAAGATGCATGAGAAAGGAGCCTTCCGGCTGCCAGAC 1566
QY 615 rValGlySerGlyLysValTyrProThrValHisThrSerProProProGluIleLeuLy 635
Db 1567 AATAGGATA-GGGAGGAATTTCC-----ATCAT 1595
QY 635 sAspLysAlaLeuValGluValAlaProSerProGlyProProThrThrLeuThrSerPheAs 655
Db 1596 GAATCAGTCGCTGCTCAGCATC-----CCAGGCTCGCCCTTCTTCCCGACACAA 1646
QY 655 nIlePro-----ProGlyProPhe----- 661

Db 1647 CAGCAAAAGCAGCATCTTCACTTTCGGGGTCTTGAGCGGTTCCGGACCCCGGTTCCGA 1706
QY 662 -----SerSerMetHisLysLeuLeuGluThrGlnSer-ThrGlyAlaCysH 677
Db 1707 GAACGAGTTCCGACAGCAGACAGACACAGCAGTGAAGAAAGTAGAGCGCGCGACTC 1766
QY 677 lSerSerCysLysIleSerSerProCysSer----- 687
Db 1767 GCTCTCATCCCGA---TCCGCGCCCGCAGAGCGCGCAGAGCTACAGCGGCTACAGCGG 1823
QY 688 -----LysAlaAspSerGlyAlaCysGlyPro----- 696
Db 1824 CTACAGCCAGTGACGCCGCTGCTCGCGCATCTTCCCAAGCCTGCGCGCAGCGTGAACG 1883
QY 697 -----AspSerCysProTyrCysAlaArgThrGlyAlaGlyGluProGluS 712
Db 1884 CAACAGCACCGTGAGCTGCAATGGCGGTGTCTCATCGGGCTT-GGC-----TCGC 1936
QY 712 erAlaAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspA 732
Db 1937 ACATCGGCGGCTCCTCGCTGAGGCAACAACAGTGAAGATTAAAG----- 1983
QY 732 lAGlHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProA 752
Db 1984 -----A 1984
QY 752 spAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLys- 771
Db 1985 AGAAGGCCCTGGATCGCTCTTAAGTCCATGGAACAACCTCGCTCCTAAGCAGCAGAGG 2044
QY 772 --IleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrL 791
Db 2045 ACAGAAATCAACAGT-----ATAATGAGCGTTGTCAACAACACAC 2083
QY 791 eu----- 791
Db 2084 TAGTGGAAGNN 2143
QY 791 ----- 791
Db 2144 NNN 2203
QY 791 ----- 791
Db 2204 NNN 2263
QY 792 --SerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleS 811
Db 2264 NNN 2323
QY 811 erAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrG 831
Db 2324 NNNNNNNNNNGTGTTCACACTGGGATCTTCACGCGCGGAATGTTCCTGAAGCTCATAGCCATGG 2383
QY 831 lyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleS 851
Db 2384 ATCCCTACTATTACTTCCAAGAGGCTGGAACATTTTGAACGGAATTATTCGTCTCCCTCA 2443
QY 851 erValTrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgL 871
Db 2444 GTTTAATGAGCTGGGCTTGACAGACGTGAGAGGGCTCTCAGTGCGCATCTTCCGAT 2503
QY 871 euMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValL 891
Db 2504 TGCTCCGAGTCTTCAAAATTGGCCAAGTCTGGCCCACTGAACATGCTGATCAAGATCA 2563
QY 891 euMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheI 911
Db 2564 TTGGGAACCTCGTGGCGCCCTGGGCAACCTGACCCTGTGCTGGCCATCATTTGCTTCA 2623
QY 911 lePheSerIleLeuGlyMetHisLeuPheGly-----CysLysP 924
Db 2624 TCTTGGCGGTGGTGGAATGACGCTCTTGGAAAGAGCTTACAAGAGTGCGTCTGTAAAG 2683

QY 924 heAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuT 944
Db 2684 TCAGCCAGAG-----TGCAAGCTCCCG---CGCTGGCACATGAACACTTCTTCC 2731
QY 944 rPAlaIleValThrValPheGlnIleLeuThrGlnGlu-----AspTrpAsnLysValL 962
Db 2732 ACTCCTTCCTCATCGTCTTCCGAGTGCTGTGGGAGTGCATCGAGACCAGTCTGAAC 2791
QY 962 euTyraSnGLyMetAlaSerThrSerSerTrpAlaIleLeuTyrrPheIleAlaLeuMetT 982
Db 2792 TTATTTCTGGCCTTGCTTCTGAG----- 2814
QY 982 hrPheGlyAsnTyrrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnA 1002
Db 2815 -----CTCCTTCAGCGCAGACAAT 2833
QY 1002 laGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAspG 1022
Db 2834 CTGGCGGCCACGACGACGCGGGAATGA-----CAACCTGCAGATATCG 2881
QY 1022 LysArgLysArgLysArgLysArgLeuAlaLeuValAlaLeuGlyGluHisAlaGluLeuA 1042
Db 2882 GTGATCCGGATCAAGAAGGGCGT-----GGCCTGGGCCAA----- 2916
QY 1042 rGlySerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerHisProL 1062
Db 2917 -----AGTGAAGGTG 2926
QY 1062 ySerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArgArgThrSers 1082
Db 2927 CATGCCCTTCATGCAGGCACTTCAAGCAACGGAGGCTGATGAAGTGAACCTTTAGAC 2986
QY 1082 erGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysProProSerAlaArgS 1102
Db 2987 GAGCTGTATGAGAAGAGGCCAATCGCATCGCCA----- 3021
QY 1102 erSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgA 1122
Db 3022 -----CCACACCG-GCGTGACATTCACAGGAACGGCGACTTCCAGAAATAATGAATCG 3075
QY 1122 snSerLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgSerL 1142
Db 3076 CACCACTAGCGGCATCGGCAAACTG----- 3101
QY 1142 euLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluAspArgA 1162
Db 3102 -----GACGATACCAGCTCCTCAGAA----- 3122
QY 1162 laSerProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSers 1182
Db 3123 -----GGGAGTA 3129
QY 1182 erPheAspLeu---ProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyA 1201
Db 3130 CCATCGACATCAAGCCTGAGGTGGAAGAAGTCCCA----- 3164
QY 1201 rgSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaA 1221
Db 3164 ----- 3164
QY 1221 rgThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluGlyAsnL 1241
Db 3165 -----GTGAGCAGCCTGAGGAATACTTGATCCAGACGCCCTGCTTACGGAGGGTTGTG 3219
QY 1241 euSerLysGlyGluArgIleGlnAlaTrpValArgSerArgLeuProAlaCysCysArgG 1261
Db 3220 TCCAGAGGTTCAAG-----TGCTGCCAGG 3243
QY 1261 LuArg-----AspSerTrpSerAlaTyrrIlePheProProGlnSerA 1275
Db 3244 TCAACATCGAGAGAGACTAGGCAAGTCGTG-----TGGATC----- 3281

QY 1275 rgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValValLeuV 1295
Db 3282 --CTGCGAAACCTGCTTCTCCTCATTTGGAGCACAAATTGGTTGAGACCTTCATCATTT 3339
QY 1295 alIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHis 1315
Db 3340 TCATGATTTCTCTCAGCAGTGAGCCCTGGCTTCGAGACATCTAATTGAGCAGAGGA 3399
QY 1315 erAlaGluArgIlePheLeuThrLeuSerAsnTyrrIlePheThrAlaValPheLeuAlaG 1335
Db 3400 AGACCATCCGTACCATCTCGAGTATGCGGACAAGGCTTACCTACCTAATGAGCTCTGG 3459
QY 1335 LuMetThrValLysValValAlaLeuGlyTyrrCysPheGlyGluGlnAlaTyrrLeuArgS 1355
Db 3460 AGATGTTGCTCAATGGACAGCCTATGGCTTCGTC-----AAGTTCTTACCA 3507
QY 1355 erSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValS 1375
Db 3508 ATGCCCTGGTGTGGTTGGACTTCTCCTCATTTGGCTNNNNNNNNNNNNNNNNNNNNNNNN 3567
QY 1375 erMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuA 1395
Db 3568 NNN 3627
QY 1395 rgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluT 1415
Db 3628 NNNNN-----NN 3678
QY 1415 hrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheT 1435
Db 3679 CCTGGTGGCGGCATCCCTCCATCATGAACGTGCTGCTGTGTCATCTTCTGGC 3738
QY 1435 leIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyG 1455
Db 3739 TGATTTTCAGCATCATGGCGGCTTAACCTGTTTCTGGGAATACCACTACTGCTTCAACG 3798
QY 1455 LuAspThrArg-----AsnIleThrAsnLysSerAspCysAlaGlu- 1468
Db 3799 AGACTTCAGAAATCCGCTTCGAATCGACGAGGTGAACAATAAACCGACTGTGAGAAGC 3858
QY 1469 -----AlaSerTyrrArgTrpValArgHisLysTyrrAsnPheAspAsnL 1483
Db 3859 TCATGGAGGGCAACAACAAGATCCGATCGAAGGAAGAGCTCAAGATCACTTCGACAACG 3918
QY 1483 euGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTyrrValAspIleM 1503
Db 3919 TCGGGGCAAGCTACCTGGCCCTTCTTCAAGTGGCAACCTTCAAAAGCTGATGACATCA 3978
QY 1503 euTyrrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProT 1523
Db 3979 TGTATGCAGCTGTAGATTCCCGAAGCCGGACGACAGCCTGATTAAGGGCAACATCT 4038
QY 1523 rpMetLeuLeuTyrrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetP 1543
Db 4039 ACATGTACATCTACTTCGTATCTTCATCTTCCGCTCCTTCTTCAACCTCAACCTGT 4098
QY 1543 heValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluA 1563
Db 4099 TCATCGGTGCATCATCGACAATTCAATCAACAGAAAGAAAGTTGGAGGTCAGAGACA 4158
QY 1563 la---ArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgSerLysG 1582
Db 4159 TCTTCATGACAGAGAACAGAGAAGTACTACAACGCCATGAAGAGCTAGGCTCCAAGA 4218
QY 1582 LuLysGlnMetAlaGluAlaGlnCysLysProTyrrTyrrSerAspTyrrSerArgPheArgL 1602
Db 4219 AGCCACAG-----AAGCCCATCCCCGACCTTTGAACAAATCCAAG 4260
QY 1602 euLeuValHisHisLeuCysThrSerHisTyrrLeuAspLeuPheIleThrGlyValIleG 1622
Db 4261 GGATTTGCTTTGATTTGTCACGCAACAAGCCTTGCACATCGTATCATGATGCTCATCT 4320
QY 1622 LysLeuAsnValValThrMetAlaMetGluHisTyrrGlnGlnProGlnIleLeuAspGluA 1642

Db	4321	GCCTTAACATGGTGCACCATGATGTGGAGACAGACACACAGAGCAAGCAGATGGAGACA	4380
QY	1642	laLeuLysIleCysAsnTyrllePheThrValIlePheValPheGluSerValPheLysL	1662
Db	4381	TTCTCTACTGATTAATCTGTGCTCTTCATCTTCTTCACTGGAGTGTGTCTCAAAA	4440
QY	1662	euValAlaPheAlaPheArgArg--PhePheGlnAspArgTyrAsnGlnLeuAspLeuA	1681
Db	4441	TG-----TTTGCCTTGAGACACTACTATTTCACCATTTGGCTGGAACATCTTTGACTTTG	4494
QY	1681	laIleValLeuLeuSerIleMetGlyIleThrLeuGluIuIleGluValAsnLeuSerL	1701
Db	4495	TGTTGTCATCTCTCCATTTGTGGAAATGTTCCGTGGATATCATTTGAGAAGTACTTC-	4553
QY	1701	euProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuL	1721
Db	4554	-----GTCTCCCGACCCCTATTCCGGCTCATCCGATGGCCGATCGGCGCATCTTGC	4608
QY	1721	ysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLeuP	1741
Db	4609	GTCTGATCAAGGGCGCCCAAGGATCCGCACCCCTGCTTTTGCCTTAATGATGTCCCTGC	4668
QY	1741	roGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaIleuG	1761
Db	4669	CCGCCCTGTTCAACATCGGCTCTCTGCTCTTCCGTGATGTTCATCTTCCATCTTTG	4728
QY	1761	lyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyA	1781
Db	4729	GGATGTCCAACCTTCGCGTACGTGAAGCAGAG-----GCCGGCATTTATG	4773
QY	1781	rgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrg	1801
Db	4774	ACATGTTCAACTTCGAGACGTTTGGCAACAGCATGATCTGCCTGTTCCAGATCAGACCT	4833
QY	1801	lyAspAsnTyrAsnGlyIleMet-----LysAspProSerArgAspCysA	1816
Db	4834	CTGCTGGTTGGATGGCTTACTGCTGCCAATCCTGAACGCCCCCTGACTGCAGCTTGG	4893
QY	1816	spGlnGlu-----SerThrCysTyrAsnThrValIleSerProI	1829
Db	4894	ACAAGAGCACCCAGAGAGTGCCCTTCAAGGGGAGCTGCCGGAAACCCCTCCGTGGGCATCT	4953
QY	1829	leTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlav	1849
Db	4954	TCTTCTTCGTACGATCATCATCATCTCTTCTTGATCGTGGTAACATGTACATTGCCA	5013
QY	1849	alleuMetLysHisLeuGluGluSerAsnLysGluAlaLysGlu-----GluAlag	1866
Db	5014	TCATCTTGAGAACTTCAGCGTAGCCACAGAGGAAGCGCGATCCTCTGAGCGAGAGCG	5073
QY	1866	IuLeuGluAlaGluLeuGluLeuMetLysThrLeuSerProGlnProHisSerProL	1886
Db	5074	ACTTCGAGACTTCTATGAG-----	5093
QY	1886	euGlySerProPheLeuTyrProGlyValGluGlyValAsnSerThrAspSerProLysP	1906
Db	5094	-----ATCTGGAGAAAGTTGAT-----	5111
QY	1906	roGlyAlaProHisThrThrAlaHisIleGly-----AlaAlaSerGlyPheS	1922
Db	5112	-----CCTGATGCCACCCAGTTCATCGAGTACTGTAACTGGCCGACTTTGCCGACG	5163
QY	1922	erLeuGluHisProThrMetValProHisProGluGluValProValProLeuGlyProA	1942
Db	5164	CCCTGGAGCATCCGCTCCGAGTACCAGGCCCAACACCACATCGAGCTC--ATCGGCATGG	5220
QY	1942	spLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerT	1962
Db	5221	ACCTGCCCATGTG-----AGCGGA--GATCGAATCCACTGCTTG-----GACATCC	5265
QY	1962	yrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTyrGlyLeuP	1982

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Db      5266 TTTTC-----GCCTTCACCAAGCAGTCTCTGGAGACAGTGGC----- 5303
QY      1982 rOlYsAlaGInSerGlySerIleuSerValHisSerGlnProAlaAspThrSerCysI 2002
Db      5304 -----GAGTTGACATCTCTGGCGACAGATGAGGACGGCTTCG 5343
QY      2002 lElEuGInLeuProLYsAspValHisTYrLeuLeuGlnProHisGlyAlaProThrTrg 2022
Db      5344 TGGCGTCCAATCCTTCCAAAGTGTCTTAC----- 5372
QY      2022 lYAlaIleProLYsLeuProProGluYArgSerProLeuAlaGlnArgProLeuArgA 2042
Db      5373 -----GAGCCTATCAGACCACTTGCGCGCA 5400
QY      2042 rglAlaIaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspL 2062
Db      5401 AGCAG----- 5405
QY      2062 euleuSerGluValSerGlyPro-SerCysProLeuThrArgSerSerSerPheTrpGly 2081
Db      5406 -----GAAGAGGTGTCTGCAGTGTGTTGCAGCGTGCTTACAGGGGACACTGGCTAGGC 5460
QY      2082 GlySerSerIleGlnValGlnArgSer-----GlyIleGlnSerLYs 2096
Db      5461 GGGGCTTCA-----TCTGCAGAAAGATCACTTCCAACAAGCTGGAGATGGAGGCACCC 5514
QY      2097 ValSerLYsHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLYs 2116
Db      5515 ACCGAGAGAAGAGAGAGACACCCCGTCCACAGCTCCCTCCCTCTTACGACAGCGTGA 5574
QY      2117 AspProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGly 2136
Db      5575 CAAAGCCCGACAGAGAGAGCAGC-----AGCGGG 5604
QY      2137 AspleuLeuProSerSerGlnGluProLeuPheProArgAspleuLYs 2154
Db      5605 CAGAGGAAGGCAGAGGGAAGAG-----CCAAGAGGCAGAAAGAG 5646

RESULT 8
CF548698      879 bp      mRNA      linear      EST 22-SEP-2003
LOCUS      CF548698
DEFINITION      AGENCOURT_15594508 NICHD_XGC_Brn1 Xenopus laevis cDNA clone
IMAGE:7018586 5', mRNA sequence.
ACCESSION      CF548698
VERSION      CF548698.1 GI:34885530
KEYWORDS      EST.
SOURCE      Xenopus laevis (African clawed frog)
ORGANISM      Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM14738 row: j column: 24
High quality sequence stop: 646.
Location/Qualifiers
1..879
/organism="Xenopus laevis"
/mol_type="mRNA"

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/db_xref="taxon:8355"
/clone="IMAGE:7018586"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD_XGC Brn1"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN

Alignment Scores:
Pred. No.: 4.09e-78 Length: 879
Score: 1275.00 Matches: 250
Percent Similarity: 91.19% Conservative: 19
Best Local Similarity: 84.75% Mismatches: 17
Query Match: 10.60% Indels: 9
DB: Gaps: 2

US-09-611-257A-24 (1-2287) x CFS48698 (1-879)

QY 1497 ASpgLYTRpValAspIleMetTyrAspGLyLeuAspAlaValGLyAlaSpGLnInPro 1516
Db 1 GACGGATGGGTGACATCATGTATGATGACTGTGCTGCGAATTGACCAAGCAGCCA 60
QY 1517 ILeMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAla 1536
Db 61 GTGATGATATTACACCCCTTGATGCTGTATATTATTCATCTCATTTTGTGATTTGGCA 120
QY 1537 PhePheValLeuAsnMetPheValGLyValValAlaGLuAsnPheHisLysCysArgGLn 1556
Db 121 TTTTGTGCTCAACATGTTTGTGGGTGTGTGGTGGAGAAGCTTCCATAAGTGCCGGCAG 180
QY 1557 HisGLnGLuGLuGLuAlaArgArgArgGLuGLuLysArgLeuArgLeuGLuLys 1576
Db 181 CATCAGAA 240
QY 1577 LysArgArgSerLysGLuLysGLnMetAlaGLuAlaGLnCysLysProTyrTyrSerAsp 1596
Db 241 AAGAGAAGG-----AAGGCCAGTGTAAACCTTACTATTTCGGAG 279
QY 1597 TyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPhe 1616
Db 280 TATTCACACCTTCGGCTCCATCCATCAGATCTGTACAAGTCATATTGATTTGTTT 339
QY 1617 IleThrGLyValIleGLyLeuAsnValValThrMetAlaMetGLuHisTyrGLnInPro 1636
Db 340 ATTACTGGGGTCATTGGATTGAATGTTATCATCTATGCAATGAGCAGACTATCAGCAACC 399
QY 1637 GlnIleLeuAspGLuAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPhe 1656
Db 400 CAGGTAATTGGTTGAAGCTTAAAAATCTGTAAATATACATCTTTACCCCTCATTTTCGTA 459
QY 1657 GluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGlnAspArgTTrpAsn 1676
Db 460 GAACTCTGGGTGCAAAATGATAGCTTTTGCTCCGCGAATCTTTAAAGACAGGTGAAC 519
QY 1677 GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGLyIleThrLeuGLuIleGLu 1696
Db 520 CAGTTGGATCTGGCCATCGTTCTTCTCCATCATGGGAATCACACGTGAAGAGATTGAA 579
QY 1697 ValAsnLeuSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle 1716
Db 580 GTCAATGCATCACTGCCCATTAACCAACAATCATCCGAATAATGAGGGCTTGCGGATT 639
QY 1717 AlaArgValLeuLysLeuLeuLysMetAlaValGLyMetArgAlaLeuLeuHisThrVal 1736
Db 640 GCTCGGCTGCTGAAGTATTAAAGATGGCAGTCGGTATCGAGCCCTGCTGATACGGTT 699
QY 1737 MetGlnAlaLeuProGlnValGLyAsnLeuGLyLeuLeuPheMetLeuLeuPhePheIle 1756
Db 700 CTGCAAGCGCTTTCAGAGTGGGAATCTCGGCCCTGCTTTATGCTGCTCTTTTAA 759

QY 1757 pheAlaAlaLeuGLyValGLuLeuPheGLyAspLeuGLuCysAspGLuThrHisProCys 1776
Db 760 TTTGCCGCTCTGGAGACTTGAACCTTTTGGTGACTTAAAAAGCACTGATCCATCCCTGT 819
QY 1777 Glu-GlyLeuGLyArgHisAlaThrPheArgAsn---PheGLy 1789
Db 820 GAAAGTCTTGGCAGACTTGCCACTTTCAAGGAATTTTCGGG 862

RESULT 9
CA319705 793 bp mRNA linear EST 09-JUL-2003
LOCUS CA319705
DEFINITION UI-M-FW0-cca-d-09-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
IMAGE:6816826 5', mRNA sequence.
ACCESSION CA319705
VERSION CA319705.1 GI:24537829
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE 1 (bases 1 to 793)
JOURNAL NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bs-rc@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: PYX-5.

FEATURES
source location/Qualifiers

1. 793
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6816826"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 6.7e-77 Length: 793
Score: 1256.50 Matches: 241
Percent Similarity: 92.40% Conservative: 2
Best Local Similarity: 91.63% Mismatches: 9
Query Match: 10.45% Indels: 11
DB: Gaps: 1

US-09-611-257A-24 (1-2287) x CA319705 (1-793)

QY	1444	LeuphelySGLYLysPhePheValCysGlnGlyLAspThrArgAsnIleThrAsnLys	1463
DB	3	CTCTTCAAGGGAAGTCTTCTGCTGTCAAGGTGAGGACACCAAGACATCACTAACAAAG	62
QY	1464	SerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeu	1483
DB	63	TCCGACTGCTCTGAGGCCAGTTACCGGTGGTCCGGCACAAAGTACAACTTTGACAACCTG	122
QY	1484	GlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMet	1503
DB	123	GGCCAGGCTCTGATGTCCCTGTTGTGCTGGCCTCCAAGATGGCTGGTTGACATCATG	182
QY	1504	TyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrp	1523
DB	183	TATGATGAGCTGATGTGTGGAGTGAGACCAAGCACCATCATGAACCAACCCCTTGG	242
QY	1524	MetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPhe	1543
DB	243	ATGCTGCTCTACTTCATCTCTCTCTCCATCGTGGCCTCTTCTGTAACATGTTT	302
QY	1544	ValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAla	1563
DB	303	GTGGCGCTGTGTGTGAGAACTTCCATAAGTGCAAGGCAGCACCAAGAGAGAGGCGG	362
QY	1564	ArgArgArgGluGluLysArgLeuArgLeuGluLysLysArgArg-----	1579
DB	363	CGGCGGCGGAGAGAAAGCACTAAAGAGGCTGAGAAAGAGAAAGAAATCTAATGTTG	422
QY	1580	-----SerLysGluLysGlnMetAlaGluAlaGlnCysLysPro	1592
DB	423	GACGATGTAATTCCTTCGGCAGCTCAGCCAGCGCTGCTGCAGAAAGCCAGTGCAAAACC	482
QY	1593	TyrTyrSerAspTyrSerArgPheArgLeuValHisLysLeuCysThrSerHisTyr	1612
DB	483	TACTACTGTGACTACTCGCGCTTCGGCTCTCGTCCACCACTGTGTACCAGCACTAC	542
QY	1613	LeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHis	1632
DB	543	CTGACCTCTTCATCACTGTGTGTCATCGGGCTGAATGTGTCAAGATGGCCATGGAACAT	602
QY	1633	TyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrVal	1652
DB	603	TACCAGCAGCCCCAGATCCTGACGAGGCTCTGAAGATCTGCAACTACATCTTTACCGTC	662
QY	1653	IlePheValPheGluSerValPheLysLeuValAlaPheAlaPheArgArgPhePheGln	1672
DB	663	ATCTTGTCTTGGAGTCAGTATTCAACTTGTGGCCTTCGGCTTCGCCGGTTCTTCCAG	722
QY	1673	AspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeu	1692
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QY	1693	GluGluIle	1695
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DEFINITION genomic survey sequence.
ACCESSION AY416499
VERSION AY416499.1 GI:39772459
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 5943)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

TITLE Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 5943)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES location/Qualifiers
source 1..5943
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="SCN8A"
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Alignment Scores:
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Best Local Similarity: 21.84% Mismatches: 840
Query Match: 10.23% Indels: 664
DB: 9 Gaps: 83

US-09-611-257A-24 (1-2287) x AY416499 (1-5943)

QY	25	ProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGluArgAlaProArg	44
DB	22	CCACCAGGCCCTGATAGTTTCAAGCCTTTCACC-----CCTGAG	60
QY	45	SerArgAspSerProValAlaSerArgSerSerThrCysProGlyProGlyAlaAla	64
DB	61	TCACCTGGCAACATTTGAGAGCGCATTTCTGAGAGCAAGCTCAAGAAACCAAGGCC	120
QY	65	GlyAlaGlySerThrGluLysAspProGlySer-----AlaAspSerGlu	79
DB	121	GATGGAGTCATCGGAGGAGCATGAGACAGCAAGCCCAAGCCAAACGACGACCTGAA	180
QY	80	Ala-----GluGlyLeu-----	83
DB	181	GCAGGGAAGAGTTTGCCCTTTCATCTACGGGACATCCCCCAAGGCCCTGGTTGCA	240
QY	84	-----ProTyr-----	85
DB	241	CTGAGGACTTTGACCCATCTATTGACGCGAGAAACCTTTGTAGTATTAAACAGAGGG	300
QY	86	-----ProAlaLeuAlaProValValPhePheTyrLeu	96
DB	301	AAAACCTCTTCAGATTAGTCCACGCCCTGCCTG-----TACATTTTA	345
QY	97	SerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGlu	116
DB	346	AGTCCTTTTAACCTGATAGAGAATAAGCTATTAAATTGTGATACATTCATTTTAC	405
QY	117	ArgValSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgPro---	135
DB	406	ATGATCATTAATGTGACCTATTTTTGAACCAACTGTGTATTTCATGACTTTTGTAA	465
QY	136	-----CysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAsp	153
DB	466	GACTGTGGAAGATGTG-----	483
QY	154	AspPheIlePhe---AlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	172


```
Db 484 GAGTACACGTTACAGGAGATTATACATTTGAATCAGTAGTGAATAATCATTGCAAGAGGT 543
      ::::: ||| :::: ||| :::: ||| :::: ||| :::: |||
Qy 173 IlePheGlyLysLeuCyS-----TyrLeuGlyAspThrTrpAsnArgLeu 187
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 544 TTC-----TGCATAGATGGCTTACCTTTTACGGGACCACGAACTGGTGA 591
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 188 AspPheIleValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSer 207
      ||||| ::::: ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 592 GATTTCAGTGCATCATGATGGCGTATATACAGAGTTGTAAACCTAGGCAATGTT--- 648
      ||||| ::::: ::::: ||| ::::: ||| ::::: ||| ::::: |||
Qy 208 PheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValPro 227
      ||||| ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 649 ---TCAGCTCAGCACTTTCAGGGTACTGAGGGCTTGAATACTATTTCGGTAATCCCA 705
      ||||| ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 228 SerMetArgIleLeuValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeu 247
      ::::: ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 706 GGCCTGAAGACAATGTGGGTGCCCTGATTCACTGTGAAGAAACTGTCAAGATGTGATG 765
      ||||| ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 248 LeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGly 267
      ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 766 ATCTGCACAGTGTCTGCCTGAGTGTGTTTGCCTTGATCGGACTGCGCTGTCATGAGGG 825
      ||||| ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 268 LeuLeuArgAsnArgCysPheLeu---ProGluAsnPheSerLeuProLeuSerValAsp 286
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 826 AACCTTGGAAACAAGTGTGTGTGTGGCCCATTAAC----- 867
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 287 LeuGluProTyrTyrGln-----ThrGluAsnGluAspGluSerProPheIleCysSer 304
      ||||| ||| ::::: ||||| ||||| ||||| ||||| ||||| |||||
Db 868 ---GAGAGCTATCTTGAATAATGCCACCAAGGCTTTGATTGGGAAGATATATC----- 918
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 305 GlnProArgGluAsnGlyMetArgSerCysArgSerVal-----ProThr 319
      ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 919 -----AACAAATAAAACAATTTCTACACAGTTCTCGCATGCTGGAACCTTTA 966
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 320 LeuArgGlyGlyGlyGlyGlyProProCysSerLeuAspTyrGluThrTyrAsnSer 339
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 967 CTCTGTGGGAACAGTCTGATGCTGGCAATGCCAGAGGATACCA----- 1014
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 340 SerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGlu 359
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1015 -----TGTATGAAAGCAGGA 1029
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 360 HisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIle 379
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1030 AGGAACCCCAACTATGTTACACAAGTTTGAACCTTTAGCTGGGCTTCTTGCCATTA 1089
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 380 PheGlnValIleThrLeuGlyGlyTyrValAspIleMetTyrPheValMetAspAlaHis 399
      ||||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 1090 TTTCGCCTTATGACCCAGGACTATTGGAAAACCTGTATCAATTGACTTACGAGCAGCC 1149
      ||||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Qy 400 SerPheTyrAsnPheIleTyrPheIleLeuLeuIleValGlySerPhePheMetIle 419
      ||||| ::::: ||||| ::::: ||||| ||||| ||||| ||||| |||||
Db 1150 GGGAAACATACATGATCTTCTGCTCTGTCATCTTTGTGGTCTTCTATCTGCTG 1209
      ||||| ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 420 AsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLysGlnArgGluSerGln 439
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1210 AACTTGATCTTGGCTGTGGTGGCCATGCGCTTATGAAGAA----- 1248
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 440 LeuMetArgGluGlnArgValArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSer 459
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1249 -----CAGAAITCAGGCCAACACACTGGAGAGGACGAGAA 1278
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 460 GluProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAla 479
      ::::: ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 1279 CAATAAAGAGGCTGAATTTAAACAATGTTGGAGCAACTT-----AAGAA 1323
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 480 AlaArgArgLeuAlaGlnValSerArgAlaIleGlyValArgAlaGlyLeuLeuSerSer 499
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 1324 CAACAGGAAGAGCAGAGGCTGCT--GCGATGGCACTTCAGCAGAACTGTCTCAGAA 1380
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 500 ProValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArg 519
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
```

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Db 1381 GATGCCATAGAG-----GAAGAAGGTGAAGAAGAGGCGGCTCCCTCGAGCTCTTCT 1434
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 520 ArgLeuSerValHisHisLeuValHisHisHisHisHisHisHisIleTyrHisLeu 539
      ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 1435 GAAATCTCT-----AAATCTC 1449
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 540 GlyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArg-AspAlaAs 559
      ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
Db 1450 AGCTCA-----AAGAGTCAAGGAAGAACGTTACAGAGGAAGAAG 1491
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 559 nGlySerArgArgLeuMetLeuProProProSerThrProThrProSer----- 575
      ||||| ::::: ||||| ||||| ||||| ||||| ||||| |||||
Db 1492 AGGAAGCAAAAGAACTCTCTGAAGAGAGAGAAAGGGAATCCGAGAAGGTGTTAAG 1551
      ||||| ::::: ||||| ||||| ||||| ||||| ||||| |||||
Qy 576 -----GlyGlyProProArgGlyAlaGluSerVal----- 585
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1552 TCAGAGTCAGAGATGGCATGAGAAGAGAGCCTTTCGGCTGCCAGACAACNNNNNNNN 1611
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 586 -----HisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysValAlaPr 603
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1612 NNNNNNNNNNNNNNNNNNNNNNNNTCACTGCTCAGCATCCAGCGCTCGCCCTTCTCTCC 1671
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 603 O-----ProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyLysVa 621
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1672 CGCCACACAGCAGCAGACGACATCTTCAGTTTCAGGGGACCTGGCGGCTCCGAGACCCG 1731
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 621 lTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuValGl 641
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1732 GGCTCCGAAATGATGTTGCGCG-----ATGACGAGCAGCAGCAGCGGTGAG 1776
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 641 uValAlaProSerProGlyProProThrLeuThrSerPheAsnIleProProGlyProPh 661
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1777 GAGAGCGAGGCGCGCGGACTCCCTCT-----TCATCCCATCCGGCGCCG 1824
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 661 eSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysHisSerSerCysLy 681
      ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 1825 GAGCGCC-----GAGCAGACTACAGCGGCTACAGCGGTACAGCCAG 1866
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 681 sIleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyPro----- 696
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 1867 GGCAGCGCTCT-----CGCGCATCTTCCCAAGCCTGCGGCGCAGCGTGAAGCGCAAC 1920
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 697 -----AspSerCysProTyrCysAlaArgThrGlyAlaGlyLupProGluSerAl 713
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1921 AGCAGCGGTGACTGCAACGCGGTGTGCTCATCGCGCGCGGCTCCACATCGGC 1980
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 713 aAspHisValMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGl 733
      ||||| ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 1981 GGG-CGTCTCTGCCAGAGGCTACAACTGAGGTGAATTAAG----- 2022
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 733 nHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAl 753
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2023 -----AAGAA 2027
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 753 aGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLys---Il 772
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2028 AGGCCCTGATCTCTTTAGTTCCATGGAACCAATTAGCCTCTTACGGCGGAGAGCAG 2087
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 772 eValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeu-- 791
      ::::: ||||| ::::: ||||| ::::: ||||| ::::: |||||
Db 2088 AATCAACAGT-----ATAATGAGTGTGTTACAATACTACTAGT 2126
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 791 ----- 791
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2127 AGAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 791 ----- 791
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2187 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2246
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 792 -----Se 792
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2247 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2306
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


[illegible]

QY	1100	laArgSerSerProHisSerProTTPSerAlaIalaserTrp-----ThrserArgA	1118
Db	3180	GAGAAATGGCAATGGCACAACCGGCGCATTTGGCAGCGGTGAGAATACTATT-C	3238
QY	1118	rgSerSerArgAsnSerLeuGlYargAlaProSerLeuLysArgArserProserGlYg	1138
Db	3239	ATGAGACCACATGTCTTCATCAACAACCCCACTTGACTGTACGGGTACC-----	3291
QY	1138	luArgArgSerLeuLeuSerGlYglUgly-----GlnGluserglInaspGlUglUs	1156
Db	3292	-----ATTGCTGTGGCGAGTCTGACTTTGAGAACCCTCAACACAGAGATGTTA	3340
QY	1156	erSerglUgluaSpArgAlaserProAlaglYSerAsphIsArgHIsArgGlySerleug.	1176
Db	3341	GCAGCGAGTCGGAT-----CCTGAAGGCAGCAAAGATAAAGTAGACACCAGCT	3391
QY	1176	luArgGlualalysSerSerPheAspleu---ProAspThrleuGlnValProglYleuH	1195
Db	3392	CCTCTGAAGGA---AGCACCATTTGATATCAAACGAAAGTAGAAGAGGTTCCT----	3441
QY	1195	isArgThrAlaserGlYArgSerSereralaserGluHIsGlnAspCyAsnGlyLysSera	1215
Db	3441	-----	3441
QY	1215	laserglYargLeuAlaArgThrLeuArgThrAspaSProGlnLeuAspglyAspaSPA	1235
Db	3442	-----GTGAACAGCCTTGAGGAATACTTGATCCAAGATGCCCT	3478
QY	1235	sPaAsnspGlUglYasnLeuSerLySglYgluaRglleglnAlatrpvalArgSerArgL	1255
Db	3479	GCTTCACAGAAGGTTGTCTCCAGCGGTTCAAG-----	3510
QY	1255	eUProAlaCySySarGluArg-----AspserTrpSerAlaTyrl	1269
Db	3511	-----TGCTGCCAGGTCACATCGAGGAAGGCTAGGCAAGCTTGG-----TGGA	3556
QY	1269	IepheProGlnSerArGrPheArgleuleuCysHIsArglleileThHislysmetP	1289
Db	3557	TC-----CTGCGGAAAACCTGTCTTCCTCATCTGTGAGCACAACCTGCT	3598
QY	1289	heaSPHISValleuVallleilepheleuAsnCysilleThrIleAlametGluArgP	1309
Db	3599	TTGAGACCTTCATCATCTTCATGATTCTGCTGAGCAGTGCGCCCTTGCGATGAGACA	3658
QY	1309	rolYSIlEasprroHisserAlagluArgliepheleuthrLeuSerXsnTyrllepHet	1329
Db	3659	TCTACATTGAGCAGAGAAGAACCATCCGACCATCCTGAATATGCTGACAAGTCTTCA	3718
QY	1329	hralavalPheleualaGlumethrVallysValValAlaleuGlYtrpCysPheglYg	1349
Db	3719	CCTATATCTTCATCTCGAGAGATGTGCTCAAGTGGACAGCAGCCTATGGCTTCGTC-	3771
QY	1349	IuGlnAlaTyrlEuArgSerSerTrpAsnValleuAspglyleuleuValleuIleserv	1369
Db	3772	----AAGTTCCTTCAACAATGCCTGGTGTGGCTGGACTTCCTCATTTGTGGCTNNNNNNN	3826
QY	1369	allEaspIleuValsermetValserAspserGlyThrLysIleleuGlyMetLeua	1389
Db	3827	NN	3886
QY	1389	rgValleuArgleuLeuArgThrLeuArgProleuArgValIleserArgAlaGlnGlyL	1409
Db	3887	NN	3937
QY	1409	eulysleuValValgluThrleuMetSerSerleuLysProIleglyAsnIleValValI	1429
Db	3938	NNNNNGTGTGTGAATGCCTTGTGTGGCGGCATCCCTCCATCATGAATGCTGCTGG	3997
QY	1429	IeCySySaAlaphetheilleIephегlylleleuGlyValGlnleuPheLysGlyLysP	1449
Db	3998	TGTGTCTCATCTTCTGGCTGATTTTCAGCATCATGGGAGTTAACTTGTTGGGGAAGT	4057
QY	1449	hepheValCySGlnGlyGlu-----AspThrArgAsnIleThrAsnL	1463

[illegible]

Db	5093	TGTTTCAATGACAACCTCAGCTGGTTGGATGGCTCTGCTGTCGCCATCTTAACCGCC	5152
QY	1810	spProSerArgaspCysaspGlnGlu-----SerThrCysTyrA	1823
Db	5153	CCCCTGACTGACGCTTAGATTAAGGAACACCAGGAGTGGCTTTAAGGAGATGTGGGA	5212
QY	1823	snThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuV	1843
Db	5213	ACCCCTCAGTGGGCACTTCTTCTTTGTAGCTACATCATCATCTCTTCCATAATTGCG	5272
QY	1843	alaSnaValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlnAlaLysG	1863
Db	5273	TGAACATGTACATTCATCCATCATCTCGAGAACTTCAGTGTAGCCACAGAGAAAGTGCA	5332
QY	1863	Iu-----GluAlaGluLeuGluAlaGluLeuGluLeuMetLysThrLeuSerP	1880
Db	5333	ACCCTCTGAGTGAAGATGACTTTGAGACCTTCTATAG-----	5370
QY	1880	roGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyValAsn	1900
Db	5371	-----ATCTGGAGAAAGTTCGAC-----	5388
QY	1900	erThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGly-----	1916
Db	5389	-----CCCGATGCCACCAGTTTCATTGAGTACTGTAAAGC	5422
QY	1917	--AlaAlaSerGlyPheSerLeuGluHisProThrMetValProHisProGluGluValP	1936
Db	5423	TGGCAGACTTTGGAGATGCCTTGGAGCATCCTCTCCGAGTGGCCCAAGCCAAATACCAT	5482
QY	1936	roValProLeuGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHis	1956
Db	5483	AGCTC--ATCGCTATGATCTGCCAATGCTG-----AGCGGG--GATCGCATCCACT	5530
QY	1956	erLeuProAsnAspSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyH	1976
Db	5531	GCTTG-----GACATCCTTTT-----GCCTTCACCAAGCGGCTCTGGAG	5572
QY	1976	isArgGlyTrpGlyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnP	1996
Db	5573	ATAGCGGG-----GAGTTGACATCCTGCGGCAGC	5602
QY	1996	roAlaAspThrSerCysIleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProH	2016
Db	5603	AGATGGAAGAGCGGTTCTGGCATCCCAATCCTTCCAAAGTGTCTTAC-----	5649
QY	2016	isGlyAlaProThrTrpGlyAlaIleProLysLeuProProGlyArgSerProLeuA	2036
Db	5650	-----GAGCCAAATCA	5659
QY	2036	laGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyL	2056
Db	5660	CAACCACTGCGCTGCAAGCAG-----	5682
QY	2056	eugLysSerArgGluAspLeuLeuSerGluValSerGlyPro-SerCysProLeuThrArg	2075
Db	5683	-----GAGGAGGTATCTGCAGTGTCTCTGCAGCGTGCT--	5716
QY	2076	serSerSerPheTrpGlyGlySerSerIleGlnValGlnGlnArgSerGlyIleGlnSer	2095
Db	5717	ACCGGGACATTTGGCAAGCGCGGCTTCATCTGCAAAAAAGCAACTTCTAATAAGCTGG	5776
QY	2096	LysValSerLysHisIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAla	2115
Db	5777	AGATGGAAGCACAACCGGAGAAAGAAAGAGCAAGCAAGCCCATCTACAG-----	5824
QY	2116	LysAspProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSer	2135
Db	5825	-----CCTCCCTCCCGCTCTATGACAGTGTACTAAACCTGAAAGAGAGAAACAGCAGC	5878
QY	2136	GlyAspLeuLeuProSerSerGlnGluGluProLeuPheProArgAspLeuLysLys	2154
Db	5879	GGG-----CAGAGGAAGGAAGGAGAAAGAGCCAAAGACAAAGAGAGG	5923

RESULT 11
CF745071 715 bp mRNA linear EST 10-OCT-2003
LOCUS UI-M-GV0-clu-p-15-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone
DEFINITION IMAGE:30622742 5', mRNA sequence.
ACCESSION CF745071
VERSION CF745071.1 GI:37641411
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 715)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: PYX-5.
FEATURES
source
1. 715
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30622742"
/tissue_type="whole brain"
/dev_stage="1,5, and 15 days newborn"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_GV0"
/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction. ligated with
EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

ORIGIN
Alignment Scores: 6.63e-73 Length: 715
Pred. No.: 1198.00 Matches: 233
Score: 1198.00
Percent Similarity: 98.73% Conservative: 1
Best Local Similarity: 98.31% Mismatches: 3
Query Match: 9.96% Indels: 0
DB: 7 Gaps: 0

US-09-611-257A-24 (1-2287) x CF745071 (1-715)

QY 918 HisleuPheGlyCysIysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLys 937
Db 3 CACCTTTTGGTTGCAAGTTGCATCTGAACGGGATGGGACACGTTGCCAGACCGGAAG 62

QY 938 AsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnIuAsp 957
Db 63 AATTGTGACTCCCTGCTCTGGGCATGTGCACTGTTCTGAGATTCTGACTCAGGAAGAC 122

QY 958 TrpAsnIysValLeuTyrrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrrPhe 977
Db 123 TGGAAATAAAGTCCCTTTACAAACGGCATGGCCCTCCACGTCATCTTGGGCTGCTTACTTC 182

QY 978 IleAlaLeuMetThrPheGlyAsnTyrrValLeuPheAsnLeuLeuValAlaIleLeuVal 997
Db 183 ATGCCCTCATGACTTTTGGCAACTACGAGTGTCTTTAACTGCTTGTGCCATTCTCGTG 242

QY 998 GluGlyPheGlnAlaGluGlyAspAlaThrIysSerGluSerGluProAspPhePheSer 1017
Db 243 GAGGTTTCCAGGCAGAGGAGATGCCACCAAGTCTGAGTCAGAGCCTGATTTCTTTTCG 302

QY 1018 ProSerValAspGlyAspGlyAspArgLysIysArgLeuAlaLeuValAlaLeuGlyGlu 1037
Db 303 CCAGTGTGATGTGATGGGGACAGGAAGACGCTTGGCCCTGTGGCTTGAGAGAA 362

QY 1038 HisAlaGluLeuArgIysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrPro 1057
Db 363 CACTCGAAGTACGAAAGAGCCTTTGGCCACTCTCATCATCCACAGAGCTGACACCG 422

QY 1058 MetSerHisProIysSerSerSerThrGlyValGlyGluAlaLeuGlySerGlySerArg 1077
Db 423 ATGTCACTGCCCAAGAGCTCCACAGAGTGTGGGGGAACACTGGGCTCTGCGC 482

QY 1078 ArgThrSerSerSerGlySerAlaGluProGlyAlaAlaHisHisGluMetLysCysPro 1097
Db 483 CGCACAGTAGCAGTGGTTCGCTGAGCCTGGAAGTCCCATCATGATGAATCACC 542

QY 1098 ProSerAlaArgSerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSerArg 1117
Db 543 CCAAGTCCCGGAAGCTCCCGCACAGTCCCTGGAGCCGACAGCAAGCAGCTGACAGCAGG 602

QY 1118 ArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuIysArgArgSerProSerGly 1137
Db 603 CGCTCCAGCCGGAACAGACGCTGGGCCGGCCCCCAGCCTGAAGCGTAGAGCCCAAGCGGG 662

QY 1138 GluArgArgSerLeuLeuSerGlyGluGlyGlnIuSerGlnAspGlu 1154
Db 663 GAGCGGAGGTCCCTGCTGTCTGAGAGAGGTGACAGAGACGAGATGAGAG 713

RESULT 12
BU709095 810 bp mRNA linear EST 15-JUL-2003
LOCUS UI-M-EW0-caz-e-20-0-UI.r1 NIH_BMAP_EW0 Mus musculus cDNA clone
DEFINITION IMAGE:6419323 5', mRNA sequence.
ACCESSION BU709095
VERSION BU709095
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 810)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
http://image.llnl.gov

US-09-611-257A-24 (1-2287) x CF745071 (1-715)

QY 918 HisleuPheGlyCysIysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLys 937
Db 3 CACCTTTTGGTTGCAAGTTGCATCTGAACGGGATGGGACACGTTGCCAGACCGGAAG 62

QY 938 AsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnIuAsp 957
Db 63 AATTGTGACTCCCTGCTCTGGGCATGTGCACTGTTCTGAGATTCTGACTCAGGAAGAC 122

/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6419323"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP Ew0"
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonafo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is GTGCGTGGAA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 9.53e-73 Length: 810
Score: 1197.00 Matches: 246
Percent Similarity: 91.51% Conservative: 2
Best Local Similarity: 90.77% Mismatches: 11
Query Match: 9.95% Indels: 15
DB: 5 Gaps: 1

US-09-611-257a-24 (1-2287) x BUI709095 (1-810)

QY 1369 ValIleAspIleLeu-ValSerMetValSerAspSerglyThrlyslleleuglyMetle 1388
Db 1 GTCATCGACATCCTGTGTGTCATGTTCTTGACAGCGGCACCAAGATTCTCGGCATGCT 60
QY 1388 uArgValleuArgleuArgThrleuArgProleuArgValIleSerArgAlaGlnG1 1408
Db 61 GAGGGTGTCGCGGTGTCGCGGACCCCTACGTCCTCAGGGTCATCAGCGGCCAGGG 120
QY 1408 yleuLysleuValValGluThrleuMetSerSerleuLysProIleGlyAsnIleValVa 1428
Db 121 GCTGAAGCTGTGTGTAAGACTGTGATGTCAATCCCTCAAAACCATGGCAACATTGTGCT 180
QY 1428 IileCysCysAlaPhePheIleIlePheGlyIleleuGlyValGlnleuPheLysGlyLy 1448
Db 181 CATCTGCTGTGCCTTCTTCATCATTTTGGAAATCTTGGGGTGACAGCTTCAAGGGA 240
QY 1448 sPhePheValCysGlnGlyAspThrArgAsnIleThrAsnLysSerAspCysAlaG1 1468
Db 241 GTTCTTGTGTGTCAAGGTGAGGACACCAAGACATCACTAACAAAGTCCGACTGTGCTGA 300
QY 1468 uAlaSerTyrArgTyrValArgHisIleTyAsnPheAspAsnleuGlyGlnAlaLeuMe 1488
Db 301 GGCCAGTTACCGGTGGTCCGGCACAAGTACAACTTTGACAACTGGGCCAGGCTCTGAT 360
QY 1488 tSerleuPheValleuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAs 1508
Db 361 GTCCCTGTTTGTGTGCTGCTCCCAAGATGGCTGGTTGACATCATGTATGATGACTGA 420
QY 1508 pAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTyrMetSerleuTyrPh 1528
Db 421 TGCTGTGGAGTGGACCAAGCCCATCATGAACCAACCCCTTGATGCTGCTACTT 480
QY 1528 eIleSerPheleuLeuIleValAlaPhePheValleuAsnMetPheValGlyValValVa 1548
Db 481 CATCTCTTCTCTCTCATCGTGGCTTCTTCTGCTGAACATGTTTGTGGCGGTGTGCT 540
QY 1548 lGluAsnPheHisIleLysCysArgGlnHisGlnGlyGluGluValAlaArgArgGluG1 1568
Db 541 GGAGAACTTCCATATAGTGCAGGACAGCAACCAAGAGAGAGAGGCGCGCGCGGAGGA 600

QY 1568 ulysArgleuArgArgleuGlyLysLysArgArg----- 1579
Db 601 GAAGCGACTTAAGAGCGCTGAGAAAAAGAGAAGAACTTAATGTTGACGATGTAATTGC 660
QY 1580 -----SerLysGlyLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTy 1597
Db 661 TTCCGGCAGCTCAGCCAGCGCTGCGTCAGAAAGCCAGTGCAACCCTACTACTGACTA 720
QY 1597 rSerArgPheArgleuLeuValHisIleuLysCysThrSerHisTyrLeuAspLeuPheI1 1617
Db 721 CTCGCGCTTCCGCTCCC-TCGTCAACCTGTGTACAGC-CACTAAGCTGNA-CTCTTCAT 777
QY 1617 eThrGlyValIleGlyLeuAsnValValThr 1627
Db 778 CACTGTGTATCGGGCTGAATGTGTACG 808

RESULT 13
CF584866 952 bp mRNA linear EST 24-SEP-2003
LOCUS AGENCOURT_11360281_updated NIH_MGC_137 Mus musculus cDNA clone
DEFINITION IMAGE:6431076 5', mRNA sequence.

ACCESSION CF584866
VERSION CF584866.1 GI:35198128
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 952)
NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Daniela S. Gerhard, Ph.D.
COMMENT Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
cDNA Library Preparation: Catherine Lee, Endocrine Pancreas
Consortium

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: IRBD12 row: f column: 01
High quality sequence start: 15
High quality sequence stop: 571.

FEATURES

source 1..952
Location/Qualifiers
1..952
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6431076"
/lab_host="DH10B"
/clone_lib="NIH_MGC_137"
/note="Organ: pancreas; Vector: pSPORT1; Site 1: SalI;
Site 2: NotI; Library consists of a pool of clones
rearrayed from the following libraries: Melton normalized
mixed mouse pancreas 1 N1-MS1, Amplified Melton mouse
islets 1 M1S1-A, and Kaestner ng3 wt. Clones rearrayed in
the laboratory of K. Kaestner (University of
Pennsylvania). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 1.57e-72 Length: 952
Score: 1195.50 Matches: 250
Percent Similarity: 81.88% Conservative: 3
Best Local Similarity: 80.91% Mismatches: 31
Query Match: 9.94% Indels: 25
DB: 7 Gaps: 7

US-09-611-257A-24 (1-2287) x CF584866 (1-952)

QY 1746 LeuGLyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGLyValGLuLeuPhe 1765
Db 34 CTGGGACTTCTCTTCATGCTATATATTTTCATCTTTGCACTCTGGGCGTGAGCTCTTT 93
QY 1766 GLYAsPLeuGLuCYsAsPGLuThrHisProCYsGLuGLyLeuGLYARGHIsAlaThrPhe 1785
Db 94 GGAGACCTGGAGTGTGATGAGACACACCTTGTGAGGGCTTGGGCGGCATGCCACTTT 153
QY 1786 ArgAsnPheGLyMetAlaPheLeuThrLeuPheArgValSerThrGLYAsPAsnTPAsn 1805
Db 154 AGGAACCTTGTATAGCCCTTCTTGACCTCTCCGAGTCCCACTGTGACCACTGGAAT 213
QY 1806 GLYIleMetLYsAsPProSerArgAsPCySAsPGLInGLuSerThrCYsTYrAsnThrVal 1825
Db 214 GGTATTATGAGAGACACCCCTCCGGAGCTGTGACCAAGAGTCCACCTGCTACAACACCGTC 273
QY 1826 IleSerProIleTYrPheValSerPheValLeuThrAlaGLInPheValLeuValAsnVal 1845
Db 274 ATCTCACCCCACTTACTTCGTGTCCTTCCTGCTGACGCGCCCACTTGTGCTGCAACGTG 333
QY 1846 ValIleAlaValLeuMetLYsHisLeuGLuGLuSerAsnLYsGLuAlaLYsGLuAla 1865
Db 334 GTCATAGCCGTGCTGATGAAGCACCTGGAAGAGACAAAGAGAGCCCAAGGAGGAGCG 393
QY 1866 GLuLeuGLuAlaGLuLeuGLuLeuGLuMetLYsThrLeuSerProGLInProHisSerPro 1885
Db 394 GAGTTGAGGCGGAGCTGAGAGCTAGAGTAGAAGACACTCAGCCCGCAGCCCACTCCCG 453
QY 1886 leuGLySerProPheLeuTrpProGLyValGLuGLyValAsnSerThrAspSerProLYs 1905
Db 454 CTGGGACAGCCCTTCTCTGCGCTGGGGTGGAAGTGTCAATAGCCCTGACAGCCCTAAG 513
QY 1906 ProGLYAlaProHisThrThrAlaHisIleGLYAlaAla---SerGLyPheSerLeuGLu 1924
Db 514 CCTGGGGCTCCACACACACGCGCCCATTTGGAGCAGCCCTTTCAGGCTTCTCCCTTGAG 573
QY 1925 HisProThMetValProHisProGLuGLuValProValProLeuGLYProAsPLeuLeu 1944
Db 574 CACCCACGATGGTAACTCACACTGAGAGGGGGCCAGTCCCTTAAGACCAAGACTGCTG 633
QY 1945 ThrValArgLYsSerGLyValSerArgThrHisSerLeuProAsnAspSerTYrMetCys 1964
Db 634 ACTGTAGGAAGTCTGTGTGTCAGCCGACACACTCTCTGCCAATGACAGCTAATGTGC 693
QY 1965 ArgAsn-GLySerThrAla-GLuArgSerLeuGLYHisArgGLYTrpGLyLeu---ProLY 1983
Db 694 CGCAATGGGAGCCCTGCGCCGAGAGATCCCTAAGACACAAAGGGGCTGGGCGCTCCCAA 753
QY 1983 ySAlaGLnSerGLy---SerIleLeuSerValHisSerGLnProAlaAspThrSerCysI 2002
Db 754 AAGCCAGTCAGGGCTCCAAATCTTGTCTGTTCACCTCCCAACAAGCAGAACAAC---- 809
QY 2002 IeLeuGLnLeu-----ProLYsAsPValHisTYrLeuLeuGLnProH 2016
Db 810 -----CAGCTGGCATTTAAAGCTTTCCCAAAAATGCCCAA-----CTATCTGGGT 858
QY 2016 isGLYAlaProThrTrpGLYAlaIlePro-----LYsL 2027
Db 859 TCCAGACCCCTCTCTTGGGGGGCGTCCCAACCTGGGGGGGCGCCCTTACCCCTTAATAAAC 918
QY 2027 euProProProGLYArgSerPro 2034
Db 919 TAACCCCCCCCACTTGGGGCCC 941

RESULT 14
AK083220 4675 bp mRNA linear HTC 03-APR-2004
LOCUS AK083220
DEFINITION Mus musculus adult male hippocampus cDNA, RIKEN full-length
enriched library, clone:C630029C19 product:sodium channel,
voltage-gated, type VIII, alpha polypeptide, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK083220
AK083220.1 GI:26101130
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4675)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

COMMENT

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>

URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
1..4675
/organism="Mus musculus"
/mol_type="mRNA"
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/clone_id="RIKEN full-length enriched mouse cDNA library"
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1..3589
misc_feature
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sodium channel, voltage-gated, type VIII, alpha
polypeptide (MGD|MGI:103169, GB|NM_011323, evidence:
BLASTN, 99%, match=3589)"
ORIGIN
Alignment Scores:
Pred. No.: 4.62e-71 Length: 4675
Score: 1190.50 Matches: 407
Percent Similarity: 43.22% Conservative: 265
Best Local Similarity: 26.17% Mismatches: 537
Query Match: 9.90% Indels: 349
DB: 3 Gaps: 55
US-09-611-257A-24 (1-2287) x AK083220 (1-4675)
QY 810 IleserA nileVal pheThrSerLeu pheAlaLeuGluMetLeuLeuLysLeuVal 829
Db 4 GTAGGGAACCTGGTGTTCACCTGGGATCTTACCGCGGAATGTTCTCGAAGCTCATAGCC 63
QY 830 TyrgLyProPheGlyTyriLeLysAsnProTyra nilePheAspGlyValIleValVal 849
Db 64 ATGATCCCTACTATTACTTCCAAAGAGGCTGGAACATTTTGACGGATTATCGTCTCC 123
QY 850 IleserValTrpGluIleValGlyGlnGlyGlyLeuSerValLeuArgThrPhe 869
Db 124 CTCAGTTTAATGAGCTGGGCTTGACAGACGTGAGGGGCTTCAGTGTGCGATCTTTC 183
QY 870 ArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuVal 889
Db 184 CGATGTCTCCGAGTCTTCAAAATTGGCCAAAGTCTGCGCCACCTGAACATGCTGATCAAG 243
QY 890 ValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIle 909
Db 244 ATCATTTGGGAACCTCCGTTGGCGCCCTGGGCAACCTGACCCTGTGCTGCCATCTTCTC 303
QY 910 PheIlePheSerIleLeuGlyMetHisLeuPheGly-----Cys 922
Db 304 TTCATCTTTGCCGTGGTGGGATGACAGCTCTTGGAAGAAGCTACACAGAGTCCGTCTGT 363
QY 923 LysPheAlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeu 942
Db 364 AAGATCAGCCAGAG-----TGCAAGCTCCG---CGCTGGCAGATGAACGACTTC 411
QY 943 LeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeu 962
Db 412 TTCACCTCCTTCCTCATCGTCTTCCGAGTGTGTGGGAG---TGATCGAGACCATG 468
QY 963 TyrAsnGlyMet---AlaSerThrSerSerTrpAlaAlaLeuTy rPheIleAlaLeuMet 981
Db 469 TGGGATTCATGGAAGTGGCGCGCCAGGCCATGTCCTTATCGTGTTCATGATGTCATG 528
QY 982 ThrPheGlyAsnTy rValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGln 1001
Db 529 GTCATCGGCAACCTGGTGTGCTGAACCTATTCTGACCCTTGCTTCGAGCTCCTTCAGC 588
QY 1002 AlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerValAsp 1021
Db 589 GCAGACAATCTGGCG-----GCCACGGAC 612

QY 1022 GlyAspGlyAspArg-----LysLysArgLeuAla 1031
Db 613 GACGACGGGAAATGAACAACCTGCAGATATCGGTATCCGGATCAAGAAAGGCGTGCC 672
QY 1032 LeuValAlaLeuGlyGluHisAlaGluLeuArgLysSerLeuLeuProProLeuIleIle 1051
Db 673 TGGGCCAAAGTGAAGTGCATGCCCTCATGCAG----- 705
QY 1052 HisThrAlaAlaThrPrometSerHisProLysSerSerSerThrGlyValGlyLysAla 1071
Db 706 -----GCACACTTCAAGCAACGGAGGCTGATGAAGTAACT 744
QY 1072 LeuGly-SerGlySerArgArgThrSerSerSerGlySerAlaGluProGly----- 1088
Db 745 TTAGACGAGCTGTATGAGAAGAGCCCACTGCATCGCCCAACCAACACCGCGTGACATT 804
QY 1089 -----AlaAlaHisHisGluMetLysCysProProSerAlaArgSerProHis 1105
Db 805 CACAGAACCGGACCTTCCAGAAAATGGAATGGCACCACTAGCGGCATCG----- 856
QY 1105 sSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlu 1125
Db 857 -----GCAGCAGCGGTGAGAAGTACATCATGCAGCAGACACACA----- 895
QY 1125 YArgAlaProSerLeuLysArgArgSer---ProSerGlyGluArgArgSerLeuLeuSe 1144
Db 896 ---TGTCTTCAATTAACAACCCAACTGACCGTGGCG-----TGCCCATGTCTGTG 945
QY 1144 rGlyGlyGly-----GlnGluSerGlnAspGluGluGluSerSerGluLysAspArgAl 1162
Db 946 -GGCAGTCTGATTTCCAGAACCTCAACACAGAGGATGTTAGCAGCGAGTCAGAC----- 999
QY 1162 aserProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSe 1182
Db 1000 ----CCGGAAGCAGCAAAAGACAACCTGGAAGATACCAAGCTCTCAGAAAGG--AGTAC 1052
QY 1182 rPheAspLeu---ProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyAr 1201
Db 1053 CATCGACATCAAGCTTGAGGTGAAGAGTCCCA----- 1086
QY 1201 gSerSerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaAr 1221
Db 1086 ----- 1086
QY 1221 gThrLeuArgThrAspAspProGlnLeuAspGlyAspAspAspAsnAspGluLysnLe 1241
Db 1087 ----GTGAGCAGCCTGAGGAATACTTGATCCAGACCGCTTCAAGGAGGTGTGT 1142
QY 1241 uSerLysGlyGluArgGlnGlnAlaTrpValArgSerArgLeuProAlaCysCysArgGlu 1261
Db 1143 CCAGAGGTTCAAG-----TGCTGCCAGGT 1166
QY 1261 uArg-----AspSerTrpSerAlaTyriLePheProProGlnSerAr 1275
Db 1167 CAACATCGAGAGAGACTAGCAAGTCTGG-----TGATC----- 1203
QY 1275 gPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHisValIleuVa 1295
Db 1204 -CTGCGGAADAACCTGCTCTCATTTGTGAGCACAATTTGGTTTGAACCTTCATCATTTT 1262
QY 1295 IileIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSe 1315
Db 1263 CATGATTCCTCTCAGCAGTGAAGCCCTGGCTTCGAGGACATGTATGAGCAGAGAA 1322
QY 1315 rAlaGluArgIlePheLeuThrLeuSerAsnTyriLePheThrAlaValPheLeuAlaGlu 1335
Db 1323 GACCATCCGTACCATCTCGAGTATGCGGACAAGGCTTTCACCTTACATCTTCAGGA 1382
QY 1335 uMetThrValLysValValAlaLeuGlyTy rPysPheGlyGluGlnAlaTy rLeuArgSe 1355
Db 1383 GATGTTGCTCAAAATGACAGACCTATGCTTCGTC-----AAGTTCTTACCAA 1430

Qy	1355	rSerTrpAsnValLeuAspGlyLeuValLeuIleSerValIleAspIleValSe	1375
Db	1431	TGCCTGGTGTGGTTGGAAGCTTCCTCATTTGGCTGTCTTTAGTCAGCCTTAATAGCTAA	1490
Qy	1375	rMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuAr	1395
Db	1491	TGCCCTG-----GGCTACTCGGAAGTAGTGCCATAAAGTCCCTTAGAACCTTAAG	1541
Qy	1395	gThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGlutH	1415
Db	1542	AGCTTTGAGACCCCTTAAGACCCTTATCAGATTGTAAGGATGAGGGTGGTGAACGC	1601
Qy	1415	rLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheI	1435
Db	1602	CTTGGTGGGCCCATCCCTCCATCATGAACGTCGTCTGTGTCTCATCTTCTGGCT	1661
Qy	1435	eilePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGl	1455
Db	1662	GATTTTCAGCATCATGGCGGTTAACTGTTTGGTGGAAATACCACTACTGCTTCAAACA	1721
Qy	1455	uasPTyrArg-----AsnIleThrAsnLysSerAspCysAlaGlu--	1468
Db	1722	GACTTCAGAAATCCGGTTCGAATCGACGAGGTGAACAATAAAACGACTGTGAAGAAGCT	1781
Qy	1469	-----AlaserTyrArgTrpValArgHisLysTyrAsnPheAspAsnIe	1483
Db	1782	CATGAGGCGCAACAACACAGAGATCCGATGGAAGAACGTCAAGATCAACTTCGACAAAGT	1841
Qy	1483	uGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMe	1503
Db	1842	CGGGCAGGCTACCTGGCCCTTCTCAAGTGGCAACCTTCAAAGCTGATGACATCAT	1901
Qy	1503	tTyrAspGlyLeuAspAlaValGlyValAlaSpGlnGlnProIleMetAsnHisAsnProTr	1523
Db	1902	GTAATGACGCTGTAGATTCCGAAAGCCGACGACGACCTGATTATGAGGGCACATCTA	1961
Qy	1523	pMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPh	1543
Db	1962	CATGTACATCTACTTCGTATCTTCATCATCATCTTGGGCTCTTCTTCAACCTCAACCTGTT	2021
Qy	1543	eValGlyValValValGlnAsnPheHisLysCysArgGlnHisGlnGluGluGluAl	1563
Db	2022	CATCGGTGCATCATGCACAATTTCAATCAACAGAAAAGTTTGAGGTCAAGACAT	2081
Qy	1563	aArgArgArgGluGlu-----LysArgLeuArgArgLeuGluLysLysArgArgSerLy	1581
Db	2082	CTTCATGACAGAGAACAGAGAAGTA-CTACAAAGCCATGAAGAAGTAGGGC-TCCA	2139
Qy	1581	sGluLysGlnMetAlaGluAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheAr	1601
Db	2140	GAAAGCCACAG-----AAGCCCATCCCCGACCTTTGAACAAATCCA	2181
Qy	1601	gLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIl	1621
Db	2182	AGGAGATTGTCTTGATTTCGTCAAGCAACAAGCCCTTGACATCGTATCATGATGCTTAT	2241
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Db	2242	CTGCCTTAACATGTGTGACCATGATGTGTGAGACACACACAGAGCAAGCAGATGGAGAA	2301
Qy	1641	uAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValPheGluSerValPheLy	1661
Db	2302	CATTCTCTACTGATTAATCTGTCTTCGTATCTTCTTCACTGCGAGTGTGTCTCAA	2361
Qy	1661	sLeuValAlaPheAlaPheArgArg--PhePheGlnAspArgTrpAsnGlnLeuAspLe	1680
Db	2362	AATG-----TTTGCCCTGAGACACTACTATTTCACCAATTGGCTGGAACATCTTGACTT	2415
Qy	1680	uAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnLeuSe	1700
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Db	2476	C-----GTTCCCGACCACTATTCCGGCGTCATCCGATTGACCCCGCATCGGCATCTT	2529
Qy	1720	uLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuHisThrValMetGlnAlaLe	1740
Db	2530	GGCTGTGATCAAGGGCGCCAAAGGATCCGACACCTGCTCTTGGCTTAATGATGTCGT	2589
Qy	1740	uProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaIaLe	1760
Db	2590	GCCCCCGCTGTTCACATCGGCGCTCTGCTCTTCCGTGTCATGTTCATCTTCCATCTT	2649
Qy	1760	uGlyValGluLeuPheGlyAspLeuGlyCysAspGluThrHisProCysGluGlyLeuG	1780
Db	2650	TGGGATGTCCAACTTCGCGTACGTGAACGACGAG-----GCCGGCATTGA	2694
Qy	1780	YArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerTh	1800
Db	2695	TGACATGTTCACTTCGAGACGTTTGGCAACAGCATGATCTGCGTGTCCAGATCAGCAG	2754
Qy	1800	rGlyAspAsnThrAsnGlyIleMet-----LysAspProSerArgAspCys	1815
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Oy 2081 lyglYserSer1leg1nValg1nGlnArgSer-----Gly1leg1nSerL 2096
Db 3382 GCGGGGCTTCA-----TCTGCAGAAAGATCACTTCCACAAGCTGGAGAATGAGGCGAC 3435
Oy 2096 ysValserLysh1s1leargLeuProAlaProCysProglYleuGluProSerTrpAlaL 2116
Db 3436 CCACCGAGAGAGAGAGAGACACCCCGTCCACAGCCTCCCTCTTACGACAGCGCT 3495
Oy 2116 ysAspProProgluThrArgSerSerleuGluLeuAspThrGluLeuSerTrp1leSerg 2136
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Oy 2195 erProSerSerleuGlyGlnProleuGlyGlyProglYserArgProLysLysLysL 2215
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Db 3708 -----CCAAACATA----- 3716
Oy 2235 erProglYValCysLeuArg-----ArgArgAlaProAlaSerAsps 2249
Db 3717 -----GTCTGCTTACACGTGACACGTTGCACTCTGAGCGGTGACTGCTGGGACA 3768
Oy 2249 erLyAspProSerValSerSerProleuAspSerThrAlaAlaSerProSerProLysL 2269
Db 3769 AAGACCCCTGCTCCCTGGACTCACAGATTTTCTATCGCTTGGGACAGCTTACTGCAT 3828
Oy 2269 ysAspThrleuSerleuSerGlyleuSerSerAspProThr 2282
Db 3829 GTTCCACACTCGGTCAATGCACTTAGAGTAACCTTAACA 3869

RESULT 15
BU058818 771 bp mRNA linear EST 26-AUG-2002
LOCUS UI-M-FRO-cak-a-11-0-UI.r1 NIH_BMAP_FRO Mus musculus cDNA clone
DEFINITION IMAGE:6413458 5', mRNA sequence.
ACCESSION BU058818
VERSION BU058818.1 GI:22499107
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 771)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
CDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
FEATURES
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/clone_1ib="NIH BMAP_FRO"
/note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN
Alignment Scores:
Pred. No.: 4.03e-72 Length: 771
Score: 1187.50 Matches: 238
Percent Similarity: 94.09% Conservative: 1
Best Local Similarity: 93.70% Mismatches: 15
Query Match: 9.87% Indels: 2
DB: Gaps: 0

US-09-611-257a-24 (1-2287) x BU058818 (1-771)
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Db 10 AGCTCAGCCAGCGCTGCCGTACAGAGCCCAAGTCAACCTACTACTGACTACTCGCGC 69
Oy 1600 pheArgLeuValHis1sleuCysThrSerHisTyTrpLeuAspLeuPhe1leThrGly 1619
Db 70 TTCCGGCTCCTCGTCCACCACTGTGTACAGCCACTACCTGACTTTCATCATCTGCT 129
Oy 1620 ValTlegLyLeuAsnValValThrmelAlaMetGluHisTyTrpGlnProGlnleLeu 1639
Db 130 GTCATCGGGCTGAATGTGTGTCACGATGGCCATGGAACATTACAGACAGCCAGATCCTG 189
Oy 1640 AspGluAlaLeuLys1leCysAsnTyTrlePheThrVal1lePheValPheGluSerVal 1659
Db 190 GACGAGGCTCTGAAGATCTGCAACTACATCTTACCGTCATCTTGTCTTGAGTCACTA 249
Oy 1660 PheLySleuValAlaPheAlaPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAsp 1679
Db 250 TTCAAACTTGTGGCTTTCGGCTTCGCGGCTTCTTCCAGAGACAGGTGGAACAGCTGAC 309
Oy 1680 LeuAla1leValleuLeuSer1leMetGly1leThrleuGluGlu1legLValAsnLeu 1699
Db 310 CTGGCTATTGTCTTCTGTCCATCATGCGCATCAAGCTGGAAGAGATTGAGTCAATGCT 369
Oy 1700 SerleuPro1leAsnProThr1le1leArg1leMetArgValleuArg1leAlaArgVal 1719
Db 370 TCACTGCCCATCAACCCACCATCATCCGTATCATGAGGAGTGTCCGCAATTGCTCGAGTT 429
Oy 1720 LeuLySleuLeuLysMetAlaValAlaGlyMetArgAlaLeuLeuHisThrValMetGlnAla 1739

Db	430	CTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGCACCTGCTGGACACGGTGATGCAGGCC	489
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Qy	1760	LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu	1779
Db	550	CTGGGCGTGAGCTCTTTGGAGACCTGGAGTGATGAGACACACCCTTGAGGGGCTTG	609
Qy	1780	GlyArgHisAlaThrPheArgAsnGlyMetAlaPheLeuThrLeuPheArgValSer	1799
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Qy	1800	ThrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluSer	1819
Db	670	ACTGCTGACAACTGGAATGTATTGAAAGACACCCCTCCGGGACTGTGNACAGAGTC-	728
Qy	1820	ThrCysTyrAsnThrValIleSerProIleTyrPheValSer	1833
Db	729	ACCTGCTACAC-ACCGTCATCTCACCCATCTACTTCGTGTCC	769

Search completed: September 19, 2005, 15:13:17
Job time : 14571.6 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2005, 16:30:41 ; Search time 20656.3 Seconds
(without alignments)
5315.550 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEBDAGAEESGQPRSFM.....PKKDVLSLGSISDPADLDP 2266

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 segs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US09611257/runat_15092005_134300_25171/app_query.fasta_1.4878
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09611257@cgn2.1_1_29545@runat_15092005_134300_25171 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
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2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	11895	99.9	6801	9	AF227751	AF227751 Homo sapi
2	11877.5	99.8	6822	6	AR201014	AR201014 Sequence
3	11877.5	99.8	6822	9	AF227744	AF227744 Homo sapi
4	11877.5	99.8	7741	6	AR201015	AR201015 Sequence

5	11872	99.7	6855	9	AF227749	AF227749 Homo sapi
6	11843.5	99.5	6966	9	AF227745	AF227745 Homo sapi
7	11838	99.4	6999	9	AF227750	AF227750 Homo sapi
8	11815.5	99.3	7648	9	AF134986	AF134986 Homo sapi
9	11758.5	98.8	7253	9	AF126965	AF126965 Homo sapi
10	11741	98.6	7274	9	AF126966	AF126966 Homo sapi
11	11741	98.6	7349	9	AF190860	AF190860 Homo sapi
12	11735.5	98.6	6786	9	AF227747	AF227747 Homo sapi
13	11707	98.3	6897	9	AF227746	AF227746 Homo sapi
14	11703	98.3	6921	9	AF227748	AF227748 Homo sapi
15	11251.5	94.5	7030	9	AF134985	AF134985 Homo sapi
16	11246.5	94.5	7030	6	CQ724231	CQ724231 Sequence
17	11133.5	93.5	7625	10	MMU012569	AJ012569 Mus muscu
18	11111	93.3	7129	6	BD224078	BD224078 T-type ca
19	11111	93.3	7285	6	BD224079	BD224079 T-type ca
20	11111	93.3	7286	10	AF125161	AF125161 Rattus no
21	10945	91.9	6942	10	AF290212	AF290212 Rattus no
22	10945	91.9	7542	10	RNCAL1G	AF027984 Rattus no
23	10913	91.7	7527	10	BC057399	BC057399 Mus muscu
24	10890.5	91.5	7540	6	AX068898	AX068898 Sequence
25	8977	75.4	5475	9	AB032949	AB032949 Homo sapi
26	7705	64.7	4903	9	AB012043	AB012043 Homo sapi
27	6573	55.2	4944	10	AK129294	AK129294 Mus muscu
28	6315.5	53.1	3993	9	AF124351	AF124351 Homo sapi
29	6224.5	52.3	7044	9	HSA420779	AJ420779 Homo sapi
30	6223	52.3	8447	6	AX068900	AX068900 Sequence
31	6222.5	52.3	7868	10	AF290213	AF290213 Rattus no
32	6215.5	52.2	7898	6	BD087035	BD087035 Calcium c
33	6215.5	52.2	7898	9	AF073931	AF073931 Homo sapi
34	6214.5	52.2	7898	6	BD087032	BD087032 Calcium c
35	6211.5	52.2	7762	9	AF051946	AF051946 Homo sapi
36	5713	48.0	6941	6	BD087036	BD087036 Calcium c
37	5637.5	47.4	6924	6	CQ730788	CQ730788 Sequence
38	5496.5	46.2	6390	9	AF142567	AF142567 Homo sapi
39	5493	46.1	6911	10	AF086827	AF086827 Rattus no
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41	5492.5	46.1	6816	6	AR352550	AR352550 Sequence
42	5484	46.1	6855	6	AR175748	AR175748 Sequence
43	5484	46.1	6855	6	AR352551	AR352551 Sequence
44	5484	46.1	9886	9	AF393329	AF393329 Homo sapi
45	5432.5	45.6	6740	9	AF129133	AF129133 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS AF227751 Homo sapiens voltage-dependent calcium channel alpha 1G subunit
DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1G subunit
isoform be (CACNA1G) mRNA, complete cds.
ACCESSION AF227751 GI:7159274
VERSION AF227751
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 6801)
AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.
TITLE Molecular and functional properties of the human alpha(1G) subunit
that forms T-type calcium channels
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE 20158909
PUBMED 10692398
REFERENCE 2 (bases 1 to 6801)
AUTHORS Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France
FEATURES
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gene
CDS

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RCQAPPRSPSEASGRIVSGKVYPVHTISPEETLKEKALVEVAASGPPTLTSLNI
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REMPDSDSEAVEYFTQDQHSDLRDPHSRRQSLGPDAEPSSVLAFWRLICDTFRKIV
DSKYFGRGIMAIIVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLIKLIVYG
PFGYIKNPYNI FDGVIIVVISWEIVGQGGGLSVLRTFRMLRVLKVRFPLAQRLV
VLMKTMNVATFCMLMLFI FIFISILGMHLPGCKFASERDGTLPDRKNFDSLMAIV
TVEQILTQEDMNKVLXNGMASTSSWAALFYIALMTFGNYVLFNLLVAILVEGFOABEI
SKREDASGQLSCIQLPYVDSQGDANKSESEPDFSPSLDGDGRKKCLALVSLGEHPE
LRKSLPLLIHTAATPMSLPKSTSTGLGALGPASRTSSGSAEPGAHEMKSPPS
ARSSPHSPWSAASWTSRRSSRNSLGRAPSLKRSPSGERRSLSGEQESQDEEBSS
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SGRLARALRPDDPPLDGDADDEGNLSKGERVAMIRARLPACCLERDSWSAYIFPQ
SRRLLRHRIITHKMPDHVLYIIFLNCITIAMERPKIDPHSAERIFLTLSNYIFTAV
FLAEMTVKVALGWCFGEOAYLRSSMNVLDELVLISVIDILVSNVSDGTKILGMLR
VLRILRTLRLRVISRAGIKLVETLMSLKEIGNIVICCAFIIIGILGVQLFKG
KFVFCQGEDTRNITNKSDCABASRWVRHKNFNQLGOALMSLFVLASKDGVMDIMYD
GLDVGVDQQPI MNHNPMLLYFISFLIVAFVLMFVGVVFNHFKCRQHOEBEA
RRREKRRLRLLEKKRKAQCKPYSDYSRFLVHLLCTSHYLDLFTGVLGNVMT
AMEHYQQPQILDALKICNYIFTVIFVLESVFLVAFGRRFQDRNQDLDAIVLS
IMGITLBEIEVNASLPINPTIIRIMRVLRIRAVLKLKMAVGMRALDVTMQALLPQV
NLGLFMLLFFIFALGVELFGDLECEDTHPCGLGRHATFRNFGMAFVTLFRVSTGD
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AKEBAELEAELEMKTLSPQHPSPIGSPFLMGVEGPDSPSPKGFALHPAARSA
SHSLSLHPTMQPHPTLPGPDLITVRKSGVSRTHSLPNDSYMCRHGSTAEGPLGRGW
GLPKAQSGSVLSVHSDPADTSYIQLPKDAPHLQPHSATWGTIPKLPQQRSPLAQ
RPLRQAIRITDSLVDQGLSGREDLAEVSGSPPLARAYSFWGQSTQAQSHRSPLA
KISKMTTPAPCPGPEPNMGKPEPTRSLELDELISWISGDLPPGGOEPPSPRDL
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ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 6801
Score: 11895.00 Matches: 2265
Percent Similarity: 99.96% Conservative: 0
Best Local Similarity: 99.96% Mismatches: 1
Query Match: 99.92% Indels: 0
DB: 9 Gaps: 0

US-09-611-257A-37 (1-2266) x AFD227751 (1-6801)

QY 1 MetAspGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
DB 1 ATGACGAGAGAGATGAGCGGCGCCGAGAGATCGGGAACGCCCGAGCTTCATG 60
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp 40
DB 61 CGGCTCAACGACCTGTCTGGGGGCGCGGGGCGCGGGGCGGTCTACGAGAAAGAC 120

QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
DB 121 CCGGCGACGCGCGACTCCGAGAGCGGAGGGGTGCCGTACCCGCGCGTGGGTGTT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
DB 181 TTCCTTACTTGAGCCGACGACAGCCGCCCGCGAGCTGGTGTCTCCGACGGTCTGTAAAC 240
QY 81 ProTrpPheGluArgLieserMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
DB 241 CCCTGGTTTGAGCGCATCAGCATGTTGGTCATCTTCTCAACTGCGTGACCCCTGGCATG 300
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
DB 301 TTCGGCCATGCGAGGACATCGCTGTGACTGCCAGCGCTGCCGATCTGCAGGCCCTTT 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
DB 361 GATGACTTCATCTTGGCTTCTTGGCCGTGAGATGGTGTGAAGATGGTGGCCTTGAGGC 420
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
DB 421 ATCTTTGGAAAAAGTGTAACTGGGAGACACTTGGAACCGGCTTGACTTTTCATCGTC 480
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
DB 481 ATCGGAGGATGCTGAGTACTCGCTGACCTGAGAAACGTCAAGCTTCAGCTGTCAAG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
DB 541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCACGATGCGCATCTT 600
QY 201 ValThrLeuLeuLeuAspThrLeuPrometLeuGlyAsnValLeuLeuLeuCysPhePhe 220
DB 601 GTCACTTCTGCTGCTGATACGCTGCCCATGCTGGGCAACGTCCTGCTCTGCTTCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
DB 661 GTCTTCTTCATCTTCGCGATCGCTGCGGCTCCAGCTGTGGCAGGGCTGCTTCGAAACCGA 720
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
DB 721 TGCTTCTCACTGAGAAATTCAAGCTCCCCCTGAGCGTGGAACCTGAGCGCTATTACCAAG 780
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
DB 781 ACAGAGAACGAGATGAGAGCCCTTCATCTGCTCCACGACGAGAAACGGCATGCGG 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
DB 841 TCCTTCAGAAAGCGTGCCCAAGCTGCGCGGGGAGCGGGGGCGTGGCCCACTTGCGGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrCysValAsnTrpAsnGlnTyrTyr 320
DB 901 GACTATGAGGCTTACAACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTAC 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnPropheLysGlyAlaIleAsnPheAspAsnIle 340
DB 961 ACCAAGTGTCTCAGCGGGGAGCAACACCTTTCAGGGCGCCATCACTTTGACAAACATT 1020
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
DB 1021 GGCTATGCCCTGATCGCCATCTTCCAGTCAATCAACGCTGGAGGGCTGGGTCGACATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
DB 1081 TACTTTGTATGATGATGCTCATCTCTTCAATTCATCTACTTCACTCTCCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
DB 1141 GTGGGCTCTTCTTCATGATCAACCTGTGCTGTGTGATTGGCACGAGTTCTCAGAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420

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Db 1201 ACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTTCTGTCCAAGCC 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
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Db 1261 AGCAACCCTGCTAGCTTCTTGAGCCCCGGCAGCTGCTATGAGAGCTGCTCAAGTACTTG 1320
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
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Db 1321 GTGTACATCCTTCGTAAGGAGCAGCCCGCAGGCTGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
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Db 1381 CCGGTTGGGCTGCTCAGCAGCCCGCAGCACCCTCGGGGGCCAGGAGACCAGCCAGCAGAC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
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Db 1441 AGCTGCTCTCGCTCCACCGCGCCTATCCGTCCACCACCTGTGCACCAACCACCAACCAC 1500
QY 501 HisHisHisHisTyrHisLeuGlyValAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
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Db 1501 CATCACCACTACCTACCACTGGGCAATGGGAGCTCAGGGCCCCCGGGGCCAGCCCGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
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Db 1561 ATCCAGGACAGGGATGCCAATGGGTCCCGCGCTCATGCTGCCACCACTCGACGCT 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
|||||
Db 1621 GCCCTCTCGGGGCCCCCTGTGTGGCGCAGAGTCTGTGCACAGCTTCTTACCATGCGGAC 1680
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1681 TGCCACTTAGAGCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTGAGGCATCC 1740
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
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Db 1741 GGCAGGACTGTGGGCAAGGGAAGTGTATCCACCGTGACACACCAAGCCCTCCACCGAG 1800
QY 601 ThrLeuLysGluLysValLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
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Db 1801 ACGCTGAAGAGAGGACCTAGTAGAGGTGGCTGCCAGCTTGCGGCCCAACCTCACC 1860
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
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Db 1861 AGCTCAACATCCCAACCGGGCCCTACAGCTCCATGCACAAGCTGTGAGACACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
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Db 1921 ACAGGTGCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTGAAGCAGACAGTGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
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Db 1981 GCCTGTGTCAGACAGCTGCCCTACTGTGCCGGGGCCGGGGCAGGGAGGTGAGCTC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
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Db 2041 GCCGACCGTGAAATGCTGACTCAGACAGCGAGGAGTTTATGAGTTTACACACAGATGCC 2100
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
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Db 2101 CAGCACAGCAGACTCCGGGACCCCAACAGCCGGGGCAACGAGCCTTGGGCCCATGCA 2160
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
2161 GAGCCAGCTCTGTGCTGCTTCTGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2221 GACAGCAAGTACTTTGGCGGGGAATCATGATGCCATCTGTGCAACACACTCAGCATG 2280
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
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Db 2281 GGCATCGAATACACAGCAGCCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2340
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe 800
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Db 2341 GTCTTACCAAGCTCTTGTGCCCTGAGATGCTGTGAAGCTGCTGTGTATGTTCCCTTT 2400
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820
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Db 2401 GGCTACATCAAGAAATCCCTACAACATCTTCGATGTTGTGTCATCAGCGTGTGG 2460
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
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Db 2461 GAGATCGTGGCCAGCAGGGGGCGGCTGTGCTGTGCGGACCTTCCGCTGATGCTG 2520
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
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Db 2521 GTGCTGAAGCTGTGCGCTTCTCGCGGCGCTGCAGCGGCACTGTGTGCTCATGAAG 2580
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
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Db 2581 ACCATGACACAGTGGCCACCTTCTGCATGCTGCTTATGCTTTCATCTTCATCTTCA 2640
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGlyLysArgAspGlyAspThrLeu 900
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Db 2641 ATCTGGGCATCATCTCTTCGGCTGCAAGTTTGCTCTGACGGGAGTGGGACACCCCTG 2700
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
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Db 2701 CCAGACCGGAAGAAATTTGACTCTTGTCTGTGGCCATCGTCACTGTCTTCAAGATCTTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
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Db 2761 ACCCAGAGGACTGGAACAAGTCTCTCAATGATGCTTCCACGTCCTGCTGGCG 2820
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal 960
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Db 2821 GCCCTTATTTCATTGCCCTCATGACCTTGGCAACTACGTGCTTCAATTGTGCTGTC 2880
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSerGly 980
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Db 2881 GCCATTCTGTGTGAGGGCTTCCAGGCGGAGGAATCAGCAACGGGAAGATGCGAGTGA 2940
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyLysAspAlaAsnLysSerGlu 1000
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Db 2941 CAGTTAAGCTGTATTCAGCTGCTGTGACTCCAGGGGGAGATGCCAACAAAGTCCGAA 3000
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
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Db 3001 TCAGAGCCCGATTTCTTCCACCAGCTCGATGTGATGGGGCAGAGAAAGTGTCTTG 3060
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040
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Db 3061 GCCTTGTGTCCCTGGGAGAGACACCCGAGCTGCGGAAGAGCTGCGCCTCTCATC 3120
QY 1041 IleHisThrAlaAlaThrPrometSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
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Db 3121 ATCCACACGGGCCCAACCACTGTGCTGCCCAAGAGCACACGAGCGGCTGGCGGAG 3180
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
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Db 3181 GCGCTGGGCCCTGCTGCGCGCGCACACAGCAGCAGCGGTTGCGGAGAGCTGGGGCGGCC 3240
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
3241 CACGAGATGAAGTCAACCGCCAGCGCCGAGCTTCCGACAGCCCTGGAGCGCTGCA 3300
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
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Db 3301 AGCAGCTGACACAGAGCGCTCCAGCGGAAACAGCTCGGCCGTGCACCCAGCTGAAG 3360
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140
|||||
Db 3361 CGAGGAAGCCCAAGTGAAGAGCGGCGGTCTCTGTGTGCGGAGAAAGCCAGAGAGCCAG 3420

QY	1141	AspGluGluGluSerSerGluGluGluValArgAlaSerProAlaGlySerAspHis	1160
Db	3421	GATGAAGAGGAGACTCAGAAGAGGAGCGGGCCAGCCCTCGGGCAGTGACCATCGCCAC	3480
QY	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3481	AGGGGCTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCAGACACACTGCAGGTG	3540
QY	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
Db	3541	CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTGTCTTGAGCACCAGACTGCAAT	3600
QY	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	3601	GGCAAGTCGGCTTCAGGCGCCCTGGCCCCGGCCCTGCGGCTGATGACCCCCCACTGGAT	3660
QY	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrrPile	1240
Db	3661	GGGATGACGCCGATGACGAGGGCAACTTGAGCAAAAGGGAAAGGGTCCGCGCTGGATC	3720
QY	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro	1260
Db	3721	CGAGCCCGACTCCCTGCTGCTGCTCGAGCGAGACTCTTGTCAGCCTACATCTTCCCT	3780
QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
Db	3781	CCTCAGTCCAGGTTCCGCCCTCCTGTGTCAACCGGATCATCACCAAGATGTTGCACCAAC	3840
QY	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
Db	3841	GTGGTCTTGTATCATCTTCTTAACTGCATCACCATCGCCATGGAGCGCCCAAAATT	3900
QY	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320
Db	3901	GACCCCCACAGCGGTGAACGCATCTTCTGACCCCTTCCAATTACATCTTCAACCGCAGTC	3960
QY	1321	PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlnAla	1340
Db	3961	TTTCTGGCTGAATGACAGTGAAGTGGTGGCACTGGGCTGTGCTTCGGGAGCAGGCG	4020
QY	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp	1360
Db	4021	TACCTCGGAGACGAGTTGGAACGTGCTGACGCGGCTGTGTCTCATCTCCGTATCGAC	4080
QY	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
Db	4081	ATTCTGTGTCCATGGTCTCTTGACAGCGGCACCAAGATCTGGGCATGTGAGGGTGTG	4140
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
Db	4141	CGGCTGCTGCGACCTGGGCCCGCTCAGGGTGATCAGCGGGCGCAGGGGCTGAAGCTG	4200
QY	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys	1420
Db	4201	GTGGTGAGACGCTGATGTCTCACTGAAAACCATCGGCAACATTGTAGTCATCTGCTGT	4260
QY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal	1440
Db	4261	GCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAAGGGAAGTTTTCGTG	4320
QY	1441	CysGlnGlyGlyAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
Db	4321	TGCCAGGGCGAGATACCAAGAACATCACCAATAAATCGACTGTGCCGAGGCCAGTTTAC	4380
QY	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
Db	4381	CGGTGGGTCCGGCACAAAGTACAACCTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTTC	4440
QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4441	GTTTGGCCTCCAAAGATGGTGGGTGACATCATGTACGATGGGCTGGATGCTGTGGGC	4500

QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTTrpMetLeuLeuTyrPheIleSerPhe	1520
DB	4501	GTGGACCAAGACCCCATCATGAACCAACACCCCTGGATGCTGCTGACTTCACTCTCGTTC	4560
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsn	1540
DB	4561	CTGCTCATTTGTGGCCTTCTTTGTCTTGAACATGTTTGTGGTGTGGTGGAGAACTTC	4620
QY	1541	HisLysCysArgGlnHisGlnGluGluValArgArgArgGluLysArgLeu	1560
DB	4621	CACAGTGTCCGGACGACCAAGAGAGAGAGGCGCGCGGAGAGAGAACGCCCTA	4680
QY	1561	ArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSer	1580
DB	4681	CGAAGACTGGAGAAAAAGAGAGAAAGCCAGTGCACAACTTACTACTCCGACTACTCC	4740
QY	1581	ArgPheArgLeuLeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleThr	1600
DB	4741	CGCTTCGGGCTCCCTCGTCCACCACTTGTGCACCAACCACTACCTGAGCTTTCATCACA	4800
QY	1601	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1620
DB	4801	GGTGTCATCGGGCTGAACGTGTCAACCATGGCCATGGAGCACTACCAAGACCCCAAGATT	4860
QY	1621	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer	1640
DB	4861	CTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCATCTTTGTCTTGAGTCA	4920
QY	1641	ValPheLysLeuValAlaPheGlyPheArgArgPheGlnAspArgTrpAsnGlnLeu	1660
DB	4921	GTTTTCAACTTGTGGCCTTGTGTTTCGTCGGTTCCTCCAGACAGGTGAACCAAGCTG	4980
QY	1661	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1680
DB	4981	GACCTGGCCATGTGCTGTCTGCCATCATGAGGCACTACGCTGGAGAAATCGAGGTCAAC	5040
QY	1681	AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1700
DB	5041	GCCTCGCTGCCATCAACCCCAACCATCATCCGCATCATGAGGGTCTCGCATTCGCCGA	5100
QY	1701	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln	1720
DB	5101	GTGCTGAAGCTGTGAAGATGCTGTGGCATGGGGCGCTGCTGACACGGTGATGCAG	5160
QY	1721	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAla	1740
DB	5161	GCCCTGCCCAAGGTGGGGAACCTGGGACTTCTCTCATGTGTGTTTTCATCTTTGCA	5220
QY	1741	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly	1760
DB	5221	GCTCTGGGCGTGAGCTCTTTGGAGACCTGAGTGTGACGACACACACCCCTGTGAGGGC	5280
QY	1761	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1780
DB	5281	CTGGGCCCTCATGCAACCTTTCGAACTTTGGCATGGCCTTCTAACCCCTTCCGAGTC	5340
QY	1781	SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu	1800
DB	5341	TCCACAGGTGACAAATTGGAATGGCATTATGAAGACACCCCTCCGGACTGTACCAAGAG	5400
QY	1801	SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla	1820
DB	5401	TCCACCTGCTACAACACGGTCACTCGCCTATCTACTTTGTGTCTTCGTGCTGACGGCC	5460
QY	1821	GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsn	1840
DB	5461	CAGTTCTGTCTAGTCAACGTGTGATGCGCGTGTGATGAAGCACCTGGAGAGAGCAAC	5520
QY	1841	LysGluAlaLysGluGluValGluLeuGluValAlaGluLeuGluLeuGluMetLysThrLeu	1860
DB	5521	AAGAGGCCAAGAGAGAGGCGGAGCTAGAGGCTGAGCTGGAAGCTGAGATGAAGACCCCTC	5580
QY	1861	SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro	1880

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Db 5581 AGCCCCCAGCCCACTGGCCACTGGGAGCCCTTCTGCTGGGCTGGAGGGCCCC 5640
QY 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900
Db 5641 GACAGCCCCGACAGCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCCAAGAGATCAGCC 5700
QY 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyPro 1920
Db 5701 TCCCACTTTTCCCTGGAGCACCCCAAGATGACCCCAACCCACGAGACTGCGAGACCA 5760
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LOCUS Sequence 3 from patent US 6358706.
DEFINITION AR201014
ACCESSION AR201014
VERSION AR201014.1 GI:20251902
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6822)
AUTHORS Dublin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.
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Score: 11877.50 Matches: 2264
Percent Similarity: 99.65% Conservative: 1
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 99.78% Indels: 7
DB: 6 Gaps: 1
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QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyLysArgProGlyProGlySerAlaGluLysAsp 40
Db 61 CGGCTCAACGACTGTGCGGGGCCGGGGCCGGCGGGGGGTGACAGAAAAAGAC 120
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
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DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1g subunit
isoform ae (CACNA1G) mRNA, complete cds.
ACCESSION AF227744
VERSION AF227744.1 GI:7159260
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6822)
AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and
Nargeot,J.

TITLE Molecular and functional properties of the human alpha(1g) subunit
that forms T-type calcium channels
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE 20158909
PUBMED 10692398
REFERENCE 2 (bases 1 to 6822)
AUTHORS Monteil, A., Mennesier, G., Bourinet, E., Lory, P. and Nargeot, J.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France
FEATURES
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ORIGIN
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Score: 11877.50
Percent Similarity: 99.65%
Best Local Similarity: 99.60%
Length: 6822
Matches: 2264
Conservative: 1
Mismatch: 1

Query Match:	99.78%	Indels:	7
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RESULT 4
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LOCUS AR201015
DEFINITION Sequence 4 from patent US 6358706.
ACCESSION AR201015
VERSION AR201015.1 GI:20251903
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 7741)
AUTHORS Dubin,A.E., Galindo,J.E., Pyati,J., Zhu,J.Y. and Erlander,M.G.
TITLE DNA encoding human alpha1g-C T-Type calcium channel
JOURNAL Patent: US 6358706-A 4 19-MAR-2002;
FEATURES location/Qualifiers
source 1..7741

ORIGIN
/organism="unknown"
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Alignment Scores:
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Score: 11877.50 Matches: 2264
Percent Similarity: 99.65% Conservative: 1
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 99.78% Indels: 7
DB: 6 Gaps: 1

US-09-611-257A-37 (1-2266) x AR201015 (1-7741)

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VERSION AF227749.1 GI:7159270
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 6855)
AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennesier,G., Lory,P. and
Nargeot,J.
TITLE Molecular and functional properties of the human alpha(1G) subunit
that forms T-type calcium channels
JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE 20158909
PUBMED 10692398
REFERENCE 2 (bases 1 to 6855)
AUTHORS Monteil,A., Mennesier,G., Bourinet,E., Lory,P. and Nargeot,J.
TITLE Direct Submission
JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France
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SOURCE			
ORGANISM			Homo sapiens (human)
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REFERENCE			
AUTHORS			Monteil,A., Chemln,J., Bourinet,E., Mennessier,G., Lory,P. and
			Nargeot,J.
TITLE			Molecular and functional properties of the human alpha(1g) subunit
JOURNAL			that forms T-type calcium channels
MEDLINE			J. Biol. Chem. 275 (9), 6090-6100 (2000)
PUBMED			20158909
			10692398
REFERENCE			
AUTHORS			2 (bases 1 to 6966)
TITLE			Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.
JOURNAL			Direct Submission
			Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.)
			U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France
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ORIGIN

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US-09-611-257A-37 (1-2266) x AF227745 (1-6966)

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QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValIleLeuGlyMet	100
Db	241	CCCTGTTTGAGCGCATCAGCATGTTGGTCACTTCTTCAACTGCGTGACCTGGGCATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	301	TTCCGGCCATGCGAGGACATCGCCTGTGACTCCACGCGCTCCGATCTGCAGGCCCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGly	140
Db	361	GATGACTTCATCTTGCCCTTCTTTGCGGTGAGATGGTGTGAAGATGGTGCCCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
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QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
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QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	541	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCACAGCATGCGCATCTT	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValIleuLeuLeuCysPhePhe	220
Db	601	GTCACGTTGCTGCTGSGATAACGCTGCCCATGTGGCAACGTCCTGCTGTCTTCTTCTT	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
Db	661	GTCTTCTTCATCTTCGGCATCGTCGGCTCCAGCTGTGGCAGAGGCTGTCGGAACCGA	720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTrpGln	260
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QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
Db	781	ACAGAGAACGAGATGAGAGCCCTTCATCTGTCTCCAGCCACGCGAGAACGGCATGCGG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
Db	841	TCCTGCAAGCGTGCCCAACGCTGCGCGGGAACGGGGCGGTGGCCACCTTGGGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrCysValAsnTrpAsnGlnTyrTyr	320
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QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
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QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
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QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
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QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
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QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
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QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440

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QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
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QY 501 HisHisHisHisTyrHisHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
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RESULT 7

AF227750 6999 bp mRNA linear PRI 06-MAR-2000

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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AUTHORS

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1. .6999

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ORIGIN

Alignment Scores:
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Score: 11838.00 Matches: 2264
Percent Similarity: 97.13% Conservative: 1
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Query Match: 99.45% Indels: 66
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US-09-611-257A-37 (1-2266) x AF227750 (1-6999)

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DB	121	CCGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCGCGGCTGGCCCGGTGTT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
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QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	301	TTCCGGCCATGCGAGACATCGCCTGTGACTCCAGCGCTGCGGATCCTGCAGGCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	361	GATGACTTCATCTTGTCTTCTTGGCTGAGAGATGTTGTGAAGATGTTGGCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrTrpLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
DB	421	ATCTTTGGGAAAAAGTGTACTCGGAGACACTTGGAACGGGCTTGACTTTTCATCGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180

DB	481	ATCCGAGGGATGCTGAGTACTCGCTGGACCTGCAGAAAGTCAGCTTCTCAGCTGTCAAG	540
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DB	541	ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCCTT	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	601	GTCACGTGCTGCTGATACGCTGCCCATGCTGGGCCAACGTCCTGCTGCTTCTTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
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QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
DB	721	TGCTTCTCACTGAGAAITTCAGCTCCCTCCAGCGTGGAACCTGGAGCGCTATTACCAAG	780
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
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QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
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QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrCysValAsnTrpAsnGlnTyrTyr	320
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QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
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QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
DB	1081	TACTTGTGATGATGATGCTCATCTTCTTCAAAITTCATCTTCACTTCCTCATCATC	1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
DB	1141	GTTGGCTCTTCTTTCATGATCAACTGTGCTGTGTGATTGCCACGCAGTCTCAGAG	1200
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
DB	1201	ACCAAGCAGCGGGAAGCCAGCTGATGCGGAGCAGCGTGTGCGTCTCTCAACAGCC	1260
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QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluTrpGlnProSerSer	480
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QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
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QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
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QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
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QY	2015	AlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGly	2034
Db	6241	GCTCAGAGGCCACTCAGCGGCCAGGACGAATAAGACTGACTCCTTGAGACGTTCAGGGT	6300
QY	2035	LeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArg	2054
Db	6301	CTGGGCAGCCGGGAGACTCTGTGGCAGAGGTAGTGGCCCTCCCGCCCTGGCCCGG	6360
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Db	6361	GCCTACTCTTTCTGGGGCAGTCAAGTACCAGGCACAGCAGCACTCCGCGACACAGC	6420
QY	2075	LysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTyrPgly	2094
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QY	2095	LysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTyrIleSer	2114
Db	6481	AAGGGCCCTCCAGAGACCAAGACAGCTTAGAGTTGGACACGAGCTGAGATTTC	6540
QY	2115	GlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLys	2134
Db	6541	GGAGACCTCTGCCCCCTGGCGGCCAGGAGAGCCCCCATCCCCACGGACCTGAAGAG	6600
QY	2135	CysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTyrLeuAspGluGln	2154
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QY	2155	ArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThr	2174
Db	6661	AGGAGACACTCTATCGCCGTCAGCTGCTGACAGCGGCTCCCAACCCCACTGGGCACA	6720
QY	2175	AspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLys	2194
Db	6721	GACCCCTTAACCTTGGGGGCCAGCCTCTTGGGGGGCCTGGGAGCCGGCCCAAGAAAAA	6780
QY	2195	LeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrProPro	2214
Db	6781	CTCAGCCCCCCTAGTATCACCATAGACCCCCCGAGAGCCAAGTCTCTGGACCCCGCC	6840
QY	2215	SerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAla	2234
Db	6841	AGCCCTGTATCTGCTCCGAGGAGGGCTCCGTCCAGCACTCCAAGATCCCTTGGCC	6900
QY	2235	SerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeu	2254
Db	6901	TCTGGCCCCCTGACAGCATGCTGCTCGCCCTCCCAAGAAAGATGTCTGAGTCTC	6960
QY	2255	SerGlyLeuSerSerAspProAlaAspLeuAspPro	2266
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RESULT 8
AF134986
LOCUS
DEFINITION

AF134986 7648 bp mRNA linear PRI 20-MAR-2000
Homo sapiens T calcium channel alpha1g subunit (CACNA1G) mRNA,

complete cds.

AF134986
AF134986.1 GI:6625658

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 7648)

Mittman, S., Guo, J. and Agnew, W.S.

Structure and alternative splicing of the gene encoding alpha1g, a human brain T calcium channel alphasubunit

Neurosci. Lett. 274 (3), 143-146 (1999)

20014446

10548410

2 (bases 1 to 7648)

Mittman, S., Guo, J. and Agnew, W.S.

Submitted (15-MAR-1999) Anesthesiology/Critical Care Medicine, The Johns Hopkins University School of Medicine, 600 N. Wolfe Street, Meyer 297, Baltimore, MD 21287-7294, USA

FEATURES

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ORIGIN

Alignment Scores:

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Score:	11815.50	Matches:	2264
Percent Similarity:	95.29%	Conservative:	1
Best Local Similarity:	95.25%	Mismatches:	1
Query Match:	99.26%	Indels:	111
DB:	9	Gaps:	2

US-09-611-257A-37 (1-2266) x AF134986 (1-7648)

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DB	61	CGGCTCAACGACCTGTGCGGGGCCGGGGGCGGGCCGGGGCGGGGTGACAGAAAGAC	120
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
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QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
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QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	361	GATGACTTCATCTTTCCTTCTTGGCCGTGAGATGATGTTGTAAGATGTTGGCTTGGGC	420
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DB	421	ATCTTTGGGAAAAGTGTACTCGGAGACACTTGAAACGGCTTGACTTTTCATCGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	481	ATCGCAGGGGATGCTGAGTACTCGCTGCACTGCAGAACGTCACTTCTCAGCTGTCAAG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	541	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCTCCAGCATGCCATCTT	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	601	GTCACGTTGCTGCTGAGTACGCTGCCATGTCTGGCAACGTCTGCTGTGCTTCTTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg	240
DB	661	GTCTTCTTCATCTTCGCGCATGTCGGCGTCCAGCTGTGGGCAAGGCTGCTTCGAAACCGA	720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
DB	721	TGCTTCCTACTGAGAAATTTCAGCCTCCCTTGAGCGTGGAAGCTGGAAGCGCTATTACCAAG	780

QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
DB	781	ACAGAGAACGAGATGAGAGCCCTTCATCTGCTCCAGCACGCGAGAACGGCATGCGG	840
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DB	841	TCCTGCAGAACGTCGCCACGCTGCCGGGAGCGGGGGCGGTGGCCACCTTGCGGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerAsnThrCysValAsnTyrAsnGlnTyrTyr	320
DB	901	GACTATGAGCCCTACAACAGCTCCAGCAACACCACCTGTGTCACTGGAACCACTACTAC	960
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
DB	961	ACCAACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGCCATCAACTTGACAACATT	1020
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DB	1021	GGCTATGCCCTGGATCGCCATCTTCCAGTCACTCAGTCAAGGGCTGGGTGACATCATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle	380
DB	1081	TACTTGTGATGATGATGCTCATCTTCTTACAATTTCATCTTCACTTCTCATCATC	1140
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QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
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QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640

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QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3841 GTGTCTTGTATCATCTTCTTAATGTGCATCACCATCGCCATGGAAGCCCCCAAAATT 3900
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
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QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340
Db 3961 TTTCTGCTGAATGACAGTGAAGTGTGGCACTGGGCTGTGCTTCCGGGAGCAGGCG 4020
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 4021 TACCTCGGAGCAGTTGGAACGTGCTGACGGGCTGTTGTGTCTCATCTCCGTATCGAC 4080
|||||

QY	1361	ILEuValSerMetValSerAspSerGlyThrLysILEuGlyMetLeuArgValLeu	1380
Db	4081	ATTCTGTGTCATGCTCTTGACAGCGGCACCAAGATCTGGGCATGTGAGGCTCTG	4140
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValILESerArgAlaGlnGlyLeuLysLeu	1400
Db	4141	CGGCTGCTGCGGACCCCTGCGCCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTAAGCTG	4200
QY	1401	ValValGluThrLeuMetSerSerLeuLysProILEGlyAsnILEValValILECysCys	1420
Db	4201	GTGTGTGAGACCGCTGATGTCCTCACTGAACCCCATCGGCAACATTGTAGTCATCTGCTGT	4260
QY	1421	AlaPhePheILEILEPheGlyILEuGlyValGlnLeuPheLysGlyLysPhePheVal	1440
Db	4261	GCCTTCTTCATCATTTTCGGCATCTTGGGGTGCAGCTCTTCAAGGGAAGTTTTCGTG	4320
QY	1441	CysGlnGlyGluAspThrArgAsnILEThrAsnLysSerAspCysAlaGluAsnSerTyr	1460
Db	4321	TGCCAGGGCGAGATACCAAGAACATCACCAATAATCGACTGTGCCGAGGCCAGTTAC	4380
QY	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlnAlaLeuMetSerLeuPhe	1480
Db	4381	CGGTGGGTCCGGCACAGTACACTTGTGACACCTTGCGCAGGCCCTGATGTCCCTGTC	4440
QY	1481	ValLeuAlaSerLysAspGlyTrpValAspILEMetTyrAspGlyLeuAspAlaValGly	1500
Db	4441	GTTTGGCCTCCAGAGATGCTGGGTGGATCATGTACATGGGCTGATGCTGTGGGC	4500
QY	1501	ValAspGlnGlnProILEMetAsnHisAsnProTrpMetLeuLeuTyrPheILESerPhe	1520
Db	4501	GTGACACGACGACCCCATCATGAACACCAACCCTGATGCTGCTACTTCATCTGCTTC	4560
QY	1521	LeuLeuILEValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe	1540
Db	4561	CTGCTCATGTGTGCTTCTTGTCTGTAACATGTTGTGGGTGTGTGTGAGAACTTC	4620
QY	1541	HisLysCysArgGlnHisGlnGlnGluGluGluAlaArgArgGluLysArgLeu	1560
Db	4621	CACAAGTGTCCGACGACCAAGAGAGAGAGAGGCCCCGGGGAGAGAGAACGCTTA	4680
QY	1561	ArgArgLeuGluLysLysArgArg-----	1568
Db	4681	CGAAGACTGGAGAAAAGAGAGGAATCTAATGCTGACGATGTAATTGCTTCCGGCAGC	4740
QY	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe	1582
Db	4741	TCAAGCAGCGCTGCTGAGAAAGCCAGTGCAAACTTAATACTCCGACTACTCCGCTTC	4800
QY	1583	ArgLeuLeuValHisLysLeuCysThrSerHisTyrLeuAspLeuPheILEThrGlyVal	1602
Db	4801	CGGCTCCTCGTCCACCACTGTGTGACACGACCACTACTGGAACCTTCATCACAGGTCTC	4860
QY	1603	ILEGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnILEuAsp	1622
Db	4861	ATCGGGCTGAACGTGTGCATGCCATGGCCATGGAGCACTACAGACCCCAAGATTCTGGAT	4920
QY	1623	GluAlaLeuLysILECysAsnTyrILEPheThrValILEPheValLeuGluSerValPhe	1642
Db	4921	GAGGCTCTGAAGATCTGCACTACATCTTCACTGTTCATCTTTGTCTTGAGTCAGTTTTTC	4980
QY	1643	LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu	1662
Db	4981	AAACTTGTGCTTGTGTTCCGTCGGTTCCTTCCAGGACAGGTGAACCAAGCTGGAACCTG	5040
QY	1663	AlaILEValLeuLeuSerILEMetGlyILEThrLeuGluGlnILEGluValAsnAlaSer	1682
Db	5041	GCCATTGTGCTGCTGCATCATGGGCATCACGCTGAAGAAATCGAGTCAACGCTCG	5100
QY	1683	LeuProILEAsnProThrILEILEArgILEMetArgValLeuArgILEAlaArgValLeu	1702
Db	5101	CTGCCCATCAACCCCAACCATCATCCGCATCATGAGGGTGTCCGCATTGCCCGAGTGTCTG	5160

QY	1703	LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu	1722
Db	5161	AAGTGTCTGAAGATGGCTGTGGCATGCGGGCGCTGTGACACAGGTGATGCAGGGCCCTG	5220
QY	1723	ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaIleu	1742
Db	5221	CCCAGGTGGGAACCTGGGACTTCTTCATGTGTGTTTTCATCTTTGCAGCTCTG	5280
QY	1743	GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly	1762
Db	5281	GGCGTGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCCTTGGC	5340
QY	1763	ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr	1782
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QY	1783	GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr	1802
Db	5401	GGTGACAATTGGAATGGCATTATGAAGGACACCCTCCGGACTGTGACCGAGATCCACC	5460
QY	1803	CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe	1822
Db	5461	TGCTACAACACGCTCATCTCGCCTATCTACTTGTGTCTTCCGTGTCAGGCCAGTTTC	5520
QY	1823	ValLeuValAsnValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu	1842
Db	5521	GTGCTAGTCAACGTGTGATCGCCGTGCTGATGAAGCACCTGGAGGAGCAACAAGGAG	5580
QY	1843	AlaLysGluGluAlaGluLeuGluValaGluLeuGluLeuGluMetLysThrLeuSerPro	1862
Db	5581	GCCAAGAGAGAGGCCGAGCTAGAGGCTGAGCTGAGAGTGAAGACCTCAGCCCC	5640
QY	1863	GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValaGluGlyProAspSer	1882
Db	5641	CAGCCCCACTCGCCACTGGGCAGCCCCCTTCTCTGGCCTGGGGTCGAGGGCCCCGACAGC	5700
QY	1883	ProAspSerProLysBProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis	1902
Db	5701	CCCCAGACCCCCAAGCTGGGGCTCTGCACACCAGCGGCCACGCGAGATCAGCTCCAC	5760
QY	1903	PheSerLeuGluHisProThr-----	1909
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QY	1909	-----	1909
Db	6001	ACGGATGACTTTTGCTGATGACATGCACACACTTACTTAGTGCCCTGAGAGCAAT	6060
QY	1910	MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValaArgLysSerGly	1929
Db	6061	ATGCAGCCCCACCCACGAGCTGCCAGGACCACTTACTGACTGTGCGGAAGTCTGGG	6120
QY	1930	ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla	1949
Db	6121	GTCAGCCGAACGCACTCTGTGCCCAATGACAGCTACATGTGTGCGCATGGGAGCACTGCC	6180
QY	1950	GluGlyProLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeu	1969
Db	6181	GAGGGGCCCCCTGGGACACAGGGGCTGGGGGCTCCCAAGCTCAGTCAAGCTCCGCTTGG	6240
QY	1970	SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro	1989

Db	6241	TCCGTTCACTCCAGCAGACAGATACCAAGTACATCCTGCAGACTTCCCAAGATGACACT	6300
Qy	1990	HisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProPro	2009
Db	6301	CATCTGCTCCAGCCCCACAGCGCCCCCACTGGGGCACCATCCCAAACCTGCCCCACCA	6360
Qy	2010	GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer	2029
Db	6361	GGACGCTCCCTTGGCTCAGAGGCCACTCAGCGCCACAGGCAATTAAGACTGACTTCC	6420
Qy	2030	LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer	2049
Db	6421	TTGGACGTTCAAGGCTCGGGCAGCCGGAGAACCTGCTGGCAGAGGTGAGTGGCCCTCC	6480
Qy	2050	ProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHis	2069
Db	6481	CCGCCCCCTGAGCCGGGCTACTCTTCTGGGGCCAGTCAAGTACCAGGCAACAGCAGCAC	6540
Qy	2070	SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro	2089
Db	6541	TCCCCGAGCCACAGCAAGATCTCCAAGCACATGACCCCCCAGCCCTTGCCACAGGCCCA	6600
Qy	2090	GluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu	2109
Db	6601	GAACCCCACTGGGGCAAGGGCCCTCCAGAGACCAAGACAGCTTAGAGTTGGACACCGGAG	6660
Qy	2110	LeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGlnGluProProSerPro	2129
Db	6661	CTGAGCTGGAATTTCAGAGAACCTCCTGCCCCCTGGCGGCGCAGAGAGCCCCCATCCCA	6720
Qy	2130	ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer	2149
Db	6721	CGGGACCTGAAGAAGTGCTACAGCGTGAGGCCAGAGCTGCCAGCGCCGCTTACGTCC	6780
Qy	2150	TrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln	2169
Db	6781	TGGCTGGATGAGCAGAGAGACACTCTATCGCCGTCAAGCTGCCTGGACAGCGGCTCCAA	6840
Qy	2170	ProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySer	2189
Db	6841	CCCCACCTGGGCACAGACCCCTCTAACCTTGGGGGCCAGCCTCTTGGGGGGCCTGGAGC	6900
Qy	2190	ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGly	2209
Db	6901	CGGCCCCAAGAAAAAATCAGCCCCGCTAGTATCACATAGACCCCCCGAGAGCCAAAGGT	6960
Qy	2210	ProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer	2229
Db	6961	CCTCGGACCCCGCCAGCCCTGTATCTGCTCCGAGAGAGGCTCCGCTCCAGCACTCC	7020
Qy	2230	LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys	2249
Db	7021	AAGGATCCCTTGCCCTCTGCCCCCTGACAGCATGGCTGCCTCGCCCTCCCAAGAA	7080
Qy	2250	AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266
Db	7081	GATGTGCTGAGTCTCTCCGGTTTATCTCTGACCACGACAGACCTGACCCCC	7131

RESULT 9
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LOCUS Homo sapiens voltage-dependent calcium channel alpha 1g subunit b
DEFINITION Isoform (CACNA1G) mRNA, complete cds.
ACCESSION AF126965
VERSION AF126965.1 GI:4761538
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 7253)
AUTHORS Montell,A., Chemin,J., Bourinet,E., Mennesier,G., Lory,P. and

TITLE	Nargeot,J. Molecular and functional properties of the human alpha(1g) subunit that forms T-type calcium channels
JOURNAL	J. Biol. Chem. 275 (9), 6090-6100 (2000)
MEDLINE	20158909
PUBMED	10692398
REFERENCE	2 (bases 1 to 7253)
AUTHORS	Montell,A., Mennesier,G., Bourinet,E., Lory,P. and Nargeot,J.
TITLE	Direct Submission
JOURNAL	Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R. 1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France
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CDS	176..6907 /gene="CACNA1G" /note="CACNA1G-b; T-type" /product="voltage-dependent calcium channel alpha 1g subunit b isoform" /protein_id="AAD29400.1" /db_xref="GI:4761539"

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Percent Similarity:	98.94%
Best Local Similarity:	98.94%
Query Match:	98.78%
	Length: 7253
	Matches: 2242
	Conservative: 0
	Mismatches: 1
	Indels: 23

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QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyLysArgProGlyProGlySerAlaGluLysAsp	40
Db	236	CGGCTCAACGACCTGTCGGGGGCGGGGGCGGGCGGGGGTCAAGAAAGAC	295
QY	41	ProGlySerAlaAspSerGlyAlaGlyLysLeuProTyrProAlaLeuAlaProValVal	60
Db	296	CCGGGACGGCGGACTCCGAGGGCGAGGGGCTGCCGTACCCTGGCGCTGGCCCCGGTGGTT	355
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
Db	356	TTCTTCTACTTGAGCCAGACAGCCGCCCGGAGCTGGTGTCTCCGACGGTCTTAAC	415
QY	81	ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
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QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	476	TTCCGGCCATGCGAGGACATCGCCTGTGACTCCACGGCTGCCGATCCTGCAGGGCTTT	535
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
Db	536	GATGACTTCACTTTTGCCCTTCTTTGCCGTGGAAGATGGTGGTGAAGATGGTGCCCTTGGGC	595
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal	160
Db	596	ATCTTTGGAAAAAGTGTACCTGGAGACACTTGGAACCGGCTTGACTTTTTCATCGTC	655
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
Db	656	ATCGCAGGAGATGCTGAGTACTCGCTGGAACCTGCAGAAACGTCACTTCTCAGCTGTACGG	715
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	716	ACAGTCCGTGTCTGCGACCGCTCAGGGCCATTAAACCGGGTGCACGATGCGCATTCCTT	775
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	776	GTCACGTGTGCTGATACGCTGCCCATGCTGGGCAACGTCTGCTGCTCTTC	835
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg	240
Db	836	GTCCTTCTTCACTTTCGGCATCGTCGGCGTCCAAGCTGTGGGCAAGGCTGCTTCGGAACCGA	895
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
Db	896	TGCTTCTTACTGAGAAATTTCAGCCTCCCTGAGCGTGAACCTGGAAGCTATTATCCAG	955
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
Db	956	ACAGAGAACGAGATGAGAGCCCTTCATCTGCTCCCAAGCCACGAGAACGGCAATGCCG	1015
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
Db	1016	TCCTGCAGAAAGCTGCCACGCTGCGGGGGAACGGGGCGGTGGCCACCTTGCGGTCTG	1075
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr	320
Db	1076	GACTATGAGGCTTACAACAGCTCCAGCAACACCACTGTGTCACTGGAACCACTACTAC	1135
QY	321	ThrAsnCysSerAlaGlyGlyHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
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QY	341	GlyTyrAlaIleTyrPheAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet	360

Db	1196	GGCTATGCCCTGGATCGCCATCTTCCAGGTCAATCAGCTGAGGAGGCTGGGTGCACATCATG	1255
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
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QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
Db	1316	GTGGGCTCTTCTTCAATGATCAACCTGTGCCCTGGTGTGATTGGCCACGAGTTCAGAG	1375
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1376	ACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTCTCTTCCAACGCC	1435
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu	440
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QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
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QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
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QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
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QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
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QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
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QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu	600
Db	1916	GGCAGACTGTGGCAGCGGGAAGGTATATCCACGTGCACACACAGCCCTCCACCGGAG	1975
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	1976	ACGCTGAAGAGAAAGGCACTAGTAGAGTGTGCTGCAGCTTGGGCCCAACCTCACC	2035
QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640
Db	2036	AGCCTCAACATCCACCCGGGCGCTTACAGCTCCATGCACAAGCTGTGAGACACAGAGT	2095
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
Db	2096	ACAGGTGCTGCCAAAGCTTTTGCAAGATCTCCAGCCCTTGCTTGAAAGCAGACAGTGA	2155
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyValGluLeu	680
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Db 3086 -----GGAGATGCCAACAAAGTCCGAA 3106
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3107 TCAGAGCCCGATTTCTTCCACCAGCCTGATGTGATGGGACAGAGAAAGTGTCTTG 3166
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Db 3227 ATCCACACGGCCGCCACACCATGTGCTGCCCAAGACACACGCGGCTGGGCGAG 3286
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QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
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QY 1121 ArgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyGluGlnGlnLeuSerGln 1140
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Db 3527 GATGAAGAGAGAGCTCAGAAGAGAGCGGGCCAGCCCTGGCGGCAGTGACCATCGCCAC 3586
QY 1161 ArgGlySerLeuGluArgGlyAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
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QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyLysArgValArgAlaTrpIle 1240
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QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
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QY 1401 ValValGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420
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QY	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlnAlaLeuMetSerLeuPhe	1480
Db	4487	CGGTGGGTCCGGCACAAGTACAACTTTGACAACCTTGCGCCAGGCCCTGATGTCCCTGTTCC	4546
QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
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QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTyrMetLeuLeuTyrPheIleSerPhe	1520
Db	4607	GTGACCAGCAGCCCATCATGAACACCAACCCCTGGATGCTGCTGACTTCATCTCGTTCC	4666
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe	1540
Db	4667	CTGCTCATGTGGCCTTCTTTGTCTGAACATGTTTGTGGGTGTGGTGTGAGAACCTTC	4726
QY	1541	HisLysCysArgGlnHisGlnGlnGluGluGluAlaArgArgGluGluLysArgLeu	1560
Db	4727	CACAAGTGTCCGACGACCAAGAGAGAGAGAGGCCCGCGCGGAGAGAGAGCCCTA	4786
QY	1561	ArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSer	1580
Db	4787	CGAAGACTGAGAAAAAGAGAAGAAAGCCAGTGCAACTTACTCTCCGACTACTCC	4846
QY	1581	ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1600
Db	4847	CGCTTCCGGCTCCTCGTCCACCACCTGTGCACCAGCCACTAACCCTGACCTTCATCACA	4906
QY	1601	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1620
Db	4907	GGTGTCATCGGGCTGAACGTGGTCAACCATGGCCATGGACACTAACAGACGCCCGAGATT	4966
QY	1621	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer	1640
Db	4967	CTGATGAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCTCATCTTGTCTTGAGTCA	5026
QY	1641	ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu	1660
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QY	1661	AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn	1680
Db	5087	GACCTGGCCATTGTGTCTGTCTTCATCATGGGCATCACGTGGAAGAAATCGAGGTCAAC	5146
QY	1681	AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1700
Db	5147	GCCTCGCTGCCATCAACCCACCATCATCCGCATCATGAGGGTGTGCGCATTGCCCGA	5206
QY	1701	ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln	1720
Db	5207	GTGCTGAAGCTGCTGAAGATGGCTGTGGGCATGCGGCGCTGTGACACGGTGAATGAG	5266
QY	1721	AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla	1740
Db	5267	GCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTGTGTTTTCATCTTGCA	5326
QY	1741	AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGlnGly	1760
Db	5327	GCTCTGGGCGTGAGCTCTTTGGAGACCTGAGTGTGACGAGACACACCCCTGTGAGGCG	5386
QY	1761	LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal	1780
Db	5387	CTGGGCCGTCATGCCACCTTTCGGAACCTTGGCATGGCCTTCCTAACCTCTCCGAGTC	5446
QY	1781	SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu	1800
Db	5447	TCCACAGGTGACAAATTGGAATGCATTATGAAGGACACCTCCGGGACTGTGACCAAGAG	5506
QY	1801	SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla	1820

Db	5507	TCCACCTGCTACAACACGGTCATCTGGCTATCTACTTGTGTCTTCCTGCTGACGGCC	5566
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Db	5567	CAGTTCTGTCTAGTCAACGTGTGATTCGCCGTGCTGATGAAGCACCTGGAGAGACAAC	5626
QY	1841	LysGIuAlaLysGIuGIuAlaGIuLeuGIuAlaGIuLeuGIuMetLysThrIleu	1860
Db	5627	AAGAGGCCAAGAGGAGGCCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCCCTC	5686
QY	1861	SerProGIuProHisSerProLeuGIuSerProPheLeuTrpProGIuValGIuGIuPro	1880
Db	5687	AGCCCCCAGCCCCACTCGCCACTGGGAGCCCCCTTCTGTGGCTGGGGTGAAGGGCCCC	5746
QY	1881	AspSerProAspSerProLysProGIuAlaIleuHisProAlaAlaHisAlaArgSerAla	1900
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QY	1901	SerHisPheSerLeuGIuHisProThrMetGIuProHisProThrGIuLeuProGIuPro	1920
Db	5807	TCCCACTTTTCCCTGGAGCACCCCAAGATGACGCCCAACCCACGAGCTGCCAGGACCA	5866
QY	1921	AspLeuLeuThrValArgLysSerGIuValSerArgThrHisSerLeuProAsnAspSer	1940
Db	5867	GACTTACTGACTGTGCGGAAGTCTGGGTCAAGCGAAGCACTCTTGCCCAATGACAGC	5926
QY	1941	TyrMetCysArgHisGIuSerThrAlaGIuGIuProLeuGIuHisArgGIuTrpGIuLeu	1960
Db	5927	TACATGTGTGGCATGGGAGACACTGCCAGGGGGCCCTGGACACAGGGGCTGGGGGCTC	5986
QY	1961	ProLysAlaGIuSerGIuSerValIleuSerValHisSerGIuProAlaAspThrSerTyr	1980
Db	5987	CCCAAGCTCAGTCAGGCTCCGTCTGTTCGTTCACTCCAGCCAGCAGATACCACTAC	6046
QY	1981	IleLeuGIuLeuProLysAspAlaProHisIleuLeuGIuProHisSerAlaProThrTrp	2000
Db	6047	ATCTGCAGCTTCCCAAGATGACCTCATCTGCTCCAGCCCAAGCGCCCAACTGG	6106
QY	2001	GIuThrIleProLysLeuProProProGIuArgSerProLeuAlaGIuArgProLeuArg	2020
Db	6107	GGCACCATCCCAAACTGCCCCCAGCAGAGCTCCCTTGGCTCAGAGGCCACTCAGG	6166
QY	2021	ArgGIuAlaAlaIleArgThrAspSerLeuAspValGIuLysLeuGIuSerArgLysAsp	2040
Db	6167	CGCCAGGCAATTAAGCACTGACTCTTGACGTTCAAGGCTCTGGGCAAGCCGGAAGAC	6226
QY	2041	IleuLeuAlaGIuValSerGIuProSerProProLeuAlaArgAlaTyrSerPheTrpGIu	2060
Db	6227	CTGCTGGCAGAGGTGAGTGGGCCCTCCCGCCCTGGCCCGGCTTACTTTTCTGGGGC	6286
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QY	2081	ThrProProAlaProCysProGIuProGIuProAsnTrpGIuLysGIuProProGIuThr	2100
Db	6347	ACCCCGCCAGCCCTTGGCCCAAGGCCAGAACCCCACTGGGGCAAGGGCCCTCCAGAGACC	6406
QY	2101	ArgSerSerLeuGIuLeuAspThrGIuLeuSerTrpIleSerGIuAspLeuLeuProPro	2120
Db	6407	AGAAGCAGCTTAGAGTTGGACACGAGCTGAGCTGATTTCAGAGAGACTTCTGCCCT	6466
QY	2121	GIuGIuGIuGIuGIuProProSerProArgAspLeuLysLysCysTyrSerValGIuAla	2140
Db	6467	GGCGGCCAGAGAGCCCCCATCCCAAGGACCTGAAGAAGTCTACAGCCTGGAGAGCC	6526
QY	2141	GIuSerCysGIuArgArgProThrSerTrpLeuAspGIuGIuArgArgHisSerIleAla	2160
Db	6527	CAGAGCTGCCAGCGCCGCCACAGCTCTGGCTGATGACAGAGAGAGACACTTATCGCC	6586
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Qy 2241 MetAlaAlaSerProSerProLyS1ySAspValLeuSerLeuSerG1yLeuSerSerAsp 2260

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RESULT 10

AF126966 7274 bp mRNA linear PRI 29-FEB-2000

LOCUS Homo sapiens voltage-dependent calcium channel alpha 1g subunit a

DEFINITION isoform (CACNA1G) mRNA, complete cds.

ACCESSION AF126966

VERSION AF126966.1 GI:4761540

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 7274) Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

AUTHORS Monteil,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.

TITLE Molecular and functional properties of the human alpha(1g) subunit that forms T-type calcium channels

JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)

PUBMED 20158909

REFERENCE 2 (bases 1 to 7274) Monteil,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.

AUTHORS Direct Submission

TITLE Submitted (09-FEB-1999) Human Genetics Institute (I.G.H.) U.P.R. 1142, C.N.R.S., 141 rue de la Cardonille, Montpellier 34396, France

JOURNAL location/Qualifiers

FEATURES

source 1..7274 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"

gene 1..7274 /gene="CACNA1G" 176..6928 /gene="CACNA1G" /note="CACNA1G-a; T-type" /codon_start=1 /product="voltage-dependent calcium channel alpha 1g subunit a isoform" /protein_id="AAD29401.1" /db_xref="GI:4761541" /translation="MDEEDGAGAEESGQPSFMRLNDLSGAGRPGSAEKDPGSA DSEAEGLPYPALAPVFFYLSQDSPRSWCLRTVCNPFWEFISMVLINCVTLGMFR PCEDIACDSQRCRILOAFDDFIFAFAVEMVVKVALGIFKKCYLGDTWNRLLDFIY IAGMLEYSLDLQNVFSASVTRVLRPLRAINRVSMRILVTLDLTLPLMGNVLLLC FVFVFIFGIVGVLMAGLLRNCFLPENFSLLPLVDLERYYCTENEDESPFCSQPRE NGMRSCRSVPTRLRGDGGPPCGLDYEAYNSSNTTCVWNQYTNCSAGEHNFKGA INFNDNIGYAMIAIPQVITLLEGVNDIMYFVMDAHSFYNTIFILLIVGSFMINICLV VIATQSETKORESOLMREQVRFLSNASTLASFSEPGSCYEELKYLVIILRKAAR LAQVSRAGVRVGLISSAPLPGQETOPSSSCSRSHRLSVHLLVHHHHHHHHYHLG NGTLRAPRASPEIODRDANGSRRLMLPPSTPALSGAPPGAESVHSFYHADCHLEPV RQAPPPRSPSEASGRTVGSKVYPTVHTSPPELTKEKALVEVAASSGPPTLTSLNI

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ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	7274
Score:	11741.00	Matches:	2241
Percent Similarity:	98.64%	Conservative:	1
Best Local Similarity:	98.59%	Mismatches:	1
Query Match:	98.63%	Indels:	30
DB:	9	Gaps:	2

US-09-611-257A-37 (1-2266) x AF126966 (1-7274)

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Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyAlaArgProGlyProGlySerAlaGluLyAsp 40

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QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
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QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
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QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1376	ACCAAGCAGCGGGAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTTCTCTCCACGCGC	1435
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440
Db	1436	AGCAACCTGGCTAGCTTCTCTGAGCCCGGCACTGCTTATGAGGAGCTGCTCAAGTACTG	1495
QY	441	ValTyrIleLeuArgGlyAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
Db	1496	GTTGTACATCTTCTGTAAGGACCCCGCAGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG	1555
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
Db	1556	CGGGTTGGGCTGCTCAGCAGCCACGACCCCTCGGGGCGCAGAGACCCAGCCACGACC	1615
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis	500
Db	1616	AGCTGCTCTCGCTCCACCGCGCCTATCCGTCACCACTGGTGCACCAACCAACACAC	1675
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1676	CATCACCACTACTACCTTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCCGGAG	1735
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540

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Qy	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheThrHisAlaAsp	560
Db	1796	GCCCTCTCCGGGGCCCCCCTGTGTGGCGAGAGTCTGTGACACAGCTTCTACCATGCCGAC	1855
Qy	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Db	1856	TGCCACTTAGACCCAGTCCGCTGCCAGCGCCCCCTCCAGAGTCCCCCATCTGAGGCATCC	1915
Qy	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu	600
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Qy	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	1976	ACGCTGAAGGAGAAGGCACTAGTAGGTGGCTGCCAGCTTGCGCCCCCAACCTCACC	2035
Qy	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640
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Qy	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
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Qy	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla	720
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Db	2696	GTGCTGAAGCTGTGCGCTTCTGCGGCGCTGCAGCGGAGCTGTGTGCTCATGAAG	2755
Qy	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer	880
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ACCESSION	AF190860			PRI 23-FEB-2000
VERSION	AF190860.1	GI:7021332		
KEYWORDS				
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ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 7349)			
AUTHORS	Cribbs,L.L., Gomora,J.C., Daud,A.N., Lee,J.H. and Perez-Reyes,E.			

TITLE Molecular cloning and functional expression of Ca(v)3.1c, a T-type calcium channel from human brain
JOURNAL FEBS Lett. 466 (1), 54-58 (2000)
MEDLINE 20115462
PUBMED 10648811
REFERENCE 2 (bases 1 to 7349)
AUTHORS Cribbs, L.L., Gomora, J.C., Lee, J.-H., Daud, A.N. and Perez-Reyes, E.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-1999) Physiology, Loyola University Medical Center, 2160 South First Avenue, Maywood, IL 60153, USA
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ICNYIFTVIIVLESVFKLVAFGFRRFQDRWNQDLAIVLSIMGITLIEIEVNASL
INPTIIRIMRVLIARVLKLLKMAVGMRALDITVMOALPOVGNLGLLFMLLFIIPAL
GVELFGDLECDETHPCGELGRHATFRNGMAFLTLFRVSTGDMNNGIMKDTLRDCCQE
STCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLSESNKEAKEAELEAELEEMK
TLPQPHSPLGSPFLMPGVEGPDSPSPKGAHLPAHARSASHFSLHPTMOPHPTF
LPSPDLTVRKSGVSRTHSLPNDSPCRHGSTABGPIGHKRWGLPKAOSGSVLSVHSQ
PADTSYIQLPKDAPHILQPHSAPTWGTIPKLPPGRSPLQORPLRQAAIRDTSDLV
OGLGSRBDLLAEVSGSPPLARAYSFWGSSTQAQOHSRSHSKISKMTPPAPCGE
PMWGKGPETRRSLELDTELISGLDLPGQEBPPSPDLKCYSVEAQSCORPT
SWLDEQRHSHIAVSCLDSDSQPHLGTDPNSNLGGQPLGGPGSRPKKLSPPSITIDPE
SQGRTPSPSGICLRRRAPSSSDSKDPLASGPPDSMAASPCKKDVLSLSGLSDPADL
DP"

ORIGIN

Alignment Scores:			
Pred. No.:	0	Length:	7349
Score:	11741.00	Matches:	2241
Percent Similarity:	98.64%	Conservative:	1
Best Local Similarity:	98.59%	Mismatches:	1
Query Match:	98.63%	Indels:	30
DB:	9	Gaps:	2
US-09-611-257A-37 (1-2266) x AF190860 (1-7349)			
QY	1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20	
DB	217 ATGACGACGAGAGAGATGAGCGCGCGCCGAGAGATCGGACACGCCCGAGCTTCATG	276	
QY	21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp	40	
DB	277 CGGCTCAACGACCTGTCCGGGCGCGGGGCGCGCCGGGCGGGGTCCAGCAGAAAGAC	336	
QY	41 ProGlySerAlaAspSerGlyAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60	
DB	337 CCGGACGCGCGACTCCGAGCGGAGGGGCTGCCGTACCCGCGGCTGGCCCCGGTGT	396	
QY	61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80	
DB	397 TTCTTCTACTTGAGCCAGACAGACGCCGCCGAGAGCTGTGTCTCCGACGGTCTTAAC	456	
QY	81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100	
DB	457 CCATGTTTGAGCGCATCAGCATGTGTGATCTTCTCACTGCGTGAACCTGGCATG	516	
QY	101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120	
DB	517 TTCGGCCATGCGAGACATCGCTGTGACTCCACGCGCTGCCGATCCTGACGGCTTT	576	
QY	121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140	
DB	577 GATGACTTCATCTTGCTTCTTGTGCGGTGAGATGTTGTAAGATGTGGCTTGCGC	636	
QY	141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal	160	
DB	637 ATCTTGGGAAAAAGTTTACTCTGGAGACACTTGGAACCGGCTTGACTTTTCATCGTC	696	
QY	161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180	
DB	697 ATGACGAGATGTGAGTACTCGCTGACCTGCAGAACGTCAGACTTCTCAGCTGTACG	756	
QY	181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200	
DB	757 ACAGTCCGTGTGCGACCGCTCAGGCCATTAAACCGGTGCCACGATGCGCATCTT	816	
QY	201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220	
DB	817 GTCAAGTGTGCTGATACGCTGCCCATGCTGGCAACGCTCTGCTTCTTCTTC	876	
QY	221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg	240	
DB	877 GTCTTCTTCACTTCGGCATCGTCGGCTCCAGCTGTGGCGCAGGCTGCTTCCGAACCGA	936	
QY	241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260	
DB	937 TGCTTCTTACCTGGAATTTCAAGCTTCCCTCCAGCGTGGACTGGAGCGCTATTACAG	996	
QY	261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280	
DB	997 ACAGAGACGAGATGAGACCCCTTCACTGCTCCACGCAACGAGACGCGATGCGG	1056	
QY	281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300	
DB	1057 TCCTGACAGAGCGTCCACGCTGCGGGGGAACGGGGCGGTGGCCACCTTGCGGTCTG	1116	
QY	301 AspTyrGluAlaTyrAsnSerSerSerAsnThrCysValAsnTyrAsnGlnTyrTyr	320	
DB	1117 GACTATGAGGCTTACACAGCTCCAGCAACACCACTGTGTCACTGGAACCACTACTAC	1176	

QY	321	ThrAsnCySSerAlaGlyGluHisAsnProPheIysGlyAlaIleAsnPhaSpAsnIle	340
Db	1177	ACCAACTGCTCAGCGGGGAGACAACCCCTTCAAGGGCGCCATCAACTTTGACAACATT	1236
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
Db	1237	GGCTATGCCTGATCGCATCTTCCAGGTATCAGCGTGAAGGGCTGGGTGCACATCATG	1296
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPhaIleTyrPheIleLeuIleIle	380
Db	1297	TACTTTGTGATGATGCTCATTTCTTACAAATTTCACTTCACTCCTCTCATCATC	1356
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
Db	1357	GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGAATTGCCAGCAGTTCTCAGAG	1416
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1417	ACCAAGCAGCGGGAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTTCTGTCTCCAACGCC	1476
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440
Db	1477	AGCAACCTGGCTAGCTTCTTGAGCCCGGCAGCTGCTATGAGGAGCTGCTCAAGTAACTG	1536
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVal	460
Db	1537	GTGTACATCCTTGTAGGAGACCCGCAGGCTGGCTCAGTCTTCTCGGCAGCAGTGTG	1596
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
Db	1597	CGGGTTGGGCTGCTCAGCAGCCACACCCCTCGGGGGGCAGAGACCAGCCACGAC	1656
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
Db	1657	AGCTGCTCTCGCTCCACCGCCGCTATCCGTCCACCACTGGTGCACCACCAACCAC	1716
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1717	CATCACCACTACTACCTGGGCAATGGACGCTCAGGGCCCCCGGGCCAGCCCGGAG	1776
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
Db	1777	ATCCAGGACAGGATGCCAATGGGTCCCGCGGCTCATGCTGCCACCACCTCGACGCTT	1836
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
Db	1837	GCCCTCTCCGGGCCCCCTGTGGCGCAGAGTGTGACACAGCTTACCATGCCGAC	1896
QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Db	1897	TGCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCTCCACAGTCCCATCTGAGGATCC	1956
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu	600
Db	1957	GGCAGGACTGTGGGCAAGGAGGTATATCCACCGTGACACCAAGCCCTCCACCGGAG	2016
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	2017	ACGCTGAAGAGAGAGGCACTAGTAGAGGTGCTGCCAGCTTGTGGCCCCCAACCTTCACC	2076
QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer	640
Db	2077	AGCCTCAACATCCACCCGGGCTTACAGCTCCATGCAACAAGCTGTGAGACACAGAGT	2136
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
Db	2137	ACAGGTGCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGA	2196
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680
Db	2197	GCCTGTGTCCAGACAGCTGCCCTTACTGTGCCCGGGCCGGGGCAGGGGAGGTGAGCTC	2256

QY	681	AlaaspArgGluMetProaspSeraspSergluAlaValTyrGluPheThrGlnaspAla	700
Db	2257	GCCGACCGGTGAATGCTCTACTCAGACGAGGAGGAGTTATGATTCACACAGGATGCC	2316
QY	701	GlnHisSeraspLeuArgaspProHisSerArgGlnArgSerLeuGlyProaspAla	720
Db	2317	CAGCACAGCGAAGCTCCGGGAGCCCAAGCCGAGCGCAACGAGAGCTGGGGCCAGATGCA	2376
QY	721	GluProSerSerValLeuAlaPheTrpArgLeuIleCysaspThrPheArgLysIleVal	740
Db	2377	GAGCCAGAGCTGTGTCTGGCCTTCTGGAGGCTAATCTGTGACACACTTCGAAAGATTGTG	2436
QY	741	AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760
Db	2437	GACAGCAAGTACTTTGGCCGGGGAATCATGATCCGCATCCTGTCAACACACTCAGCATG	2496
QY	761	GlyIleGlyTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle	780
Db	2497	GGCATCGAATACCAAGACAGAGCCGAGAGCTTACCAAGCCCTAGAAATCAGCAACATC	2556
QY	781	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe	800
Db	2557	GTCCTTACCAGCCTCTTTGCCCTGGAGATGCTGTGAAGCTGCTTGTTATGTGTCCTTT	2616
QY	801	GlyTyrIleLysAsnProTyrAsnIlePheaspGlyValIleValValIleSerValTrp	820
Db	2617	GGCTACATCAAGAATCCCTACAAACATCTTCATGTGATGTCATTTGATCATCAGCGTGG	2676
QY	821	GluIleValGlyGlnGlnGlyGlyLysLeuSerValLeuArgThrPheArgLeuMetArg	840
Db	2677	GAGATCGTGGGCCAGCAGGGGGCGGCTGTGCGTCTGCGAGCCTTCGCGCTGATGCGT	2736
QY	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
Db	2737	GTGCTGAAGCTGTGTGCGCTTCTGCGCGGCTGCAGCGGAGCTGTGTGCTCATGAAG	2796
QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer	880
Db	2797	ACCATGGACAACGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTTCAGC	2856
QY	881	IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgaspGlyAspThrLeu	900
Db	2857	ATCCTGGGCATGCATCTCTTGGCTGTGCAAGTTTGCTCTGAGCGGAGTGGGACACCCCTG	2916
QY	901	ProAspArgLysAsnPheaspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920
Db	2917	CCAGACCGGAAGAAATTTGACTCCTTGTCTGTGGCCATCGTCACGTGCTTTTCAGATCCTG	2976
QY	921	ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla	940
Db	2977	ACCCAGAGAGACTGGAAACAAGTCCCTTCAATAGTATGGCCTCCACGTCGTCTGGGCG	3036
QY	941	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal	960
Db	3037	GCCCTTATTTCAATGCCCCCTCATGACCTTCGCAACTACGTGCTCTTCAATTGCTGTGC	3096
QY	961	AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly	980
Db	3097	GCCATTCTGTGGAGGGCTTCCAGGCGGAG-----	3126
QY	981	GlnLeuSerCysIleGlnLeuProValaspSerglnGlyLysAspAlaAsnLysSerglu	1000
Db	3127	-----GGAGATGCCAACAAAGTCCGAA	3147
QY	1001	SerGluProaspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu	1020
Db	3148	TCAGAGCCCGAATTTCTCTCACCCAGCCTGATGTGATGGGACAGAGAAGTGTCTTG	3207
QY	1021	AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle	1040
Db	3208	GCCTTGGTGTCTTGGGAGAGACCCGAGCTGCGGAAGAGCCTGTGCGCGCTTCATC	3267
QY	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu	1060

|||||
Db 3268 ATCCACAGCGCCGCCACACCATGTGCTGCCAAGACACCAAGCGGCTGGCGAG 3327
QY 1061 A1aleuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
|||||
Db 3328 GCGCTGGGCCCTGCGTGGCGCCGACCAAGACGAGGGGTGCGCAAGCCTGGGGCGGCC 3387
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
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Db 3388 CACGAGATGAAGTCAACGCCGCCACGCGCCGACGCTTCCGCACAGCCCCCTGAGCGCTGCA 3447
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
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Db 3448 AGCAGCTGACCAAGCGCTCCAGCCGGAAAGCTCGGCCGTGCAACCCAGCCTGAAG 3507
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140
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Db 3508 CGGAGAAGCCCAAGTGGAGAGCGGCGGTCCCTGTGTGCGGAGAAGGCCAGAGAGCCAG 3567
QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
|||||
Db 3568 GATGAAGAGAGAGAGCTCAGAAGAGAGAGCGGGCAGCCCTGCGGAGATGACCATCGCCAC 3627
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
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Db 3628 AGGGGGTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCCAGACACACTGCAGGTG 3687
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
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Db 3688 CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTGAGACCAAGACTGCAAT 3747
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
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Db 3748 GGCAGAGTCGGCTTCAGGGGCGCTGGCCCGGGCCCTGGCGCTGATGACCCCTGATGAT 3807
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
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Db 3808 GGGGATGACGCGATGACGAGGGCAACCTGAGCAAGGGAACGGGTCCGCGCTGATC 3867
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
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Db 3868 CGAGCCCGACTCCCTGCTGCTGCTGCAGCGAGACTCCTGTGACGCTACATCTTCCCT 3927
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
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Db 3928 CTTCAAGTCCAGGTTCCGCTCTGTGTCAACCGGATCATCAACCAACAAGATGTTGCACCAC 3987
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
|||||
Db 3988 GTGGTCTTGTATCATCTTCTTAAGTGCATCAACCATGAGCGCCCAAAATT 4047
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
|||||
Db 4048 GACCCCAACAGCGCTGAACGATCTTCTGACCCCTCCCAATTACATCTTCAACCGCAGTC 4107
QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340
|||||
Db 4108 TTTCTGGCTGAATGACAGTGAAGTGTGTGCGACCTGGCTGTGCTTCGGGGAAGAGCGG 4167
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
|||||
Db 4168 TACCTGCGGAGCAGTTGGAACGTGCTGGAACGGGCTGTGCTCATCTCCGTCATCGAC 4227
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
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Db 4228 ATTCTGGTGTCCATGTTCTTGACAGCGGCAACCAAGATCTTGCGCATGTGAGGGTCTG 4287
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
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Db 4288 CGGCTGTGCGGACCCCTGCGCCGCTCAGGGTGATCAGCCGGGCGCAGGGGCTGAAGCTG 4347
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420
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Db 4348 GTGTGAGAGCGCTGATGTCTCTCACTGAACCCCATCGGCAACATTTGATCATCTGCTGT 4407
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
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Db 4408 GCCTTCTTCATATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAGGAAGTTTTCGTG 4467
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
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Db 4468 TGCCAGGGCGAGGATACCAAGAACATCACCAATAATCCGACTGTGCCAGGGCCACTTAC 4527
QY 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
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Db 4528 CGGTGGTCCGCAACAAGTACCACTTGACCAACCTTGCCAGGCCCTGATGTCCCTGTTT 4587
QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
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Db 4588 GTTTTGCCCTCCAAGATGTTGGGTGACATCATGTACGATGGGCTGATGCTGGGC 4647
QY 1501 ValAspGlnGluProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
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Db 4648 GTGAGCACAGACCCCATCATGAACCAACCCCTGATGCTGTACTTCATCTCGTTTC 4707
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
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Db 4708 CTGCTCATTTGGCCTTCTTGTCTGTAACATGTTGTGGGTGTGTGTGAGAACTTC 4767
QY 1541 HisLysCysArgGlnHisGlnGluGluGluValAlaArgArgArgGluLysArgLeu 1560
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Db 4768 CACAAGTTCGGAGCACACAGAGAGAGAGAGCCCGCGCGGAGAGAGAGCCCTTA 4827
QY 1561 ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys 1573
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Db 4828 CGAAGACTGAGAAAAGAGAGAGTAAGAGAGACAGATGGCTGAAGCCAGTGCATAA 4887
QY 1574 ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHis 1593
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Db 4888 CTTACTACTCGAATACTCCCGCTTCGGCTCCTGTCACCACTTGTCACCAAGCAC 4947
QY 1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu 1613
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Db 4948 TACCTGACCTTTCATCACAGGTGTATCGGGCTGAACGTGTCAACATGGCCATGGAG 5007
QY 1614 HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr 1633
|||||
Db 5008 CACTACAGACAGCCCAAGATTCTGATGAGGCTCTGAAGATCTGCAACTACATCTTCACT 5067
QY 1634 ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe 1653
|||||
Db 5068 GTCATCTTGTCTTGAAGTCAAGTTTCAAACTTGTGCGCTTGGTTCCGTCGTTCTTC 5127
QY 1654 GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr 1673
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Db 5128 CAGGACAGGTGAACCAAGCTGGAACCTGATGTGCTGTCCATCATGGCATCAAG 5187
QY 1674 LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693
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Db 5188 CTGAGGAATCGAGTCAACGCCCTGCTGCCCATCAACCCCATCATCGCATCAAG 5247
QY 1694 ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla 1713
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Db 5248 AGGGTCTGCGCATTTGCCAGTGTCAAGCTGCTGAAGATGGCTGTGGCATGCGGGCG 5307
QY 1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733
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Db 5308 CTGCTGACACAGGTGATGACAGCCCTGCCCCAAGGTGGGAACCTGGGACTTCTCTTCAAT 5367
QY 1734 LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp 1753
|||||
Db 5368 TTGTTGTTTTCATCTTTCAGCTCTGGGCTGTGAGCTCTTGGAGAAGCTGAGTGTGAC 5427
QY 1754 GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla 1773
|||||
Db 5428 GAGACACACCCCTGTGAGGGGCTGGGCGTGCATGCCACCTTTCGAACTTTGGCATGGCC 5487

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MTPPAPCPGPBPNWKGKPPETRSLELDTBLSWISGDLBPGQOEBPSPRDLKCYK
VEAQSCQRPTSMLEQRRHSIAVSCUDSGOPHLGTDPSNLGGQPLGGPGSPRKXKL
SPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKODPLASGPPDSMAASPPKXKDVLS
LSGLSSDPADLDP"

ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 6786
Score: 11735.50 Matches: 2241
Percent Similarity: 98.16% Conservative: 1
Best Local Similarity: 98.12% Mismatches: 1
Query Match: 98.58% Indels: 41
DB: 9 Gaps: 2

US-09-611-257a-37 (1-2266) x AF227747 (1-6786)

QY	1	MetAspGluGluuAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet	20
DB	1	ATGGACGAGGAGGATGGAGCGGGCCGAGAGTCCGGACAGCCCCCGAGACTTCATG	60
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp	40
DB	61	CGGCTCAACGACCTGTCGGGGGCCGGGGGCCGGGGCCGGGTCAGCAGAAAAAGGAC	120
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
DB	121	CCGGGACGCGCGGACTCCGAGCGGAGGGCTGCCGTACCCGGCGCTGGCCCGTGTT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80
DB	181	TTCTTCTACTTGAGCCAGACAGCCGCCCGGAGCTGTGTCTCCGACGGTCTGTAAC	240
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	241	CCCTGTGTTGAGCGGCATCAGCATGTTGTCATCTTCTCAACTGCGTGACCTGGGCATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	301	TTCCGGCATGCGAGACATCGCTGTGACTCCAGCGCTGCCGATCTTGCAAGCCCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140

DB	361	GATGACTTCATCTTGTCCCTTCTTGGCCGTGGAGATGTGTGAAGATGTGGCTTGGGC	420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
DB	421	ATCTTTGGGAAAAAGTGTACTCGGAGACACTTGGAACCGGCTTGACTTTTCATCGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	481	ATCGCAGGATGCTGAGTACTCGGTGACCTGCAGAACGTCAAGCTTCTCAGCTGTCAAG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	541	ACAGTCCGTGCTGCGACCCGCTCAGGGCCATTACCGGGTGCCACGATGCGCATCCTT	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	601	GTCACGTTGCTGCTGATACGCTGCCCATGCTGGGCAACGTCCTGCTGCTTCTTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
DB	661	GTCTTCTTCACTTTCGGCATCGTCGGCGTCCAGCTGTGGCAGGGCTGCTTGGAAACGA	720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
DB	721	TGCTTCTTCACTGAGATTTACAGCTCCCTGAGCGTGACCTGAGCGCTATTACCAAG	780
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
DB	781	ACAGAGAACGAGATGAGAGCCCCCTTCATCTGCTCCACGCCACGAGAACGCGCATGGG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
DB	841	TCCTGCAGAAAGCTGCCACGCTGCCGGGGACGGGGCGGTGGCCCACTTGGGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
DB	901	GACTATGAGGCTTCAACACAGCTCCAGCAACACCACTGTGTCAACTGGAACCAATCTAC	960
QY	321	ThrAsnCysSerAlaGlyLysHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
DB	961	ACCAACTGCTCAGCGGGGAGACAAACCTTCAAGGGCGCCATCAACTTGACAAACATT	1020
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
DB	1021	GGCTATGCTGATCGCCATCTTCCAGTTCATCAGCTGAGGGCTGGTGCATCATATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
DB	1081	TACTTGTGATGATGCTCATTTCTTCAATTTCATCTTCACTTCCTCCTCATCATC	1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
DB	1141	GTCGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGATGCCACGAGTTCTCAGAG	1200
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
DB	1201	ACCAAGCAGCGGAAAGCCAGCTGATGGGGAGACAGCGTGCCTGTCCTCAACGCC	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440
DB	1261	AGCAACCTGGCTAGCTTCTGTGAGCCCGGAGCTGTATGAGAGCTGTCAAGTACCTG	1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
DB	1321	GTTGATCATCTTGTGAAGCAGCCCGCAGCTGGCTCAGGTCCTCGGGCAGCAGCTGTG	1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
DB	1381	CGGGTTGGCTGCTCAGCAGCCACGACCCCTCGGGGGCCAGAGAACCCAGCCAGCAGC	1440
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500

Db 1441 AGCTGCTTCGCTCCACCGCGCCTATCCGTCCACCACTGGTGACACCAACCAACAC 1500
QY 501 HISHISHISTYRHisleuGlyVaNGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1501 CATCACCACTACCACTCGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCGGAG 1560
QY 521 ILeuAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1561 ATCCAGGACAGGATGCCAATGGGTCCCGCGGCTCATGTGTGCCACCACTCGAGCCT 1620
QY 541 AlaLeuSerGlyAlaProProGlyAlaGluSerValHisSerPheTyRHisAlaasp 560
Db 1621 GCCCTCTCCGGGGCCCCCCTGGTGGCGCAGACTCTGTGCACAGCTTTACCAATGCCGAC 1680
QY 561 CysHisleuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1681 TGCCACTTAGAGCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTGAGGCAATCC 1740
QY 581 GlyArgThrValGlySerGlyLysValTyRProThrValHisThrSerProProGlu 600
Db 1741 GGCAGAGACTGTGGCAGCGGGAAGGTATCCCAACCGTGACACAGCCCTCCACCGGAG 1800
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1801 ACGCTGAAGAGAGAAGCACTAGTAGAGTGGCTGCCAGCTCTGGGCCCCCAACCTCAC 1860
QY 621 SerLeuAsnIleProProGlyProTyRSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 1861 AGCCTCAACATCCACCCGGGGCCCTACAGCTCCATGCACACAGCTGTCGAGACACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysleuLysAlaAspSerGly 660
Db 1921 ACAGGTGCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGA 1980
QY 661 AlaCysGlyProAspSerCysProTyRCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 1981 GCCTGTGTCCAGACAGCTGCCCTTACTGTGCCCCGGGCGGCGGAGGTGAGCTC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyRGluphetrGlnAspAla 700
Db 2041 GCCGACCGTGAATGCCCTGACTCAGACAGCAGGAGTTTATGAGTTACACAGAGATGCC 2100
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2101 CAGCACAGCGAACCCTCCGGGACCCCAAGCCGGCGCAACGAGCCTGGGCCCAAGTGCA 2160
QY 721 GluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2161 GAGCCCAAGCTCTGTGCTGGCCTTCTGGAGGCTAATCTGTGCACCTTCCGAAAGATTGTG 2220
QY 741 AspSerLysTyRPhGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2221 GACAGCAAGTACTTTGGCCGGGGAATCATGATGCCATCTGTGTCACACACTCAGCATG 2280
QY 761 GlyIleGluTyRHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2281 GGCATCGAATACACGAGCAGCCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2340
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyRGlYProPhe 800
Db 2341 GTCTTCACCAAGCCTTTGGCCCTGGAGATGCTGTGAAGCTGCTGTGATGTCCCTTT 2400
QY 801 GlyTyRILELysAsnProTyRAsnIlePheAspGlyValIleValIleValIleSerValTrp 820
Db 2401 GGCTACATCAAGATCCCTACACACATCTTCGATGTGTGTCATGTGTCATCAGCGTGTGG 2460
QY 821 GluIleValGlyGlnGlnGlyGlyLysLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2461 GAGATCGTGGGCGCAGAGGGGGGGCGGCTGTGCTGCTGCGGACCTTCCGCTGATGCGT 2520
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 2521 GTGCTGAAGCTGTGTGCGCTTCTGCGCGGCTGCAGCGGCACTGTGTGTGCTCATGAAG 2580

QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 2581 ACCATGACACAACGTGGCCACTTCTGCATGTCTGCTTATGCTCTTCATCTTCATCTCAGC 2640
QY 881 ILeuGluMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 2641 ATCTGGGCATGATCTTTCGGCTGCAGATTGGCTCTGAGCGGAGATGGGACACCTTG 2700
QY 901 ProAspArgLysAsnPhAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 2701 CCAGACCGGAAGAAATTGACTCCTTGCTGGGCATGCTCACTGTCTTTCAGATCCTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyRAsnGlyMetAlaSerThrSerSerTrpAla 940
Db 2761 ACCCAGAGAGACTGGAACAAGTCTCTACAATGGTATGGCCTCCAGCTGTCTCGGCG 2820
QY 941 AlaLeuTyRPhIleAlaLeuMetThrPheGlyAsnTyRValLeuPheAsnLeuVal 960
Db 2821 GCCCTTATTTCATTTGCCCTCATGACCTTCGGCACTACGTGCTCTTCATTTGCTGTC 2880
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
Db 2881 GCCATTCTGTGAGGGCTTCCAGGCGAG----- 2910
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyLysAspAlaAsnLysSerGlu 1000
Db 2911 -----GGAGATGCCCAACAAGTCCGAA 2931
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 2932 TCAGAGCCCGATTCTTCTCACCCAGCCTGATGTGATGGGACAGAGAAGATGCTTG 2991
QY 1021 AlaLeuValSerLeuGlyGlnHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040
Db 2992 GCCTGTGTCCCTGGGAGAGCACCCGAGCTGCGGAAGACCTGCTGCCCTCTCATC 3051
QY 1041 ILeHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyL 1060
Db 3052 ATCCACAGCGCGCCACACCATGTGCTGCCAAGACACACAGCAGCGGCTGGGGCGAG 3111
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3112 GCGCTGGGCCCTGCTGCTCGCGCCGCACACAGCAGCGGGTGGCAGAGCCTGGGGCGGC 3171
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3172 CACGAGATGAAGTCAACGCCCAAGCGCCGAGCTCTCCGACAGCCCCCTGGAGCGCTGCA 3231
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3232 AGCAGCTGCACACAGAGCGCTCCAGCCGGAACAGCTCGGCCGTGACCCAGCCTGAAG 3291
QY 1121 ArgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140
Db 3292 CGGAGAGCCCAAGTAGAGAGCGGCGGTCCCTGTGTGCGGAGAAAGGCCAGAGAGCCAG 3351
QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3352 GATGAAGAGAGAGAGCTCAGAGAGAGAGCGGCGCAGCCCTGCGGCACTGACGCCAC 3411
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3412 AGGGGTCCCTGGAGCGGAGGCCCAAGATTCTTTGACCTGCGACAGACACTCAGAGTG 3471
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3472 CCAGGCTGCATCGCACTGCAGTGGCCGAGGGTCTCTTGAGCACCAAGACTGCAAT 3531
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
Db 3532 GGCAAGTCGGCTTCAAGGGCGCTGGCCCGGCGCTGCGGCTGATGATGACCCCACTGAT 3591

QY	1221	GI	Asp	Asp	Ala	Asp	Asp	Glu	Gly	Asn	Leu	Ser	Leu	Ser	Gly	Leu	Arg	Val	Arg	Ala	Trp	Ile	1240
Db	3592	GGG	ATG	ACG	CCG	ATG	ACG	AGG	CAAC	CTG	AGC	AAAG	GGG	AAAC	GGG	TCC	CGC	CGT	GAT	C			3651
QY	1241	Arg	Ala	Arg	Leu	Pro	Ala	Cys	Tyr	Leu	Glu	Arg	Asp	Ser	Trp	Ser	Ala	Tyr	Ile	Phe	Pro	1260	
Db	3652	CGA	GGCC	CACT	CCCT	GGCT	GTG	CTG	CCCT	CGA	CGA	AGCT	CTCT	GTG	TAC	AGCT	TACT	CTT	CCCT			3711	
QY	1261	Pro	Gln	Ser	Arg	Phe	Arg	Leu	Leu	Cys	His	Arg	Ile	Ile	Thr	His	Sly	Met	Phe	Asp	His	1280	
Db	3712	CCT	CAG	TCC	AGT	TCG	CGCT	CTCT	GTG	TCA	CCG	ATC	ATC	ACC	CA	AGAT	GTTC	GA	CCAC			3771	
QY	1281	Val	Val	Leu	Val	Ile	Ile	Phe	Leu	Asn	Cys	Ile	Thr	Ile	Ala	Met	Glu	Arg	Pro	Sly	Ile	1300	
Db	3772	GTG	TCT	CTT	GTC	ATC	TCT	CTT	AACT	GAT	CA	TCC	ATG	AGCG	CCCC	AA	ATT					3831	
QY	1301	Asp	Pro	His	Ser	Ala	Glu	Arg	Ile	Phe	Leu	Thr	Leu	Ser	Asn	Tyr	Ile	Phe	Thr	Ala	Val	1320	
Db	3832	GAC	CCCC	CA	AGC	CGT	GA	CGC	ATCT	TCT	CGA	CCCT	CTC	CA	ATT	TAC	ATCT	TCA	CGC	AGTC		3891	
QY	1321	Phe	Leu	Ala	Glu	Met	Thr	Val	Val	Syl	Val	Val	Ala	Leu	Gly	Trp	Cys	Phe	Gly	Glu	Ala	1340	
Db	3892	TTT	CTG	CTG	AAAT	GAC	GTG	AAAG	TGT	GTG	CACT	GGCT	GTG	CTT	CCG	GGG	AGC	AGCG				3951	
QY	1341	Tyr	Leu	Arg	Ser	Ser	Trp	Asn	Val	Leu	Asp	Gly	Leu	Leu	Val	Ile	Ser	Val	Ile	Asp		1360	
Db	3952	TAC	CTG	CGA	GAC	GTG	GAA	CGT	GTG	TGA	CGG	GTG	TGT	GCT	CACT	CCG	TCA	TGAC				4011	
QY	1361	Ile	Leu	Val	Ser	Met	Val	Ser	Asp	Ser	Gly	Thr	Leu	Ile	Leu	Gly	Met	Leu	Arg	Val	Leu	1380	
Db	4012	ATT	CTG	TGT	CTC	ATG	CTCT	GAC	AGC	GGC	AC	CAAG	ATC	CTG	GGC	ATG	CTG	AGG	TGT			4071	
QY	1381	Arg	Leu	Leu	Arg	Thr	Leu	Arg	Pro	Leu	Arg	Val	Ile	Ser	Arg	Ala	Gln	Gly	Leu	Syl	Leu	1400	
Db	4072	CGG	CTG	CTG	CGA	CCCT	GTG	CGCC	CGCT	CAG	GGT	GAT	CA	CGG	GGC	CGC	AGG	GGCT	GA	AGCT		4131	
QY	1401	Val	Val	Glu	Thr	Leu	Met	Ser	Ser	Ser	Leu	Syl	Pro	Ile	Gly	Asn	Ile	Val	Val	Ile	Cys	Cys	1420
Db	4132	GTG	TG	GAG	ACG	CTG	ATG	TCT	CACT	GA	AA	CCCAT	CGG	CAAC	ATT	GAT	CACT	GTG	CTGT			4191	
QY	1421	Ala	Phe	Phe	Ile	Ile	Phe	Gly	Ile	Leu	Gly	Val	Gln	Leu	Phe	Syl	Gly	Syl	Phe	Phe	Val	1440	
Db	4192	GCCT	TCT	TCA	TAT	TTT	CGG	CATCTT	GGG	GTG	CA	GCTCTT	CAA	AGG	AA	GTTT	TCGTG					4251	
QY	1441	Cys	Gln	Gly	Val	Asp	Thr	Arg	Asn	Ile	Thr	Asn	Syl	Ser	Asp	Cys	Ala	Glu	Ala	Ser	Tyr	1460	
Db	4252	TGC	CAG	GGC	GAG	GAT	ACCA	GGA	CATC	ACCA	ATA	ATC	GGA	CTGT	GCC	AGG	CC	AGTTAC				4311	
QY	1461	Arg	Trp	Val	Arg	His	Syl	Tyr	Asn	Phe	Asp	Asn	Leu	Gly	Gln	Ala	Leu	Met	Ser	Leu	Phe	1480	
Db	4312	CGG	TGG	GTCC	GGCA	CAAG	TAC	ACTTT	GAC	AACTT	GGC	CA	GGCC	CTG	ATG	TCT	CGTTTC					4371	
QY	1481	Val	Leu	Ala	Ser	Syl																	

Db	4672	TCAGCCAGCGCTGCGTCAGAAGCCAGTGCAACTTACTACTCCGACTACTCCGCTTC	4731
QY	1583	ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1602
Db	4732	CGGCTCCTCGTCCACCACCTTGTGCACCCAGCACTACCTGGACCTTTCATCAGAGTGC	4791
QY	1603	IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp	1622
Db	4792	ATCGGCTGAACGTGGTCACCATGGCCATGGAGACACTACCAGACGCCAGATTCTGGAT	4851
QY	1623	GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe	1642
Db	4852	GAGGCTCTGAAGATCTGCAACTACATCTTCATCTTGTCTTGAGTCAGTTTTC	4911
QY	1643	LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeu	1662
Db	4912	AAACTGTGGCTTTGGTTTCCGTCGGTTCCTCCAGACAGGTGGAACCACTGGACCTG	4971
QY	1663	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer	1682
Db	4972	GCCATTGTGCTGTCTGCATCATGGGCATCAGCCTGGAGAAATCGAGGTCACGCTTCG	5031
QY	1683	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1702
Db	5032	CTGCCCATCAACCCACCACCATCATCCGCATCATAGAGGGTGTGCGCATTGCCCGAGTCTG	5091
QY	1703	LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu	1722
Db	5092	AAGCTGTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGGACACGGTATGCAGGCCCTG	5151
QY	1723	ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu	1742
Db	5152	CCCCAGGTGGGAACCTGGGACTTCTTCATGTTGTGTTTTCATCTTGGACCTCTG	5211
QY	1743	GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly	1762
Db	5212	GGCGTGAGCTCTTGGAAGACCTGAGTGTGACGAGACACACCCTGTGAGGGCCTGGGC	5271
QY	1763	ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr	1782
Db	5272	CGTCATGCCACCTTTCGGAACCTTGGCATGGCCTTCCTAACCTCTTCCGAGTCTCCACA	5331
QY	1783	GlyAspAsnTyrAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr	1802
Db	5332	GGTGACAATTGGAATGGCAATTATGAAGACACCCCTCCGGACTGTGACCAGAGTCCACC	5391
QY	1803	CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe	1822
Db	5392	TGCTACAACACCGGTCACTCGCCTATCTACTTGTGTCTTCGTGCTGACGGCCCAATTTC	5451
QY	1823	ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu	1842
Db	5452	GTGCTAGTCAACGTGTGATCGCCGTGCTGATGAAGCACTGGAGAGAGCAACAGGAG	5511
QY	1843	AlaLysGluGluAlaGluLeuGluAlaGluLeuGluGluMetLysThrLeuSerPro	1862
Db	5512	GCCAAGAGAGAGCGCGAGCTAGAGCTGAGCTGAGATGAAGACCTCAGCCCC	5571
QY	1863	GlnProHisSerProLeuGlySerProPheLeuTyrProGlyValGluGlyProAspSer	1882
Db	5572	CAGCCCCACTCGCCACTGGGCAGCCCCCTTCTGTGGCTGGGGTCGAGGGCCCCGACAGC	5631
QY	1883	ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis	1902
Db	5632	CCCGACAGCCCCAAGCTTGGGGCTCTGCAACCCAGCGGCCCAACCGAGATCAGCCTCCAC	5691
QY	1903	PheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyProAspLeu	1922
Db	5692	TTTTCCCTGAGACCCCAAGATGACAGCCCAACCCCAAGAGCTGCAGGACCAAGATTTA	5751
QY	1923	LeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMet	1942

Db 5752 CTGACTGTCCGGAAGTCTGGGGTCAGCCGAAAGCACTCTCTGCCAATGACAGCTACATG 5811

Qy 1943 CysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLys 1962

Db 5812 TGTCGGCATGGGAGCACTGCCGAGGGGCCCTGGGACACAGGGGCTGGGGGCTCCCAAA 5871

Qy 1963 AlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeu 1982

Db 5872 GCTCAGTCAGGCTCCGCTTGTTCGTTCACTCCAGCCAGCAGATACAGCTACATCTTG 5931

Qy 1983 GlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThr 2002

Db 5932 CAGCTTCCCAAGATGCACCTCATCTGCTCCAGCCCCCAGCGCCCAACCTGGGGCACC 5991

Qy 2003 IleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGln 2022

Db 5992 ATCCCAAACTGCCCCCAAGAGAGCGCTCCCTTGGCTCAGAGGCCACTCAGGCGCCAG 6051

Qy 2023 AlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeu 2042

Db 6052 GCAGCAATAAGAACTGACTCCTTGACGTTCAAGGCTCTGGGCAGCCGGAAAGACTGCTG 6111

Qy 2043 AlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSer 2062

Db 6112 GCAGAGGTGATGGGGCCCTCCCGCCCTGGCCCTTCTTGCGGCGCAGTCA 6171

Qy 2063 SerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetThrPro 2082

Db 6172 AGTACCCAGGCAAGACAGCACTCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCG 6231

Qy 2083 ProAlaProCysProGlyProGlyProGlnProAsnTrpGlyLysGlyProProGluTrpArgSer 2102

Db 6232 CCAGCCCCCTTGCCCAAGGCCAGAACCAACTGGGGCAAGGGCCCTCCAGAGACCAGAAAGC 6291

Qy 2103 SerLeuGlnLeuAspThrGlnLeuSerTrpIleSerGlyAspLeuLeuProProGlyGly 2122

Db 6292 AGCTTAGATTGACACGAGAGCTGAGTTCGATTTCAGAGACCTTCTGCCCTTGCGGCGGC 6351

Qy 2123 GlnGluGlnProProSerProArgAspLeuLysLysCysTyrSerValGluAlaGlnSer 2142

Db 6352 CAGAGAGAGCCCCCATCCCAAGGACCTGAAGAAGTGTACAGCGTGAGGCCAGAGAGC 6411

Qy 2143 CysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaValSer 2162

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Qy 2163 CysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGlyGln 2182

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Db 6772 GACCTGACCC 6783

RESULT 13

AF227746

LOCUS AF227746 6897 bp mRNA linear PRI 06-MAR-2000

DEFINITION Homo sapiens voltage-dependent calcium channel alpha 1G subunit

ACCESSION AF227746

VERSION AF227746.1 GI:7159264

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 6897)

AUTHORS Montell,A., Chemin,J., Bourinet,E., Mennessier,G., Lory,P. and Nargeot,J.

TITLE Molecular and functional properties of the human alpha(1G) subunit that forms T-type calcium channels

JOURNAL J. Biol. Chem. 275 (9), 6090-6100 (2000)

MEDLINE 20158909

PUBMED 10692398

REFERENCE 2 (bases 1 to 6897)

AUTHORS Montell,A., Mennessier,G., Bourinet,E., Lory,P. and Nargeot,J.

TITLE Direct Submission

JOURNAL Submitted (21-JAN-2000) C.N.R.S., Human Genetics Institute (I.G.H.) U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France

FEATURES

source

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QY	1754	GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
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QY	1966	GlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPro	1985
Db	5992	GGCTCCGCTTGTTCCTTCACTCCACGACGACATACCACTACATCCTGCAGCTTCCC	6051
QY	1986	LysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLys	2005
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QY	2006	LeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIle	2025
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QY	2026	ArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluVal	2045
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QY	2046	SerGlyProSerProProLeuAlaArgAlaTyrSerPheThrGlyGlnSerSerThrGln	2065

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Qy	2206	GluSerGlnGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaPro	2225
Db	6712	GAGAGCCAGGTCTCGGACCCCGCCAGCCCTGTATCTGCCTCCGAGAGAGGCTCCG	6771
Qy	2226	SerSerAspSerLysAspProLeuAlaSerGlyProProAspSerMetAlaIleSerPro	2245
Db	6772	TCCAGCGACTCCAAGGATCCCTTGCCCTCTGCCCCCTGACACGATGGCTGCTGCC	6831
Qy	2246	SerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAsp	2265
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RESULT 14			
LOCUS	AF227748	6921 bp	mRNA linear PRI 06-MAR-2000
DEFINITION	Homo sapiens voltage-dependent calcium channel alpha 1g subunit		
ACCESSION	AF227748		
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KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 6921)		
TITLE	Monteil,A., Chemin,J., Bourinet,E., Mennesier,G., Lory,P. and Nargeot,J.		
JOURNAL	Molecular and functional properties of the human alpha(1g) subunit		
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FEATURES	U.P.R. 1142, 141 rue de la Cardonille, Montpellier 34396, France		
	Location/Qualifiers		

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QY 1583 ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602
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complete cds.
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VERSION AF134985.1 GI:6625656
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 7030)
AUTHORS Miltman,S., Guo,J. and Agnew,W.S.
TITLE Structure and alternative splicing of the gene encoding alpha1g, a
human brain T calcium channel alpha1 subunit
JOURNAL Neurosci. Lett. 274 (3), 143-146 (1999)
MEDLINE 20014446
PUBMED 10548410
REFERENCE 2 (bases 1 to 7030)
AUTHORS Miltman,S., Guo,J. and Agnew,W.S.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-1999) Anesthesiology/Critical Care Medicine, The
Johns Hopkins University School of Medicine, 600 N. Wolfe Street,
Meyer 297, Baltimore, MD 21287-7294, USA
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ORIGIN

Alignment Scores:

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Db	3592	GGGATGACCGCCGATGACGAGGGCACTGAGCAAAAGGGAA	CGGGTCCGCGCTGGATC	3651
QY	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro	1260	
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PR 26-OCT-1999; 99US-00426998.
XX
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XX
PI Dubin AE, Galindo JE, Pyati J, Zhu JY, Erlander MG;
XX
DR WPI; 2001-300486/31.
DR P-PSDB; AAE01019.
XX
XX
PT New nucleic acid encoding human calcium channel protein, useful for
PT identifying specific modulators and potential pharmaceuticals for
PT treating e.g. epilepsy.
XX
XX
PS Claim 2; Page 76-81; 115pp; English.
XX
XX The invention relates to isoform of human T-type low voltage activated
CC calcium channel (alphaG-c) cDNA and protein. Cells transformed with
CC calcium channel DNA to express calcium alphaG-c channel protein are used
CC to identify specific modulators (antagonists or agonists). These
CC modulators are useful as therapeutic agents and are used for treating
CC wide range of calcium alphaG-c channel-mediated disorders, e.g. stress
CC epilepsy, schizophrenia, depression, sleep disorders, Cushing's disease,
CC endocrine disorders, respiratory disorder, peripheral muscle disorder,
CC muscle excitability, fertilisation, contraception, disorders involving
CC hypertension, neuronal firing regulation, potentiation of synaptic
CC signals and cardiovascular disorders (e.g. atherosclerosis, cardiac
CC hypertrophy, angina pectoris). Calcium alphaG-c channel DNA is useful
CC for isolating and identifying related molecule mutations. It is also
CC optionally used as antisense sequences, in gene therapy. Calcium channel
CC alphaG-c DNA, protein and antibodies are useful for forensic analysis,
CC diagnosis and epidemiological studies, by standard hybridisation or
CC immunological assays. The present sequence is T-type low voltage
CC activated calcium channel alphaG-c cDNA. This sequence is isolated from
CC human thalamus cDNA library
XX
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QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
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QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
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QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
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Db	2623	CAGCACAGCAGCCTCCGGGACCCCAAGCCGGCGCAACGAGACCTGGGCCCAAGATGCA	2682
QY	721	GluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIleVal	740
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Qy	1001	SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu	1020
Db	3523	TCAGAGCCCGATTCTTCTCACCCAGCCTGGATGGTATGGGACAGAAAGAGTCTTG	3582
Qy	1021	AlaLeuValSerLeuGlyIuHisProGluLeuArgLysSerLeuLeuProIleuIle	1040
Db	3583	GCCTTGTGTCTCTGGAGAGCACCTCGAGCTGCGGAAGACCTGCTGCGCTCTCATC	3642
Qy	1041	IleHisThrAlaIaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu	1060
Db	3643	ATCCACACGGCGCCACACCCATGTGCTGCCCAAGAGCACACAGCAGGGCTTGGGCGAG	3702
Qy	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla	1080
Db	3703	GCGCTGGGCGCTGCGTCCGCCGCGCACAGCAGACGGGTCGGCAGAGCCTGGGGCGCC	3762
Qy	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSerAlaAla	1100
Db	3763	CACGAGATGAAGTCAACGCCAGCGCTCCAGCTCTCCGACACAGCCCTGGAGCGCTGCA	3822
Qy	1101	SerSerTyrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120
Db	3823	AGCAGCTGGACACAGCGCGCTCCAGCCGGAACAGCTTGGCCGTGCACCCAGCCTGAAG	3882
Qy	1121	ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnSerGln	1140
Db	3883	CGAGAAGCCCAAGTGGAGAGCGGGTCCCTGTTGCGGAGAAAGGCCAGAGACCCAG	3942
Qy	1141	AspGluGluGlnSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis	1160
Db	3943	GATGAAGAGAGAGCTCAGAAAGAGACGGGCCAGCCCTTGGGGCAGTGACCATTCGCCAC	4002
Qy	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180

Db	4003	AGGGGGTCCCTGGAGCGGGAGGCCAAGAGTTCCTTTGACCTGCCAGACACACTGCAGGTG	4062
QY	1181	PROGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
Db	4063	CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGGTCTGCTTGAGCACCAGCACTGCAAT	4122
QY	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	4123	GGCAAGTCGGCTTCAGGGCGCCTGGCCCGGGCCCTGCGGCTGATGACCCCACTGGAT	4182
QY	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTyrPhe	1240
Db	4183	GGGATGACGCCGATGACGAGGGCAACCTGAGCAAGGGAAAGGGTCCGCGCTGATC	4242
QY	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrPhePro	1260
Db	4243	CGAGCCCGACTCCCTGCTGCTGCTGCCGAGAGACTCCTGTGTCAGCTACATCTCCCT	4302
QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
Db	4303	CCTCAGTCCAGGTTCCGCCCTCTGTGTCACCGGATCATCACCACAAGATGTTGCACCAC	4362
QY	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
Db	4363	GTGGTCTTGTCATCATCTTCTTAACCTGCATCACCATGCCATGAGCGCCCCAAATT	4422
QY	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320
Db	4423	GACCCCCACAGCGCTGAACGATCTTCCTGACCCCTTCCAAATTACATCTTACCGCAGTC	4482
QY	1321	PheLeuAlaGluMetThrValLysValAlaAlaLeuGlyTrpCysPheGlyGlnAla	1340
Db	4483	TTTCTGGCTGAATGACAGTGAAGTGGTGGCAGCTGGCTGTGCTTCGGGGAGCAGCG	4542
QY	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp	1360
Db	4543	TACCTCGGAGCAGTGTGAACGTGCTGACGCGGCTGTGTCTCATCTCCGTATCGAC	4602
QY	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
Db	4603	ATTCTGTGTCCATGGTCTCTGACAGCGGCAACCAAGATCTGGGCATGCTGAGGGTCTG	4662
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerAlaGlnGlyLeuLysLeu	1400
Db	4663	CGGCTGCTGCGGACCCTGGCGCCGCTCAGGGTGATGACCGGGCGCAGGGCTGAAGCTG	4722
QY	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420
Db	4723	GTGGTGAGACGCTGATGTCTCACTGAACCCATCGCAACATTGTAGTCATCTGTGT	4782
QY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnPheLysGlyLysPhePheVal	1440
Db	4783	GCCTTCTTCATCATTTTGGGCATCTTGGGGTGACGCTTCAAAGGGAAGTTTTCGTG	4842
QY	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
Db	4843	TGCCAGGGCGAGATACCAAGAACATCACCAATAATCGACTGTGCCGAGGCCAGTTAC	4902
QY	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
Db	4903	CGGTGGGTCCGGCACAAGTACACTTTGACAACTTTGGCCAGGCCCTGATGTCTCTTTC	4962
QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4963	GTTTGGCCTCCAAGATGGTTGGGTGACATCATGATGGGTGGATGCTGTGGGC	5022
QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	5023	GTGACACAGCAGCCCATCATGAACACCAACCCCTGGATGTCTGTACTTCATCTGTTTC	5082
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe	1540

Db	5083	CTGCTCATTTGTGGCCCTTCTTTTGTCTTGAACATGTTTGTGGGTGTGGTGGAGAACTTC	5142
Qy	1541	HisLysCysArgGlnHisGlnGluGluGluValaArgArgArgGluLysArgLeu	1560
Db	5143	CACAAGTGTGGCAGCACACAGAGAGAAGAGGCCCGGGCGGAGAGAAGCGCTTA	5202
Qy	1561	ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys	1573
Db	5203	CGAAGACTGAGAAAAAGAGAGAGTAAGAGAGACAGATGGCTGAAGCCAGTGCAA	5262
Qy	1574	ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHis	1593
Db	5263	CCTTACTACTCCGACTACTCCCGCTCCGGCTCCTGTCACCACTTGTGACCAAGCCAC	5322
Qy	1594	TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrmAlaMetGlu	1613
Db	5323	TACCTGACCTCTTCATCACAGGTGTCAATCGGGCTGAACGTGTCACCATGGCCATGGAG	5382
Qy	1614	HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr	1633
Db	5383	CACCTACGACAGCCCCAGATTCTGATGAGGCTCTGAAGATCTGCACTACATCTTCACT	5442
Qy	1634	ValIlePheValLeuGluSerValaPheLysLeuValAlaPheGlyPheArgArgPhePhe	1653
Db	5443	GTCATCTTTGTTCTTGAGTCAATTCAAACTTGTGGCTTTGTTCCTCGTTCCTTC	5502
Qy	1654	GlnAspArgTTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	5503	CAGACAGGTGGAACCAAGCTGAGCCTGGCCATTGTGCTGCTGCCATCATGAGCATCAAG	5562
Qy	1674	LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
Db	5563	CTGGAGGAATCGAGGTCAACGCCCTCGCTGCCCATCAACCCACCATCATCCGCATCATG	5622
Qy	1694	ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla	1713
Db	5623	AGGGTCTGCCCATTTGCCCGAGTCTGAAGCTGTGAAGATGCTGTGGCATGCGGGCG	5682
Qy	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
Db	5683	CTGCTGACACGGTGATGACAGCCCTTGCCCCAGGTGGGAACCTGGGACTTCTCTTCATG	5742
Qy	1734	LeuLeuPhePheIlePheAlaAlaLeuGlyValaGluLeuPheGlyAspLeuGluCysAsp	1753
Db	5743	TTGTTGTTTTCATCTTTGACGCTGTGGCGCTGGAGCTCTTGAAGACCTGGAGTGTGAC	5802
Qy	1754	GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
Db	5803	GAGACACACCCCTGTGAGGCGCTGGCGCTCATGCCACCTTCGAACTTTGGCATGGCC	5862
Qy	1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr	1793
Db	5863	TTCTTAACCTCTTCCGAGTCTCCACAGGTGACAAATTGGAATGCATTATGAAGACACC	5922
Qy	1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
Db	5923	CTCCGGAGCTGTGACCAAGAGTCCACTGCTACACACCGGTCACTCGCCTATCTACTTT	5982
Qy	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
Db	5983	GTTGCTTCTGTGCTGACGGCCAGTTCTGTCTAGTCAACGTGTGATCGCCGTGTGATG	6042
Qy	1834	LysHisLeuGluGluSerAsnLysGluAlaLysGluGluValaGluLeuGluValaGluLeu	1853
Db	6043	AAGCACCTGAGAGAGACAACAGAGAGGCCAAGAGAGAGCGGAGCTAGAGGCTGAGCTG	6102
Qy	1854	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873
Db	6103	GAGCTGAGATGAAGACCTTCAGCCCCAGCCCACTCGCACTGGGACAGCCCTTCCTC	6162
Qy	1874	TyrProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro	1893
Db	6163	TGGCCTGGGGTTCAGGGCCCCCGACAGCCCCCGACAGCCCCCAAGCCTGGGGCTCTGCACCA	6222

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Db 171 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGATCCGGCGCTGGCCCCGGTGTT 230
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 231 TTCTTCTACTTGAGCCAGACAGACCGCCCGGAGCTGGTGTCTCCGACGGTCTGTAAAC 290
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 291 CCCTGGTTGAGCGCATCAGCATGTGGTCATCCTTCTCACTGCGTAGACCTGGGGCATG 350
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 351 TTCGGCCATGCGAGGACATCGCCTGTGACTCCGAGCGCTGCCGATCCTGCAGGCCCTTT 410
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 411 GATGACTTCACTTTGCTTTCCTTTCCTTTCGCGTAGAGATGGTGTGAAGATGGTGCCCTTGGGC 470
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 471 ATCTTTGGAAAAAGTTACTGTGGAGACACTTGGAAACGGGCTTGACTTTTTCATCGTC 530
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 531 ATGCAGAGGATGTGTGAGTACTCGCTGAGACCTGCAGAACGTCAGCTTCTCAGCTGTCAAG 590
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 591 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCCCAGCATGCGCATCCTT 650
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 651 GTCACTGTGCTGCTGATACGCTGCCCATGCTGGCAACGTCCCTGCTGCTCGCTTCTTC 710
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 711 GTCTTCTTCACTTTCGGCATCGTCGGCGCTCCAGCTGTGGGCGAGGGCTGCTTCGGAACCGA 770
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 771 TGCTTCTTACTGAGAATTTCAGCCTCCCTGAGCGTGAACCTGAGCGCTATTAACAG 830
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 831 ACAGAGAACGAGATGAGAGCCCTTCACTGCTCCAGCCACGCGAAGCGGCAATGCGG 890
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 891 TCCTGCAGAGCGTCCCCACGCTGGCGGGGAGCGGGGGGTGGCCCCACTTGGCGTCTG 950
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 951 GACTATGAGGCTTACAACAGCTCCAGCAACACCCTGTGTCACTGGAACCACTACTAC 1010
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
Db 1011 ACCAACTGCTCAGCGGGGAGCACAAACCTTCAAGGGCCCATCAACTTGAACAACATT 1070
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
Db 1071 GGGTATGCTGGATCGCCATCTTCCAGGTCAACGCTGAGGGGCTGGGTGCACATCATG 1130
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
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QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
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QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
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Db 1251 ACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTTCCTGCCAACGCC 1310
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluLeuLeuLysTyrLeu 440
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QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
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QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1431 CGGGTTGGCGCTCTCAGCAGCCCCACACACCCCTCGGGGGCCAGAGACCCACGACAGC 1490
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHis 500
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QY 501 HisHisHisIstYrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
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QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1611 ATCCAGGACAGGATGCCATGGGTCCCGCAGGCTCATGCTGCCACCAACCTCGAGCGCT 1670
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1671 GCGCTTCCGGGGGCCCCCTGCTGGCGCAGAGTCTGTGCACAGCTTCAACATGCCGAC 1730
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1731 TGCCACTTGAAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCACTGTAGGCATCC 1790
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
Db 1791 GGCAGACTGTGGCAGCGGGAAGGTGTATCCACCGTGACACACAGCCCTCCACCGGAG 1850
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
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QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
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QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 1971 ACAGGTGCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGA 2030
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2031 GCGTGTGCTCAGACAGCTGCCCTTACTGTGCCGGGCGGGGCAAGGGAGGTGAGCTC 2090
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2091 GCCGACCTGAATGCTGACTCAGACAGCGAGGCAAGTTATGAGTTACACAGAGATGCC 2150
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2151 CAGCAGACGACCTCCGGGACCCCAACAGCCGGCGCAACGAGCCTGGGCCACAGATGCA 2210
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
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QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2271 GACAGCAAGTACTTTGGCGGGGAATCATGATCGCCATCTGTGTCACACACTCAGCATG 2330
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluLysSerAsnIle 780
Db 2331 GGCATCGAATTAACACGAGCAGCCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACATC 2390
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QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800
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Db 2391 GTCTTCACCAGCCTCTTGGCCCTGGAGATGCTGGAAGCTGCTTGATGTGCCCTTT 2450
QY 801 GLYTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820
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Db 2451 GGCTACATCAAGAATCCCTACAACATCTTCGATGTGTCAATGTGTGCATCAGCGTGTGG 2510
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
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Db 2511 GAGATCGTGGGCCAGCAGGGGGGGCGGCTGTGCTGCTGCGGACCTTCCGCTGATGCCGT 2570
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
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Db 2571 GTGCTGAAGCTGTGTCGCTTCTGCGCGCTGCAGCGGCAGCTGTGTGCTCATGAAG 2630
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer 880
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Db 2631 ACCATGGACAACGTGGCCACTTCTGCATGCTGCTTATGCTCTTCACTTCATCTTCAGC 2690
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
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Db 2691 ATCTTGGGCATGCATCTCTTCGGCTGCAGATTGCTCTGAGCGGAGTGGGACACCCCTG 2750
QY 901 ProAspArgLysAsnPheAsnSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
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Db 2751 CCAGACCGGAAGATTGTACTCTTCTGCTGTGGGCCATCGTCACTGTCTTTCAGATCCTG 2810
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
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Db 2811 ACCCAGAGAGACTGGACAAGTCCCTTACAAATGTAATGGCCCTCCACGTCGTCCTGGCG 2870
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVal 960
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Db 2871 GCCCTTATTTCATGTGCCCTCATGACCTTGGCAACTACGTGCTCTTCAATTTGCTGTGTC 2930
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
| | | | |
Db 2931 GCCATTCTGTGTGAGGGCTTCCAGCGGAGGAATCAGCAACGCGAAGATGCCAGTGA 2990
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu 1000
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Db 2991 CAGTTAAGCTGTATTCACTGCTGCTGCACTCCAGGGGGGAGATGCCACAAGTCCGAA 3050
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
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Db 3051 TCAGAGCCCGATTCTTCTCAACCAGCCTGATGTGATGGGACAGAGAAGATGCTTG 3110
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
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Db 3111 GCCTTGGTGTCCCTGGGAGAGCAACCGAGCTGGGAAGAAGCCTGCTGCCCTCATC 3170
QY 1041 IleHisThrAlaAlaThrPrometSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
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Db 3171 ATCCACACGGCCGCCACCATGTCTGCTGCCAAGACACACGCGCCTGGGCGAG 3230
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
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Db 3231 GCGCTGGGCCCTGCGCTGCGCGCCAGCACAGCAGCGGGTCCGCCAGAGCCTGGGGCGGCC 3290
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
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QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
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Db 3351 AGCAGCTGGACACGAGCGCGCTCCAGCCGGAACAGCCTCGGCCGTGACCCAGCCTGAAG 3410
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnSerGln 1140
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QY 1141 AspGluGluLysSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
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Db 3471 GATGAAGAGAGAGCTCAGAAAGAGAGCGGGCCAGCCCTGCGGGCAGTACCATTCGCCAC 3530
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
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QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
| | | | |
Db 3591 CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACACGAGACTGCAT 3650
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
| | | | |
Db 3651 CGCAAGTCGGCTTCAGGGCGCGCTGGCCCGGGCCCTGCGGCTGATGACCCCACTGGAT 3710
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
| | | | |
Db 3711 GGGGATGACGCCGATGACGAGGGCACTGAGCAAAAGGGAAACGGGTCCGCGCTGCATC 3770
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
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Db 3771 CGAGCCCGACTCCCTGCTGCTGTAACCTCGAGCGAGACTCCTGTGTCAACCTACATCTCCCT 3830
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
| | | | |
Db 3831 CCTCAGTCCAGGTTCCGCTCCTGTGTCAACGGATCATCACCAAGATGTTCCAGCCAG 3890
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
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Db 3891 GTGTCCTTGTCATCATCTTCTTAACTGCATCACCATCGCCATGGAAGCGCCCAAAATT 3950
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
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Db 3951 GACCCCCACAGCGCTGAAGCATCTTCTGACCCCTCCCAATTACATCTTCACCGCAGTTC 4010
QY 1321 PheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340
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Db 4011 TTTCTGGCTGAATAGACAGTGAAGTGTGGCACTGGCTGTGTGCTTCGGGAGCAGCGCG 4070
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
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Db 4071 TACCTGGAGAGCAGTTGGAACGTGCTGGAACGGGCTGTGTGCTCATCTCCGTCATCGAC 4130
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
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Db 4131 ATTCTGTGTCCATGTCTCTGACAGCGGCACCAAGATCTGGGCATGCTGAGGGTGTG 4190
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
| | | | |
Db 4191 CGGCTGCTGCGAACCTGCGCCGCTCAGGGTGATCAGCGGGCGCAAGGCTGAAGCTG 4250
QY 1401 ValValGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
| | | | |
Db 4251 GTGCTGAGACGCTGATGTCTCTCACTGAACCCATCGGCAACTTGTAGTCATCTGCTGT 4310
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
| | | | |
Db 4311 GCCTTCTTCATCATTTTCGCATCTTGGGGGTGCAGCTCTTCAAAAGGGAAGTTTTCGTG 4370
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
| | | | |
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| | | | |
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QY 1481 ValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
| | | | |
Db 4491 GTTTTGGCTCCAAAGATGTTGGTGGAATCATGATGAGATGGGCTGATGCTGTGGCC 4550
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520

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Db 4551 GTGACCAGACCCCATCATGAACCAACCCCTGGATGCTGTACTTTCATCTCGTTCC 4610
QY 1521 LeuLeuIleValAlaPhePheValIleuAsnMetPheValGlyValValValGluAsnPhe 1540
Db 4611 CTGCTCATTTGGCCCTTCTTTGTCTTGAACATGTTGTGGGTGTGGTGGAGAACTTCC 4670
QY 1541 HisLysCysArgGlnHisGlnGluGluGluValAargArgArgGluGluLysArgLeu 1560
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QY 1561 ArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580
Db 4731 CGAAGACTGGAGAAAAAGAGAGAAAGCCCACTGCAACCTTACTCCGACTACTCC 4790
QY 1581 ArgPheArgLeuLeuValHisHisIleuCysThrSerHisTyrIleuAspLeuPheIleThr 1600
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QY 1601 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620
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QY 1641 ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1660
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QY 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700
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QY 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720
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QY 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1740
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QY 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760
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QY 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800
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QY 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluLysSerAsn 1840
Db 5511 CAGTTCGTGCTAGTCAACGTGTGATCGCCGTGCTGATGAAGACACTGGAGAGAGAAC 5570
QY 1841 LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeu 1860
Db 5571 AAGGAGGCCAAGAGAGAGCGCCGAGCTAGAGGCTGAGCTGGAGCTGAAGACCTTC 5630
QY 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880
|||||

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QY 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900
Db 5691 GACAGCCCCGACAGCCCCCAAGCTGGGGCTGTGCACCCAGCGGCCCAAGATCAGCC 5750
QY 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyPro 1920
Db 5751 TCCCACTTTTCCCTGGAGACCCACGATGCAGCCCAACCGAGAGCTGCAGAGACCA 5810
QY 1921 AspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSer 1940
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QY 1941 TyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTrpGlyLeu 1960
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QY 2001 GlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArg 2020
Db 6051 GGCACCATCCCAAACTGCCCAACCAAGAGCGCTCCCTTGGCTCAGAGGCCACTCAGG 6110
QY 2021 ArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp 2040
Db 6111 CGCCAGCAGCAATTAAGACTGACTCTTGGACGTTCAAGGCTGGGCACCGGGAAGAC 6170
QY 2041 LeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGly 2060
Db 6171 CTGCTGCGAGAGGTGAGTGGGCCCTCCCGGCCCTGGCCCGGCTTACTTCTTGGGGC 6230
QY 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2080
Db 6231 CAGTCAAGTACCCAGGACAGACGACACTCCCGAGCCACAGCAAGATCTCCAAGCACATG 6290
QY 2081 ThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThr 2100
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QY 2101 ArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProPro 2120
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QY 2121 GlyGlyGlnGluGluProProSerProArgAspLeuLysLysCysTyrSerValGluAla 2140
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QY 2141 GlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAla 2160
Db 6471 CAGAGCTGCAGCGCGGCTTACGTCTGCTGGATGAGCAGAGAGAGACACTTATCGCC 6530
QY 2161 ValSerCysLeuAspSerGlySerGlnProHisIleGlyThrAspProSerAsnLeuGly 2180
Db 6531 GTCAGCTGCCTGGACAGCGGCTCCCAACCCCACTGGGGCACAGACCCCTTAACCTTGGG 6590
QY 2181 GlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIle 2200
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QY 2201 ThrIleAspProProGluSerGlnGlyProArgThrProProSerProGlyIleCysLeu 2220
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QY 2221 ArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSer 2240
Db 6711 CGAGAGAGGGCTCCGTCCAGGACTCCAAGGATCCTTGGCCTTGGCCCCCTGACAGC 6770
|||||

QY 2241 MetAlaIaIaSerProSerProLySLyAspValIeuSerIeuSerGlyIeuSerSerAsp 2260
 |||
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 QY 2261 ProAlaAspIeuAspPro 2266
 |||
 Db 6831 CCAGCAGACCTGACCCC 6848
 RESULT 3
 ID ADQ89063 standard; cDNA; 7648 BP.
 XX ADQ89063;
 AC
 XX 21-OCT-2004 (first entry)
 DT
 XX Human urological disorder related protein 4421 encoding cDNA SEQ:15.
 DE
 XX urological disorder; uropathic; cytostatic; urinary incontinence;
 KM benign prostatic hyperplasia; human; gene; ss.
 KW
 XX Homo sapiens.
 OS
 XX
 XX
 XX
 FT Key Location/Qualifiers
 FT CDS 1..7134
 FT /*tag= a
 FT /product= "urological disorder related protein 4421"
 FT
 PN WO2004065576-A2.
 XX
 PD 05-AUG-2004.
 PF 14-JAN-2004; 2004WO-US000750.
 XX
 PR 15-JAN-2003; 2003US-0440318P.
 PR 04-FEB-2003; 2003US-0444783P.
 PR 27-MAR-2003; 2003US-0457901P.
 PR 08-MAY-2003; 2003US-0468775P.
 PR 19-MAY-2003; 2003US-0471614P.
 PR 16-JUN-2003; 2003US-0478742P.
 PR 18-JUL-2003; 2003US-0488529P.
 PR 30-JUL-2003; 2003US-0491156P.
 PR 02-SEP-2003; 2003US-0499594P.
 PR 26-SEP-2003; 2003US-0506332P.
 PR
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PI
 PI Karicheh V, Silos-Santiago I, Eliasof SD;
 XX
 DR WPI; 2004-562167/54.
 DR P-PSDB; ADQ89064.
 XX
 PT Use of polypeptides related to urological disorders, e.g. 44390, 54181,
 PT 211 or for identifying a compound capable of treating a urological
 PT disorder or identifying and treating a subject having a urological
 PT disorder.
 XX
 PS Claim 1; SEQ ID NO 15; 542pp; English.
 XX
 CC The present invention describes the use of polypeptides related to
 CC urological disorders for identifying a compound capable of treating a
 CC urological disorder, identifying a subject having a urological disorder,
 CC or treating a subject having a urological disorder. Also described: (1) a
 CC method for identifying a compound capable of treating a urological
 CC disorder; (2) a method for identifying a subject having a urological
 CC disorder; and (3) a method for treating a subject having a urological
 CC disorder. The compound has uropathic and cytostatic activities. The
 CC polypeptides related to urological disorders are useful for identifying a
 CC compound capable of treating a urological disorder, identifying a subject
 CC having a urological disorder, or treating a subject having a urological
 CC disorder. Disorders include urinary incontinence and benign prostatic
 CC hyperplasia. The present sequence encodes a human urological disorder

CC	related protein, which is used in the exemplification of the present invention.	XX	Sequence	7648 BP, 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;
Alignment Scores:				
Pred. No.:	0	Length:	7648	
Score:	11815.50	Matches:	2264	
Percent Similarity:	95.29%	Conservative:	1	
Best Local Similarity:	95.25%	Mismatches:	1	
Query Match:	99.26%	Indels:	111	
DB:	13	Gaps:	2	
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QY	1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20		
Db	1 ATGACGAGAGAGAGATGAGCGGGCCCGAGAGATCGGACAGCCCCGAGCTTCATG	60		
QY	21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp	40		
Db	61 CGGCTCAACGACCTGTCCGGGGCCGGGGCCGGCCGGGGCCGGGTACAGAAAAAGAC	120		
QY	41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60		
Db	121 CCGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTGCCCCGGTGT	180		
QY	61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80		
Db	181 TTCTTCTACTTGAGCCAGACAGACCGCCCGGAGCTGGTGTCTCCGACCGGTCTTAAC	240		
QY	81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100		
Db	241 CCCTGTTTGAGCGCATCAGCATGTTGTATCTTCTCACTGCTGACCTGGGCATG	300		
QY	101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120		
Db	301 TTCGGCCATGCGAGACATCGCCTGTGACTCCAGCGGCTGCCGATCCTGACGGCTTT	360		
QY	121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140		
Db	361 GATGACTTCATCTTGTGCTTCTTGTCCGTGAGATGTGTGGAAGATGTGGCCTTGGGC	420		
QY	141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal	160		
Db	421 ATCTTTGGAAAAAGTTTACTTGAGAGACACTTGGAAACGGCTTGACTTTTTCATGTC	480		
QY	161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180		
Db	481 ATCGCAGGAGATGCTGAGTACTCGCTGGACCTGCAGAAACGTCACTTCTCAGCTGTACG	540		
QY	181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200		
Db	541 ACAGTCCGTGTGCTGCGACCGCTCAAGGCCATTAAACGGGTGCCACGATGCGCATCTT	600		
QY	201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220		
Db	601 GTCAAGTTGTGCTGATACGCTGCCATGCTGAGCAACGTCCTGCTCTGCTTCTTC	660		
QY	221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg	240		
Db	661 GTCTTCTTCATCTTCCGACATCGTGGCGTCCAGCTGTGGCGAGGGCTGTTCGAAACGA	720		
QY	241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260		
Db	721 TGCTTCTTACTGAGAAATTTCAGCCTTCCCTTGAGCGTGAAGCTGAAGCGCTATTACAG	780		
QY	261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280		
Db	781 ACAGAGAACGAGATGAGAGCCCTTTCATCTGCTCCAGCCACGCGAGAACGGCATGCGG	840		
QY	281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300		

Db 841 TCCTGAGAAAGCGTGCCCAAGCTGCGGGGAGCGGGGGGTGGCCACCTTGCGGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerSeraThrCysValAsnTrpAsnGlnTyrTyr 320
Db 901 GACTATGAGGCTACACAGAGCTCCAGCAACACCACTGTGTCACTGGAACCACTACTAC 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheIysGlyAlaIleAsnPheAspAsnIle 340
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QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
Db 1021 GGCTATGCTGGATCGCCATCTTCCAGGTCAACGCTGAGAGGGCTGGTGCACATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle 380
Db 1081 TACTTTGTATGATGCTCATCTCCTTCACAATTTCATCTACTTCACTCCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValIleAlaThrGlnPheSerGlu 400
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QY 401 ThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
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QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrTyrGluGluLeuIysTyrLeu 440
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QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1321 GTGTACATCTTCTGTAAGGAGAGCCCGAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1381 CGGGTTGGGCTGCTCAGCAGCCAGCCACCTCGGGGCCAGAGACCAGCCAGCCAGCAGC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1441 AGCTGCTCGCTCCACCGCGCGCTATCCGTCCACCACTGTGTGACCAACCAACCAAC 1500
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1501 CATCACCACTACCACTGCGGCAATGGGAGCGTCAAGGGCCCCCGGGCCAGCCCGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 1561 ATCCAGGACAGGAGATGCCAATGGGTCCCGCAGGCTCATGTCTCCACCACTTCGACGCT 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1621 GCCCTCTCCGGGCCCCCCTGTGGGAGAGTGTGTGACAGCTTCTTACCATGCGAGC 1680
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1681 TGCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCATCTGAGGCATCC 1740
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
Db 1741 GGCAGGACTGTGGGAGCGGGAAGGTATCCCAACCGTGACACACAGCCCTCCACCGAG 1800
QY 601 ThrLeuIysGlyLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1801 ACGCTGAAGAGAGGCACTAGTAGAGGTGGCTGCCAGCTGTGGGCCCCCAACCTTCACC 1860
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 1861 AGCCTCAACATCCACC CGGGCTTACAGCTCATGACAAAGCTGTGAGACACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 1921 ACAGGTGCTGCAAAAGCTCTTGCAAGATCTCCAGCCCTTGTGAAAGCAGACAGAGTGA 1980

QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
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QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2041 GCCGACGTGAATGCTGAGACTCAGACAGCAGGAGGAGTTATAGATTCAACAGAGATGCC 2100
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2101 CAGCACAGCAGCTCCGGGACCCCAACAGCCGGCGCAACGAGCCTGGGCCAGATGCA 2160
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2161 GAGCCAGCTCTGTGCTGGCCTTCTGAGGCTAATCTGTGACACACCTTCCGAAAGATTGTG 2220
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QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
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QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
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QY	1021	AlaLeuValSerLeuGIyGluHisProGluLeuArgLysSerLeuProProLeuIle	1040
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QY	1041	IleHisThrAlaAlaThrPrometSerLeuProLysSerThrSerThrGlyLeuGIyGlu	1060
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QY	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla	1080
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QY	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTTPSerAlaAla	1100
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QY	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGIyArgAlaProSerLeuLys	1120
Db	3301	AGCAGCTGGACCGACGAGCGGCTCCAGCCGGAACAGCTCGGCCGTGACACCGAGCTGAAG	3360
QY	1121	ArgArgSerProSerGIyGluArgArgSerLeuLeuSerGlyGlyGluGlnSerGln	1140
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QY	1141	AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis	1160
Db	3421	GATGAAGAGAGAGACTCAGAAGAGAGCGGCGGACCTCGGGCAGTGACCATCGCCAC	3480
QY	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3481	AGGGGGTCCCTGGAGCGGGAGGCCAAGAGTTCCTTGACCTGCCAGACACATCGAGGTG	3540
QY	1181	ProGlyLeuHisArgThrAlaSerGIyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
Db	3541	CCAGGGCTGCATCGACTGCTCCAGTGCCGAGGGCTTGCTTCTGAGCACCAAGAGCTGCAAT	3600
QY	1201	GlyLysSerAlaSerGIyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	3601	GGCAAGTCGGCTTCAGGGCGCTGGCCCGGGCCCTGGGGCTGTGATGACCCCCACTGGAT	3660
QY	1221	GlyAspAspAlaAspAspGluGIyAsnLeuSerLysGlyGluArgValArgAlaTrrPile	1240
Db	3661	GGGGATGACGCCGATGACGAGGGCAACCTGAGCAAGGGGAACGGTCCGCGGTGATC	3720
QY	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro	1260
Db	3721	CGAGCCCGACTCCCTGCTGCTGCTGCCCTCGAGCGAGACTCTGTGTCAGCCTACATCTTCCCT	3780
QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
Db	3781	CCTCAGTCCAGGTCCGCTCTCTGTGCACCGGATCATCACCAAGATGTTGCACAC	3840
QY	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
Db	3841	GTGTCCTGTGCATCATCTTCCTTAACGTACATCACCAATGCCATGAGCGCCCAAAATT	3900
QY	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal	1320
Db	3901	GACCCCCACAGCGCTGAACGCATCTTCTGACCCCTCTCCAATTACATCTTCAACGCGAGTC	3960
QY	1321	PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla	1340
Db	3961	TTTCTGGCTGAATGACGTGAAGGTGTGGCACTGGGTGTGCTTCCGGGAGCAGCGCG	4020
QY	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp	1360
Db	4021	TACCTGCGGAGCAGTTGGAACGTGTGACGCGGTGTGGTCTCATCTCCGTATCGAC	4080
QY	1361	IleLeuValSerMetValSerAspSerGIyThrLysIleLeuGlyMetLeuArgValLeu	1380
Db	4081	ATTCTGCTGTCCATGCTCTTGACAGCGGCCACCAAGATCTCTGGGCATGTGAGGGTGTG	4140
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGIyLeuLysLeu	1400

Db	4141	CGGCTGCTGCGAACCTGCGCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAGCTG	4200
QY	1401	ValValGluThrLeuMetSerSerLeuIleuysProIleGlyAsnIleValValIleCysCys	1420
Db	4201	GTGGTGGAGACGCTGATGTCTCTCACTGAACCCCATCGGCAACATTTAGTCATCTGCTGT	4260
QY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheIleGlyLysPhePheVal	1440
Db	4261	GCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAGGGAAGTTTTCGTG	4320
QY	1441	CysGlnGlyGlyAspThrArgAsnIleThrAsnLysSerAspCysAlaGlyAlaSerTyr	1460
Db	4321	TGCCAGGGCGAGGATACAGAAACATCACCAATAATCGCACTGTGCGAGGCCAGTTAC	4380
QY	1461	ArgTrpValArgHisIysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
Db	4381	CGGTGGGTCCGGCACAGTACAACTTTGACAACTTGGCCAGGCCCTGATGTCCCTGTTTC	4440
QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4441	GTITTTGGCTCCAAGATGGTTGGGTGACATCATGTACGATGGGCTGCGATGCTGTGGGC	4500
QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	4501	GTGGACCAAGACGCCCATCATGAACCAACCAACCCCTGGATGCTGCTGACTTCATCTCGTTTC	4560
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
Db	4561	CTGCTCATTTGTGGCCCTTCTTGTCTGTAACATGTTGTGGGTGTGGTGTGGAAGAACTTC	4620
QY	1541	HisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeu	1560
Db	4621	CACAACTGTCCGACAGCACCAAGGAAGAGAGGCCCGCGCGGAGGAAGAAGCGCCTA	4680
QY	1561	ArgArgLeuGluLysLysArgArg-----	1568
Db	4681	CGAAGACTGGAGAAAAAGAAAGAAATCTAATGCTGACGATGTAATTGCTTCGGCAGC	4740
QY	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe	1582
Db	4741	TCAGCCAGCGCTGCGTCAAGAACCCAGTGAACAACTTACTCCGACTACTCCCGCTTC	4800
QY	1583	ArgLeuLeuValHisHisIleCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal	1602
Db	4801	CGGCTCTCTGTCACCACTTGTGCAACCAAGCCACTACTGGAACCTTTCATCACAGGTGTC	4860
QY	1603	IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp	1622
Db	4861	ATCGGGCTGAACGTGTGTCAACCATGGCCATGAGACACTAACAGACAGCCCAAGATTCTGGAT	4920
QY	1623	GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe	1642
Db	4921	GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCATCTTGTCTTGGAGTCAAGTTTTC	4980
QY	1643	LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu	1662
Db	4981	AAACTTGTGGCTTGTGGTTTCCGTGCTTCTTCCACAGACAGGTGGAACCAAGCTGGAACCTG	5040
QY	1663	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer	1682
Db	5041	GCCATTGTGCTGTCTTCATCATGGGCATCACGCTGAGGAATAATCGAGTCAACGCCCTCG	5100
QY	1683	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1702
Db	5101	CTGCCCATCAACCCCAACCATCATCGCATCATGAGGTGCTGCGCATTGCCGAGTGTCTG	5160
QY	1703	LysLeuLeuLysMetAlaValAlaGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu	1722
Db	5161	AAAGCTGTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGGAACACGCTGATGACAGGCCCTG	5220
QY	1723	ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu	1742

Db 5221 CCCAGGTGGGGAACCTGGACCTTCTTCATGTTGTTGTTTTCATCTTTGGACCTCTG 5280
QY 1743 G1yValG1uLeuPheG1yAspLeuG1uCysAspG1uThrHisProCysG1uG1yLeuG1y 1762
Db 5281 GGCCTGGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCTGGGC 5340
QY 1763 ArGHisAlaThrPheArGAsnPhG1yMetAlaPheLeuThrLeuPheArGVAlSerThr 1782
Db 5341 CGTCATGCCACCTTTGGAACTTTGGCATGGCCTTCTTAACCTCTTCCGAGTCTCCACA 5400
QY 1783 G1yAspAsnTrpAsnG1yIleMetLysAspThrLeuArGVAspCysAspG1nG1uSerThr 1802
Db 5401 GGTGACAATTGGAATGGCATTATGAAGACACCCCTCGGACTGTGACCAGAGAGTCCACC 5460
QY 1803 CysTrpAsnThrValIleSerProIleTyPheValSerPheValLeuThrAlaG1nPh 1822
Db 5461 TGCTACAACACGGTCATCTCGCCTATCTACTTTGTGTCTTGTGCTGACGGCCAGTTTC 5520
QY 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuG1uG1uSerAsnLysG1u 1842
Db 5521 GTGCTAGTCAAGTGTGATCGCCGTGCTGATGAAGCACTGGAGAGACAAAGAGAG 5580
QY 1843 AlAlysG1uG1uAlaG1uLeuG1uAlaG1uLeuG1uLeuG1uMetLysThrLeuSerPro 1862
Db 5581 GCCAAGAGAGAGCGCCGAGCTAGAGGTGAGCTGGAGCTGAGATGAAGACCCCTCAGCCCC 5640
QY 1863 G1nProHisSerProLeuG1ySerProPheLeuTrpProG1yValG1uG1yProAspSer 1882
Db 5641 CAGCCCACTGGCCACTGGGCAAGCCCTTCTCTGGCCTGGGGTCCAGGGCCCCCAGACAGC 5700
QY 1883 ProAspSerProLysProG1yAlaLeuHisProAlaAlaHisAlaArGVSerAlaSerHis 1902
Db 5701 CCCGACAGCCCCCAAGCCTGGGGCTTGACCCAGCGGCCCAAGCATCAGCCTTCCAC 5760
QY 1903 PheSerLeuG1uHisProThr----- 1909
Db 5761 TTTTCCCTGGACACCCCAAGACAGGACGCTGTTTGACACCATATCCCTGCTGATCCAG 5820
QY 1909 ----- 1909
Db 5821 GGCTCCCTGGAGTGGGAGCTGAAGCTGATGACGAGCTGGCAGGCCAGGGGCCAGCCC 5880
QY 1909 ----- 1909
Db 5881 TCTGCCTTCCCTTCTGCCCCCAGCCTGGGAGGCTCCGACCCACAGATCCCTCTAGCTGAG 5940
QY 1909 ----- 1909
Db 5941 ATGGAGGCTTGTCTCTGACGTACAGAGATTGTGTGAACCGTCTGCTCTAGCTCTG 6000
QY 1909 ----- 1909
Db 6001 ACGGATGACTTTTGCTGATGACATGCACACACTTTACTTAGTGCCCTGGAGACAAT 6060
QY 1910 MetG1nProHisProThrG1uLeuProG1yProAspLeuLeuThrValArGVLSerG1y 1929
Db 6061 ATGCAGCCCCCAACCCACGAGCTGCAGGACGAGACCACTTACTGACTGTGCGGAAGTCTGGG 6120
QY 1930 ValSerArGVThrHisSerLeuProAsnAspSerTyTrMetCysArGVHisG1ySerThrAla 1949
Db 6121 GTCAACCGAAGCACTCTCTGCCCAATGACAGCTACATGTGTCCGCATGGAAGCACTGCC 6180
QY 1950 G1uG1yProLeuG1yHisArGVTyTrpG1yLeuProLysAlaG1nSerG1ySerValLeu 1969
Db 6181 GAGGGGCCCTTGGAACAAGGGGCTGGGGGCTCCCCAAAGTCAAGTCAAGGCTCCGTTTG 6240
QY 1970 SerValHisSerG1nProAlaAspTrpSerTyTrIleLeuG1nLeuProLysAspAlaPro 1989
Db 6241 TCCGTTCACTCCAGCCAGACAGATACAGTACATCTGCACTTCCCAAAGATGACACT 6300
QY 1990 HisLeuLeuG1nProHisSerAlaProThrTrpG1yThrIleProLysLeuProProPro 2009
Db 6301 CATCTGCTCCAGCCCCACAGCGGCCCAACTGGGGCACCACTCCCAAAGTCCCCCACCA 6360

QY 2010 G1yArGVSerProLeuAlaG1nArGVProLeuArGVAlaAlaIleArGVThrAspSer 2029
Db 6361 GGACGCTCCCTTTGGCTTCAGAGGCCACTCAGCGGCCAGGCAAGCAATTAAGACTGACTCC 6420
QY 2030 LeuAspValG1nG1yLeuG1ySerArGVLeuAspLeuLeuAlaG1uValSerG1yProSer 2049
Db 6421 TTGACGTTCAAGGTCTGGGCAAGCCGGGAAGACTGTGCAAGAGGTGAGTGGCCCTCC 6480
QY 2050 ProProLeuAlaArGVAlaTySerPheTrpG1yG1nSerSerThrG1nAlaG1nHis 2069
Db 6481 CCGCCCTGGCCCGGGCTTACTTTCTGGGGCCAGTCAAGTACCAGCACAGCAGCAC 6540
QY 2070 SerArGVSerHisSerLysIleSerLysHisMetThrProProAlaProCysProG1yPro 2089
Db 6541 TCCCGAGCCACAGCAAGATCTCCAAGCACATGACCCCGCAGCCCTTGCCAGGCCCA 6600
QY 2090 G1uProAsnTrpG1yLysG1yProProG1uThrArGVSerSerLeuG1uLeuAspThrG1u 2109
Db 6601 GAACCCAACCTGGGCAAGGGCCCTCCAGAGACCAGAAAGCACTTAGAGTTGGACACGAG 6660
QY 2110 LeuSerTrpIleSerG1yAspLeuLeuProProG1yG1yG1nG1uProProSerPro 2129
Db 6661 CTGAGCTGATTTCAGAGAACCTCTCTGCCCTTGCGGGCCAGAGAGAGCCCATCCCA 6720
QY 2130 ArGVAspLeuLysLysCysTyTrSerValG1uAlaG1nSerCysG1nArGVArGVProThrSer 2149
Db 6721 CGGCACTGAAGAAGTGTACAGCGTGAAGGCCAGAGCTGCCAGCGCGGCTACGTCC 6780
QY 2150 TrpLeuAspG1uG1nArGVArGVHisSerIleAlaValSerCysLeuAspSerG1ySerG1n 2169
Db 6781 TGGCTGATGAGCAGAGAGACACTTATCGCCGTACAGCTGCTGAGACGGCTCCCAA 6840
QY 2170 ProHisLeuG1yThrAspProSerAsnLeuG1yG1nProLeuG1yG1yProG1ySer 2189
Db 6841 CCCCACTGGGCACAGACCCCTTAACCTTGGGGCCAGCCTTGGGGGGCTGGGAGC 6900
QY 2190 ArGVProLysLysLysLeuSerProProSerIleThrIleAspProProG1uSerG1nG1y 2209
Db 6901 CGGCCCAAGAAAACTCAGCCCGCCTAGTATCATCATAGACCCCCCGAGACCAAGT 6960
QY 2210 ProArGVThrProProSerProG1yIleCysLeuArGVArGVAlaProSerSerAspSer 2229
Db 6961 CCTGGACCCCGCCAGCCCTGTATCTGCTCCGAGGAGGGCTCCGTCCAGCACTCC 7020
QY 2230 LysAspProLeuAlaSerG1yProProAspSerMetAlaAlaSerProSerProLysLys 2249
Db 7021 AAGGATCCCTTGCCCTGCCCCCCTGACAGCATGGCTGCTGCCCCCAAGAAA 7080
QY 2250 AspValLeuSerLeuSerG1yLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7081 GATGTGCTGAGTCTCTCGGTTTATCTCTGACCCAGACGACCTGAGACCCC 7131

RESULT 4
ADSL6298
ID ADS16298 standard; DNA; 7648 BP.
XX
AC ADS16298;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human voltage-dependent alpha 1g subunit calcium channel (CACNA1G) DNA.
XX
KW Voltage-dependent ion channel; drug candidate;
KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
KW anticonvulsant; antiarrhythmic; human; alpha 1g subunit; ds.
OS Homo sapiens.
XX
PN US2004175761-A1.
XX
PD 09-SEP-2004.
XX

PF 01-MAR-2003; 2003US-00377139.
XX
PR 01-MAR-2003; 2003US-00377139.
XX
PA (MACK/) MACKINNON R.
PA (MACK/) MACKINNON A L.
PA (JIAN/) JIANG Y.
PA (RUTA/) RUTA V.
XX
PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
XX
DR WPI; 2004-642122/62.
XX REFSEQ; NM_018896.
XX
PT Screening drug candidates that target voltage dependent ion channel
PT protein, involves contacting screening protein with chemical compound,
PT which is drug candidate and determining whether chemical compound binds
PT to screening protein.
XX
PS Disclosure; SEQ ID NO 10; 61pp; English.
XX
CC The invention relates to the composition of matter suitable for use in
CC identifying chemical compounds that bind to voltage-dependent ion channel
CC proteins. The composition comprises a screening protein that consists of
CC an ion channel voltage sensor domain of the ion channel protein
CC immobilised on a solid support. The invention is useful for identifying
CC chemical compounds (drug candidate) that bind to voltage-dependent ion
CC channel proteins. The drug candidate of the invention is utilised for
CC treating a condition mediated by aberrant electrical activity that
CC initiates uptake or release of neurotransmitters and contraction of
CC muscles. The drug candidate of the invention is also utilised for
CC treating epilepsy and arrhythmia. The present sequence is a voltage-
CC dependent calcium channel DNA.
XX
SQ Sequence 7648 BP; 1492 A; 2419 C; 2205 G; 1532 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 11815.50 Matches: 2264
Percent Similarity: 95.29% Conservative: 1
Best Local Similarity: 95.25% Mismatches: 1
Query Match: 99.26% Indels: 111
DB: 13 Gaps: 2

US-09-611-257A-37 (1-2266) x ADS16298 (1-7648)
QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 1 ATGACGAGAGGAGGATGAGCGGGCGCCGAGAGTCCGGACAGCCCGAGACTTCATG 60
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 61 CGGCTCAACGACCTGTGGGGGGCCGGGGCCGGGGCCGGGGTACAGAAAAGGAC 120
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 121 CCGGGCAGCGCGACTCCGAGGCGGAGGGGCTGCGGTACCCGGCTGGCCCCGGTGT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 181 TTCTTCTACTTGAGCCAGGACAGCCCGCCGAGCTGTGTCTCCGACGGTCTGTAAAC 240
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 241 CCCTGGTTTGAGCGCATGATGATGTCATCTTCTCAACTGCGTGAACCTGGGCATG 300
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 301 TTCGGGCCATGCGAGGACATCGCTGTGACTCCAGCGCTGCCGATCTGCAGGCCCTTT 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 361 GATGACTTCATCTTGTGCTTTCTTTGCGGTGAGATGCTGTGAAGATGTGGCTTGGGC 420

QY 141 IlePheGlyLysLysCysTyrLeuGluYAspThrTrpAsnArgLeuAspPhePheIleVal 160
Db 421 ATCTTTGGAAAAAGTGTACTCTGGAGACACTTGAAACCGGCTTGACTTTTTCATCGTC 480
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 481 ATCGACAGGATGCTGAGTACTCGCTGACCTGCAGAACGTACAGTTCTCAGCTGTACAG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 541 ACAGTCCGTGTGCTGCGACCGCTGAGGCCATTAAACGGGTGCCAGCATGCGCATCCTT 600
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 601 GTCACGTTGCTGCTGATACGCTGCTCCATGCTGGGCAACGTCCTGCTGCTCTCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240
Db 661 GTCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCGAGGGCTGCTCGGAACCGA 720
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 721 TGCTTCTACTGAGAATTTCAGCTTCCCTGAGCGTGACCTGGAGCGTATTACAG 780
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 781 ACAGAGACGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGCGCATGCGG 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 841 TCCTGACAGAGCGTCCCGACCGCTGCGGGGAGCGGGGGCGGTGGCCACCTTGGGCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 901 GACTATGAGGCTTACAACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTAC 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
Db 961 ACCAAGTCTGACGGGGGAGACACACCCCTTCAAGGGCGGCATCACTTGACAACATT 1020
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1021 GGCTATGCTGATCGCCATCTTCCAGTTCATCACGCTGAGGGCTGGTGCAATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1081 TACTTTGTATGATGATGCTCATCTCTTCTTCAATTTCATCTCATCTCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGln 400
Db 1141 GTGGGCTCTTCTTATGATCAACCTGTGCTGTGTGATGTCACGAGTTCTCAGAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1201 ACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGTGTGCGTCTCAACGCC 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440
Db 1261 AGCACCTGTGCTAGCTTCTTGAGCCCGCAGCTGCTATGAGAGCTGCTCAAGTACTG 1320
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1321 GTGTACATCTTGTGAAGGACAGCCGAGGCTGGCTCAGGTCTCTGGGACAGAGTGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1381 CCGGTTGGGCTGTCTAGCAGCCAGCACCCCTCGGGGGCCAGAGAACCCAGCCAGCAGC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1441 AGCTGCTCTGCTCCACCGCGCTTATCTCTCCACCACTGTGTGACCAACCAACCAACC 1500

QY	501	HisHisHisHisTyrHisIleuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1501	CATCACCACTACCACTGGGCAATGGAGCGCTCAGGGCCCCCGGCCAGCCCGGAG	1560
QY	521	ILeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
Db	1561	ATCCAGGACAGGGATGCCAATGGGTCCCGCAGGCTCATGTGCCACCACTCCAGCCT	1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
Db	1621	GCCCTCTCCGGGGCCCCCTGGTGCGCAGAGTGTGTGCACAGCTTCTACCATGCCGAC	1680
QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Db	1681	TGCCACTTAGAGCCAGTCCGCTGCCAGGGCGCCCCCTCCAGGTCCCATGTGAGGATCC	1740
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
Db	1741	GGCAGGACTGTGGGCGAGGGGAAGTGTATCCACCGTGCAACCAAGCCCTCCACCGGAG	1800
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	1801	ACGCTGAAGAGAGAGCACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACC	1860
QY	621	SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuGluThrGlnSer	640
Db	1861	AGCCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAAGCTGTGAGACACAGAGT	1920
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
Db	1921	ACAGGTGCCTGCCAAGCTCTTGCAAGATCTCCAGCCCTGTGTAAGCAGACAGTGA	1980
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680
Db	1981	GCCTGTGTCAGACAGCTGCCCTACTGTGCCCGGGCCGGGCGAGGGAGGTGACCTC	2040
QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
Db	2041	GCCGACCGTGAAATGCTGACTCAGACAGCAGGAGCAGTTTATGAGTTTACACACAGATGCC	2100
QY	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla	720
Db	2101	CAGCACAGCAGACTCCGGGACCCCCACAGCCGGCGCAACGAGCCTGGGCCCAATGCA	2160
QY	721	GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal	740
Db	2161	GAGCCCAAGCTCTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAGAATTGTG	2220
QY	741	AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760
Db	2221	GACAGCAAGTACTTTGGCCGGGGAATCATGATCGCCATCTGTGTCAACACACTCAGCATG	2280
QY	761	GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle	780
Db	2281	GGCATCGAATACCAAGAGAGCCCGAGGAGCTTACCAACGCCCTAGAAATCAGCAACATC	2340
QY	781	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe	800
Db	2341	GTCTTCACCAAGCCTCTTTGCCCTGGAGATGCTGCTGAAGCTGCTGTGTATGTCCTTT	2400
QY	801	GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp	820
Db	2401	GGCTACATCAAGAATCCCTAACACATCTTCGATGGTGCATTTGTGTATCATCAGCGTGG	2460
QY	821	GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg	840
Db	2461	GAGATCGTGGCCAGCGGGGGCGGCTGTGCGTGTGCGGACCTTCCGCTGATGCGT	2520
QY	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
Db	2521	GTGCTGAAGCTGGTGGCTTCTCTGCCGGCGCTGCAGCGGCGAGCTGGTGGTCTCATGAAG	2580
QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer	880

Db	2581	ACCATGACAACGTGGCCACCCTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTTCAGC	2640
QY	881	ILEuGLyMeHISleuPheGLyCysLysPheAlaSerGLuArgAspGLyAspThrLeu	900
Db	2641	ATCCTGGGCATGCATCTCTTCGGCTGCAGTTTGCTCTGAGCGGGATGGGACACCCTG	2700
QY	901	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920
Db	2701	CCAGACCGGAAGATTGTGACTCTTGCTCTGGGCCATCGTCACTGCTTTTCAGATCCTG	2760
QY	921	ThrGlnGLuAspTrpAsnLysValLeuTrpAsnGLyMetAlaSerThrSerSerTrpAla	940
Db	2761	ACCAGAGAGACTGGAACAAGTCCCTCAATGATGAGCTCCACGTCGTCTCTGGGCG	2820
QY	941	AlaLeuTyrrPheIleAlaLeuMetThrPheGLyAsnTyrrValLeuPheAsnLeuVal	960
Db	2821	GGCCTTATTTCATTGCTCCCTCATGACCTTCGCACTACGTGCTCTTCATTTGCTGCTC	2880
QY	961	AlaIleLeuValGLyGLyPheGlnAlaGLyLutIleSerLysArgGLuAspAlaSerGLy	980
Db	2881	GCCATTCTGTGGAGGGCTTCCAGGCGGAGAAATCAGCAACGGGAGATGCGAGTGGA	2940
QY	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnGLyAspAlaAsnLysSerGLu	1000
Db	2941	CAGTTAAGCTGTATTCACTGCTGCTGTCACTCCACAGGGGAGATGCCAACAACTCCGAA	3000
QY	1001	SerGLuProAspPhePheSerProSerLeuAspGLyAspGLyAspArgLysLysCysLeu	1020
Db	3001	TCAGAGCCCGATTCTTCTCACCCAGCCTGATGTGATGGGACAGAGAAGAGTGTG	3060
QY	1021	AlaLeuValSerLeuGLyGLyHisProGlnLeuArgLysSerLeuLeuProProLeuIle	1040
Db	3061	GCCTTGTGTCTCTGGGAGAGCACCCGAGCTGCGAAGACCTGCTGCGCTCTCATC	3120
QY	1041	IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlnGLyGLu	1060
Db	3121	ATCCACACGGCGCCACACCCATGTGCTGCCCAAGACACACAGCAGCGGCTTGGGCGAG	3180
QY	1061	AlaLeuGLyProAlaSerArgArgThrSerSerSerGLySerAlaGLuProGlnAlaAla	1080
Db	3181	GGCGTGGGCGCTGCGTCCGCCGACACAGCAGCAGCGGTCCGACAGAGCTTGGGGCGCC	3240
QY	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
Db	3241	CACGAGATGAAGTCAACGCCACGCGCCGCACTCTCCGACACGCCCTTGAGACGCTGCA	3300
QY	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGLyArgAlaProSerLeuLys	1120
Db	3301	AGCAGCTGAGACCAGCAGCGCTCCAGCCGGAACAGCTCGGCCGTGACACCAGCTGAAG	3360
QY	1121	ArgArgSerProSerGLyGLuArgArgSerLeuSerGLyGLyGlnGLyGlnLysSerGln	1140
Db	3361	CGGAGAAGCCCAAGTGGAGAGCGGCGGTCTCTGTGTCCGGAGAGAAGCCAGAGACCAG	3420
QY	1141	AspGLyGlnGLySerSerSerGLyGLyArgAlaSerProAlaGLySerAspHisArgHis	1160
Db	3421	GATGAAGAGAGAGCTCAGAAGAGAGCGGGCCAGCCTCGGGGCACTGACCATCGCCAC	3480
QY	1161	ArgGLySerLeuGLuArgGLuAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3481	AGGGGCTCCCTGGAGCGGAGGCCAAGAGTTCTTTGACCTGCAGACACACTGCAGGTG	3540
QY	1181	ProGlnLeuHisArgThrAlaSerGLyArgGLySerAlaSerGlnHisGlnAspCysAsn	1200
Db	3541	CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTGAGACACAGACTGCAAT	3600
QY	1201	GlyLysSerAlaSerGLyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	3601	GGCAAGTCGGCTTCAGGGCGCCTGCGCCGGGCTTGGGCTGATGATACCCCCCACTGAT	3660
QY	1221	GlyAspAspAlaAspAspGLyGLyAsnLeuSerLysGLyGLyArgValArgAlaTrpIle	1240

Db 3661 GGGGATGACGCCGATGACGAGGGCAACCTTGACAAAGGGGAACGGGTCGCGCGTGATC 3720
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
Db 3721 CGAGCCCGACTCCCTGCTGCTGCTGCCTGCAGGAGACTCCTGGTCAGCTTACATCTTCCT 3780
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
Db 3781 CCTCAGTCCAGGTTCCGCCCTCCTGTGTGACCGGATCATCACCCACAAGATGTTGCACCAC 3840
QY 1281 ValValLeuValIleIlePheLeuAsnCyseIleThrIleAlaMetGluArgProLysIle 1300
Db 3841 GTGGTCTGTGATCATCTTCTTACTGATGATCAACCATCGCCATGGAGCGCCCAAAATT 3900
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db 3901 GACCCCAACAGCGCTGAACGCATCTTCCTGACCCCTCCCAATTACATCTTCAACCGCAGTC 3960
QY 1321 PheLeuAlaGluMetThrValLysValAlaIleuGlyTrpCysPheGlyGluGlnAla 1340
Db 3961 TTTCGTGCTGAATGACAGTGAAAGGTGGGCACTGGGCTGGTGTCTTCGGGAGCAGCG 4020
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 4021 TACCTGCGAGCAGTTGGAACGTGCTGACGCGGCTGTTGGTGTCTCATCTCCGTCATCGAC 4080
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4081 ATTCTGGTGTCCATGGTCTCTGACAGCGGCAACAAGATCCTGGGCATGCTGAGGGTGTG 4140
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
Db 4141 CGGCTGCTGCGGACCTTGCGCCCGCTCAGGGTGATCAGCCGGCGCGAGGGGCTGAAGCTG 4200
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420
Db 4201 GTGGTGAGACGCTGATGTCTCTCACTGAACCCATCGGCAACATTGTAGTCATCTGCTGT 4260
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
Db 4261 GCCTTCTTCATCATTTTCGGCATCTTGGGGGTGACGCTCTTCAAGGGAAGTTTTCGTG 4320
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
Db 4321 TGCCAGGGCGAGATACAGGAACATCACCAATAATCGACTGTGCGAGGCCAGTTAC 4380
QY 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db 4381 CGGTGGGTCCGGACAACTAACAATTGACAACCTTGCCAGGCGCTGATGTCCCTGTTTC 4440
QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
Db 4441 GTTTTGCCCTCCAAAGATGGTTGGGTGGACATCATGTACGATGGGCTGGAATGCTGTGGGC 4500
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
Db 4501 GTGAGCCAGCAGCCCATCATGAACACCAACCCCTGGATGCTGTACTTCACTCTCGTTTC 4560
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
Db 4561 CTGCTCATTTGTGGCTTCTTGTCTGAACATGTTGTGGGTGTGGGTGGAAGAACTTTC 4620
QY 1541 HisLysCysArgGlnHisGlnGlnGluGluGluAlaArgArgArgGluLysArgLeu 1560
Db 4621 CACAAGTGTGGCAGCACAGAGAGAGAGAGGCGCGGCGGAGAGAGAGCGCCTA 4680
QY 1561 ArgArgLeuGluLysLysArgArg----- 1568
Db 4681 CGAAGAAGCTGAGAAAAAGAGAGGAATCTAATGCTGAGCATGTAAATTGCTTCCGGCAGC 4740
QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1582
Db 4741 TCAGCCAGCGCTGCGTCAAGAAAGCCAGTGCAAACTTACTACTCGACTACTCCCGCTTC 4800

QY 1583 ArgLeuLeuValHisHisIleuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602
Db 4801 CGGCTCCGTGCCACCACTGTGTGACCAAGCCACTACTGGAACCTTTCATCAGAGGTGTC 4860
QY 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622
Db 4861 ATCGGGCTGAACGTGTGTACCATGAGCCATGAGACACTACAGACGCCAGATCTGGAT 4920
QY 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642
Db 4921 GAGGCTTGAGAGATCTGCAACTACATCTTCACTGTCACTTTGTCTTGAGTCACTTTTC 4980
QY 1643 LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu 1662
Db 4981 AAACCTGTGGCCTTGTGTTCCGTGGGTCTTCCAGGACAGGTGAAACAGCTGACCTG 5040
QY 1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer 1682
Db 5041 GCCATTGTGCTGTCCATCATGGGCATCACGCTGAGGAAATCGAGTCAACGCTTCG 5100
QY 1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702
Db 5101 CTGCCCATCAACCCACCATCATCGGCATCATGAGGGTGTGCGCATTGCCGAGTGTG 5160
QY 1703 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722
Db 5161 AAGCTGTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGGAACGGTGATGCAGGCCCTG 5220
QY 1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeu 1742
Db 5221 CCCAGGTGGGAAACCTGGGACTTCTCTTCATGTTGTTTTCATCTTTGACGCTCTG 5280
QY 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762
Db 5281 GGCGTGAGCTCTTGGAGACCTGAGTGTGACGAGACACCCCTGTGAGGGCTGCGGC 5340
QY 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782
Db 5341 CGTCATGCCACCTTTCGGAACCTTGGCATGGCCTTCTTAACCTCTTCCGAGTCTCACA 5400
QY 1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802
Db 5401 GGTGACAATTGGAATGGCATTAAGAGACACCTCCGGGACTGTGACCAAGATCCACC 5460
QY 1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822
Db 5461 TGCTACAACAGGTATCTCGCCTATCTACTTGTGTCTTCTGCTGACGCGCCAGTTTC 5520
QY 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842
Db 5521 GTGCTAGTCAAGTGTGATCGCGTGTGATGAAGACCTGAGAGAGAGCAACAGAGAG 5580
QY 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerPro 1862
Db 5581 GCCAAGAGAGAGCGGAGCTAGAGGTGAGCTGAGCTGAGAGATGAAGACCTCAGCCCC 5640
QY 1863 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer 1882
Db 5641 CAGCCCACTGCCCACTGGGCAAGCCCTTCTCTGCGCTGGGGTGAAGGCCCGACAGC 5700
QY 1883 ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902
Db 5701 CCCGACAGCCCCAAGCCTGGGGCTTGCAACCAAGCGGCCACCGAGATCAGCCTCCAC 5760
QY 1903 PheSerLeuGluHisProThr----- 1909
Db 5761 TTTTCCCTGAGACACCCACGAGACAGGAGCTGTTTGACACCATATCCCTGCTGATCCAG 5820
QY 1909 ----- 1909
Db 5821 GGCTCCCTGAGTGGAGCTGAAGCTGATGACGAGCTGCAAGGCCAGGGGCCAGCCC 5880

QY 1909 ----- 1909
Db 5881 TGTGCTTCCTTCTGCCCCAGCCTGGAGGCTCCGACCCACAGATCCCTTAGCTGAG 5940
QY 1909 ----- 1909
Db 5941 ATGAGGCTCTGTCTGTGACGTCAGAGATTGTGTGAACCGTCTGCTCTTAGCTCTG 6000
QY 1909 ----- 1909
Db 6001 ACGGATGACTCTTTGCTGTATGACATGCACACACTCTTACTTAGTGCCCTGGAGACCAAT 6060
QY 1910 MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSergly 1929
Db 6061 ATGCAGCCCCACCCACGAGCTGCCAGACCACTTACTGACTGTGCGGAGTCTGGG 6120
QY 1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla 1949
Db 6121 GTCAGCCGAACGCACTCTGTGCCAATGACAGCTACATGTGTGGCATGGAGCACTGCC 6180
QY 1950 GluGlyProLeuGlyHisArgGlyTTPGlyLeuProLysAlaGlnSerglySerValLeu 1969
Db 6181 GAGGGGCCCCCTGGGACACAGGGGCTGGGGGCTCCCCAAAGCTCAGTCAGGCTCCGTCTTG 6240
QY 1970 SerValHisSerglnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989
Db 6241 TCCGTTCACCTCCACGACGACAGATACCACTACATCCTGCAGCTTCCCAAAGATGCACCT 6300
QY 1990 HisLeuLeuGlnProHisSeraAlaProThrTTPGlyThrIleProLysLeuProProPro 2009
Db 6301 CATCTGCTCCAGCCCCACAGCGCCCCCAACTTGGGGCACCATCCCAAACCTGCCCCACCA 6360
QY 2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029
Db 6361 GGACGCTCCCTTTGGCTCAGAGGCCACTCAGGCGCCAGGCAACAATAGACTGACTCC 6420
QY 2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerglyProSer 2049
Db 6421 TTGGACGTTCAGGGGTCTGGGACGCCGGAAGACCTGCTGGCAGAGTGAGTGGGCCCTCC 6480
QY 2050 ProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHis 2069
Db 6481 CCGCCCCGTGGCCCGGCTACTCTTCTGGGGCCAGTCAAGTACCCAGGACACAGCAGCAC 6540
QY 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089
Db 6541 TCCCGACGCCACAGCAAGATCTCCAACACATGACCCTGGCAGCCCTTGCCCGCAGGCCCA 6600
QY 2090 GluProAsnTTPGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109
Db 6601 GAACCCAACTGGGGCAAGGGCCCTCCAGAGACCAGAAGCAGCTTAGAGTTGAGACCGAG 6660
QY 2110 LeuSerTrpIleSerglyAspLeuLeuProProGlyGlyGlnGluProProSerPro 2129
Db 6661 CTGAGCTGATTTCAGAGACCTCTGCCCCCTGGCGCCAGAGAGGCCCCCATCCCA 6720
QY 2130 ArgAspLeuLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer 2149
Db 6721 CGGGACCTGAAGAAGTGCTACAGCGTGAAGGCCAGAGCTGCCAGCGCGCTTAGCTCC 6780
QY 2150 TrpLeuAspGlnGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySergln 2169
Db 6781 TGGCTGGATGAGCAGAGAGACACTTATCGCCGTCAAGCTGCTGGACAGCGGCTCCAA 6840
QY 2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySer 2189
Db 6841 CCCACCTGGGCAAGACCCCTTAACTTGGGGGCCAGCTCTTGGGGGGCTTGGGAGC 6900
QY 2190 ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGlnSerglnGly 2209
Db 6901 CGGCCCAAGAAAAAACTCAGCCCCGCTTAGTATCACCATAGACCCCCCGAGAGCCAAAGT 6960
QY 2210 ProArgThrProProSerProGlyIleCysLeuArgArgArgAlaProSerSerAspSer 2229

Db 6961 CCTCGACCCCCGCCAGCCTGTATCTGCTCCGAGGAGGGGCTCCGACGACTCC 7020
QY 2230 LysAspProLeuAlaSerglyProProAspSerMetAlaAlaSerProSerProLysLys 2249
Db 7021 AAGGATCCCTTGCGCTTGCCCCCTGACAGCATGGCTGCCCTGCCCTCCCAAGAAA 7080
QY 2250 AspValLeuSerLeuSerglyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7081 GATGTGCTGAGTCTCCGGTTTATCCTGACCCAGACAGACCTGACCCC 7131
RESULT 5
AAX83484
ID AAX83484 standard; cDNA; 6729 BP.
XX
AC AAX83484;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCav1d) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KM activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Homo sapiens.
XX
PN W09929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
XX
DR P-PSDB; AAY14589.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 58-67; 138pp; English.
XX
CC This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCav1d. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6729 BP; 1283 A; 2168 C; 1975 G; 1303 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 6729
Score: 11758.50 Matches: 2242
Percent Similarity: 98.94% Conservative: 0
Best Local Similarity: 98.94% Mismatches: 1
Query Match: 98.78% Indels: 23
DB: 2 Gaps: 1

US-09-611-257A-37 (1-2266) x AAX83484 (1-6729)

QY 1 MetAspGluGluuAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
| | | | |
Db 1 ATGCACGAGGAGGAGATGGAGCGGGCCCGCAGAGTCCGGACAGCCCGGAGCTTCA 60
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGlyLysAsp 40
| | | | |
Db 61 CGGCTCAACGACCTGTGGGGGGCCGGGGGGGGCCGGGGGCTCAGCAAGAAAAGGAC 120
QY 41 ProGlySerAlaAspSerGluAlaGlyGlyLeuProTyrProAlaLeuAlaProValVal 60
| | | | |
Db 121 CCGGGCAGCGCGAGCTCCAGAGCGGAGGGCTGCCGTACCCGGCGCTGGCCCGGTGTT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
| | | | |
Db 181 TTCTTCTACTTGAGCCAGACAGCCGCCGGAGCTGTGTCTCCGACAGGCTGTAAAC 240
QY 81 ProTrpPheGluArgLieserMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
| | | | |
Db 241 CCCTGGTTGAGCGGCATCAGCATGTTGGTCACTCTTCAACTGCCGTGACCCCTGGGCATG 300
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
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Db 301 TTCCGGCCATGCGAGACATCGCCTGTGACTCCAGCGCTGCCGATCTGCAGAGCCTTT 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
| | | | |
Db 361 GATGACTTCATCTTGGCTTCTTTGGCCGTGAGATGGTGTGAAGATGGCGCTTGGGC 420
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
| | | | |
Db 421 ATCTTTGGGAAAAAGTGTAACTGGGAGACACTTGAAACCGGCTGACTTTTCATCGTC 480
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
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Db 481 ATGCAGAGGATGCTGGAGTACTCGCTGACCTGCAGAACGTCAAGCTTCAAGCTGTACAG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
| | | | |
Db 541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCCATCCTT 600
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
| | | | |
Db 601 GTCAAGTTGCTGCTGGATAGCTGCCCATGTGGCAACGTCTGTCTGTCTTCTTCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
| | | | |
Db 661 GTCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCAGGCGCTGCTTCGGAACCGA 720
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
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Db 721 TGTCTTCTAAGCTGAGAAATTTCAGCCTCCCGCTGAGCGTGGACCTGGAGCGCTATTACAG 780
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
| | | | |
Db 781 ACAGAGAAAGAGATGAGAGCCCTTCATCTGTCTCCAGCCACGCGAGAACGGCATGCGG 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu 300
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Db 841 TCCTGCAGAAAGCGTGCCACGCTGCGCGGGGAGCGGGCGGTGGCCACCTTGGCGGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
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Db 901 GACTATGAGGCTTACAACAGCTCCAGCAACACCACTGTGTCAACTGAACTACTACTAC 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
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Db 961 ACCAATGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGGCATCAACTTGAACAACATT 1020
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
| | | | |

Db 1021 GGCTATGCCCTGGATCGCCATCTTCCAGGTATCATCAGCGTGGAGGGCTGGGTGCATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
| | | | |
Db 1081 TACTTTGTGATGGATGCTCATTTCTTCTACATTTTCACTTCACTTCACTCTCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
| | | | |
Db 1141 GTGGGCTCTTCTTCATGATCAACTGTGCTGTGTGTGATTGCCACGAGTTCTCAGAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
| | | | |
Db 1201 ACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGGTGTGCGTTCTGTCCAAAGCC 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440
| | | | |
Db 1261 AGCACCTGGCTAGCTTCTGTAGCCCGGCAGCTGCTATGAGAGACTGCTCAAGTAACTG 1320
QY 441 ValTyrIleLeuArgLysAlaIleArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
| | | | |
Db 1321 GTGTACATCTTCTGTAAGGACAGCCCGCAGGCTGGCTCAGGTCTCTCGGCAGCAGGTGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
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Db 1381 CGGTTGGGCTGCTCAGCAGCCAGCAACCCCTCGGGGGCCAGAGAACCCAGCCAGCAGC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
| | | | |
Db 1441 AGCTGCTCTGCTCCACCGCCGCTATCCGTCCACCACCTGTGTGCACCACCAACCAACAC 1500
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
| | | | |
Db 1501 CATCACCAACCACTAACCACTGGGCATGGGACGCTCAGGGCCCCCGGGCAGCCCGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
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Db 1561 ATCCAGGACAGGATGCCAATGGGTCCCGCCGGCTCATGTGTGCCAACACCTCGAGCGCT 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyValaGluSerValHisSerPheTyrHisAlaAsp 560
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Db 1621 GCCCTCTCCGGGGCCCCCCTGTGTGGCGCAGAGTGTGTGCACACTTCTACCATGCCGAC 1680
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
| | | | |
Db 1681 TGCCACTTAGAGCAGTCCGCTGCCAGCGCCCCCTCCAGGTCCCATCTGAGGCATCC 1740
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
| | | | |
Db 1741 GGCAGACTGTGGCAGCGGGAAGGTATCCACCGTGCAACACGCCCTCCACCGGAG 1800
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
| | | | |
Db 1801 ACGCTGAAGAGAGACACTAGTAGAGTGGCTGCCAGCTCTGGCCCCCAACCTCAGC 1860
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
| | | | |
Db 1861 AGCCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAAAGTGTCTGGAGACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysLieserSerProCysLeuLysAlaAspSerGly 660
| | | | |
Db 1921 ACAGGTGCTGCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAAGACAGTGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
| | | | |
Db 1981 GCCTGTGTCCAAGACAGTGCCTTACTGTGCCCGGGCGGGGAGGAGGTGAGCTC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
| | | | |
Db 2041 GCCGACCGTGAAATGCTGACTCAGACAGCAGGAGTATTAGTTTACACAGAGATGCC 2100
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
| | | | |
Db 2101 CAGCACAGGACCTCCGGGAGCCCCACAGCCGGCGCAACGAGCCTGGGCCAGATGCA 2160

QY 721 GluProSerSerValIleuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2161 GAGCCAGAGCTCTGTGCTGGCCCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2220
QY 741 AspSerLysTrpPheGlyArgGlyIleMetIleAlaIleuValAsnThrLeuSerMet 760
Db 2221 GACAGCAAGTACTTGGCCGGGGAATCATGATCGCCATCTGTGTCAACACACTCAGCATG 2280
QY 761 GlyIleGlyTrpHisGluInProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2281 GGCATCGAATACCAAGAGCAGCCCGAGAGCTTACCACGCCCTAGAAATCAGCAACATC 2340
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800
Db 2341 GTCTTACCAAGCCTCTTGGCCCTGGAGATGCTGTGAAGCTGCTGTGTATGTCCTTT 2400
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820
Db 2401 GGCTACATCAAGAATCCCTACAACATCTTCGATGTTGTGTCATGTCATCAGCGTGTGG 2460
QY 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2461 GAGATCGTGGCCAGCAGGCGGGCGGCTGTGGTGTGGGACCTTCCGCTGATGCGT 2520
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 2521 GTGCTGAAGCTGTGCGCTTCTCGCGCGCTGACGGCAGCTGGTGTGTCATGAAG 2580
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 2581 ACCATGGAACAAGTGGCCACCTTCTGATGCTTATGCTTTCATCTTCATCTTCAGC 2640
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGlyArgAspGlyAspThrLeu 900
Db 2641 ATCTTGGGCATGATCTCTTGGCTGCAAGTTTGCTGTAGCGGGATGGGACACCTTG 2700
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 2701 CCAGACCCGGAAGATTTTGACTCTTGTCTGTGGCCATCGTCACTGTCTTTCAGATCCTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
Db 2761 ACCCAGGAGGACTGGAACAAGTCTCTTACAATGTATGGCTTCACGTCGCTTGGCG 2820
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
Db 2821 GCCCTTATTTCAATTGCCCTCATGACTTCGCAACTACGTGCTCTTCAATTTCGTGTC 2880
QY 961 AlaIleLeuValGluGlyPheGlnIleGluIleSerLysArgGluAspAlaSerGly 980
Db 2881 GCCATTCTGTGGAGGGCTTCCAGGGGAG----- 2910
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
Db 2911 -----CGAGATGCCACAAGTCCGAA 2931
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 2932 TCAGAGCCCCGATTCTTCTCACCCCAGCCTGGATGTGATGGGGAACAAGAAAGTGCCTG 2991
QY 1021 AlaLeuValSerLeuGlyLysHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040
Db 2992 GCCTTGTGTCTCTGGAGAGCACCAGACTGCGGAAGGCTGTGCGCCTTCATC 3051
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3052 ATCCACACGGCGCCACACCCCATGTGCTGCCAAGAGCACACACGCGCTGGCGAG 3111
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3112 GCGGTGGGCCCTGCGTGGCGCCGACACAGCAGCGGGTGGCAAGACCTGGGGCGGC 3171

QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3172 CACGAGATGAAGTCAACGCCCAAGCCGCCAGCTCTCCGACACAGCCCCCTGGAGCGCTGCA 3231
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3232 AGCAGCTGGACCAGCAGCGGCTCCAGCCGGAACAGCCTCGGCCGTGACCCAGCCTGAAG 3291
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnSerGln 1140
Db 3292 CGGAAGACCCCAAGTGAAGCGCGCGGTCCCTGTGTGGGAGAAGGCCAGAGAGCCAG 3351
QY 1141 AspGluGluGluSerSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3352 GATGAAGAGGAGAGCTCAGAAGAAGAGCGGGCCAGCCCTGCGGGCAGTGAACCATCGCCAC 3411
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3412 AGGGGTCCCTGGAGCGGAGGCCCAAGAGTTCTTTGACCTGCGACAGACACTGCAAGTGTG 3471
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3472 CCAGGCTGCATCGCACTGCCAGTGGCCGAGGTTCTTCTGAGCACAGACTGCAAT 3531
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAsp 1220
Db 3532 GGCAGTCCGGCTTCAAGGCGCCTGGCCCGGCCCTGCGCTGATGATACCCCACTGAT 3591
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
Db 3592 GGGGATGACCGCGATGACGAGGGCAACCTGAGCAAGAAGGGAACGGGTCCGCGGTGATC 3651
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
Db 3652 CGAGCCGCACTCCCTGCTGCTGCTCGAGCGAGACTCCTGTGTCAGCCTTACATCTTCCCT 3711
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
Db 3712 CCTCAGTCCAGGTTCCGCTCTGTGTCAACCGGATCATCACCCACAAGATGTTGACACAC 3771
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3772 GTGTCCTTGTCAATCATCTTCTTAAGTGCATGCATCCATGAGCGCCCAAAATT 3831
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db 3832 GACCCCAACAGCGCTGAAGCATCTTCCTGACCCTCTCCAATTATCATCTTCAACGCAATC 3891
QY 1321 PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla 1340
Db 3892 TTTCTGCTGAATGACAGTGAAGGTGTGGGCACTGGGCTGTGCTTCGGGAGCAGGCG 3951
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 3952 TACCTGCGGAGCAGTTGGAAGTGTGACCGGGCTGTTGTGCTCATCTCCGTATCGAC 4011
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4012 ATTCTGTGTCCATGTGTCTGACAGCGGCACCAAGATCCTGGGCATGTGAAGGTGCTG 4071
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
Db 4072 CGGCTGTGGGAGACCTGGCGCCGCTCAGGGTGATCAAGCGGCGCAGGGGCTGAAGCTG 4131
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
Db 4132 GTGGTGAAGACGCTGATGTCTCACTGAACCCCATCGGCAACATTTGTATCATCTGCTGT 4191
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
Db 4192 GCCTTCTTCATCATTTTCGGCATCTTGGGGGTGCAAGCTTTCAAAAGGAAGTTTTCGTG 4251
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460

Db 4252 TGCCAGGGCGAGATACCAAGAACATCACCAATAATCGACTGTGCCAGGCCAGTTAC 4311
QY 1461 ArgTrpValArgHisIySTyrrAsnPheAspAnLeuGlyAlaLeuMetSerLeuPhe 1480
Db 4312 CGGTGGGTCCGGCACAGTACAACCTTTGACACCTTGCCAGGCCCTGATGCCCTGTTCC 4371
QY 1481 ValLeuAlaSerLyAspGlyTrpValAspIleMetTyrrAspGlyLeuAspAlaValGly 1500
Db 4372 GTTTGGCCTCCAAGGATGGTTGGGTGACATCATGATGGGCTGGAATGCTGTGGGC 4431
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrrPheIleSerPhe 1520
Db 4432 GTGGACACGACGCCCATCATGAACCAACACCCTGGATGCTGTACTTCACTCGTTTC 4491
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
Db 4492 CTGCTCATTTGTGGCCTTCTTTGTCTGAAACATGTTGTGGGTGTGGTGGAGAACTTC 4551
QY 1541 HisLySCysArgGlnHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1560
Db 4552 CACAAAGTGTCCGACAGCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4611
QY 1561 ArgArgLeuGlnLysLysArgArgLysAlaGlnCysLysProTyrrTyrrSerAspTyrrSer 1580
Db 4612 CGAAGACTGGAGAAAAAGAGAAAGAAAGCCCAAGTGCACAACTTACTACTCCGACTACTCC 4671
QY 1581 ArgPheArgLeuLeuValHisHisLysLeuCysThrSerHisSTyrrLeuAspLeuPheIleThr 1600
Db 4672 CGCTTCGGCTCCTCGTCACCACTGTGTGACACCACTACCTGGACCTTTCATCACA 4731
QY 1601 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisSTyrrGlnGlnProGlnIle 1620
Db 4732 GGTGTCAATCGGGCTGAACGTGGTCAACCATGGCCATGGAGCACTACACAGAGAGAGAGAT 4791
QY 1621 LeuAspGlnAlaLeuLysIleCysAsnTyrrIlePheThrValIlePheValLeuGlnSer 1640
Db 4792 CTGGATGAGGCTCTGAAGATCTGCAACTACATCTTCATCTTGTCTTGGAGTCA 4851
QY 1641 ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1660
Db 4852 GTTTTCAAACTTGTGGCCTTGTGTTCCGTCGGTCTTCCAGGACAGGTGGAACCAAGCTG 4911
QY 1661 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGlnIleGluValAsn 1680
Db 4912 GACCTGGCCATTGTGCTGTCTTCATCATGGGCATCACGCTGGAGGAATCGAGGTCAAC 4971
QY 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700
Db 4972 GCCTCGTCCCATCAACCCCAACCATCATCCGCATCATGAGGGTGTGCGCATTGCCCGA 5031
QY 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720
Db 5032 GTGCTGAAGCTGCTGAAGATGGCTGTGGGCATGCGGGCGCTGTGACACGCTGATGCAG 5091
QY 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1740
Db 5092 GCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTGTGTTTTCATCTTTGCA 5151
QY 1741 AlaLeuGlyValGlnLeuPheGlyAspLeuGlnCysAspGlnThrHisProCysGlnGly 1760
Db 5152 GCTCTGGGCGTGAGCTCTTTGGAGAACCTGGAGTGTACGAGACACACCCCTGTGAGGGC 5211
QY 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780
Db 5212 CTGGGCGGCATGCCACCTTTGGAACTTTGGCATGGCCTTCTTAACCTTTCGAGTTC 5271
QY 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGln 1800
Db 5272 TCCACAGGTGACAATTGGAATGGCATTATGAAGACACCTCCGGAGCTGTGACAGAGAG 5331
QY 1801 SerThrCysTyrrAsnThrValIleSerProIleTyrrPheValSerPheValLeuThrAla 1820

Db 5332 TCCACCTGCTACACAGCGTATCTCGCCTATCTACTTGTGTCTTGTGCTGTGACGGCC 5391
QY 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlnGlnSerAsn 1840
Db 5392 CAGTTCTGTCTAGTCAACGTGTGTATCGCCGTGTGATGAGACACCTGGAGAGAGCAAC 5451
QY 1841 LysGlnAlaLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1860
Db 5452 AAGAGGCCAAGAGAGAGAGCGGAGTGAAGGCTGAGCTGGAGCTGAGATGAAAGACCTTC 5511
QY 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlnGlyPro 1880
Db 5512 AGCCCCAGCCCCACTCGCCACTGGGAGCCCTTCTCTGGCCTGGGCTCGAGGGCCCTC 5571
QY 1881 AspSerProAspSerProLysProGlyAlaIleuHisProAlaAlaHisAlaArgSerAla 1900
Db 5572 GACAGCCCCGACAGCCCCCAAGCCTGGGGCTCTGCACCCAGCGGCCACCGAGATACGCC 5631
QY 1901 SerHisPheSerLeuGlnHisProThrMetGlnProHisProThrGlnLeuProGlyPro 1920
Db 5632 TCCCACTTTTCCCTGGAGACACCCCAAGATGACACCCCAACGAGCTGCCAGAGCA 5691
QY 1921 AspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSer 1940
Db 5692 GACTTACTGACTGTGCGGAAGTCTGGGGTCAAGCCGAACGCACTCTGCCCCAATGACAGC 5751
QY 1941 TyrMetCysArgHisGlySerThrAlaGlnGlyProLeuGlyHisArgGlyTyrrGlyLeu 1960
Db 5752 TACATGTGTGGCATGGAGACACTGCCAGGGGGCCCTGGGACACAGGGGCTGGGGGCTTC 5811
QY 1961 ProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrr 1980
Db 5812 CCCAAAGCTCAGTCAAGCTCCGCTTGTTCGTTCACTCCACGCCACAGATATACAGCTTAC 5871
QY 1981 IleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrp 2000
Db 5872 ATCTGACAGCTTCCCAAGATGACCTCATCTGCTCCAGCCCAAGCGCCCAACTGG 5931
QY 2001 GlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArg 2020
Db 5932 GGCAACATCCCAAACTGCCCCCAACGAGACGCTCCCTTGGCTCAGAGGCCACTCAGG 5991
QY 2021 ArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlnAsp 2040
Db 5992 CGCCAGGCAGCAATGAAGACTGACTCTTGGACGTTCAAGGTTCTGGGCAAGCCGGAGAGAC 6051
QY 2041 LeuLeuAlaGlnValSerGlyProSerProProLeuAlaArgAlaTyrrSerPheTrpGly 2060
Db 6052 CTGCTGGCAGAGGTAGTGGGCCCTCCCGCCCTGGCCCGGGCTTACTCTTTCTGGGGC 6111
QY 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2080
Db 6112 CAGTCAAGTACCCAGGACAGACAGACATCCCGGACACAGCAAGATCTCCAAGCACATG 6171
QY 2081 ThrProProAlaProCysProGlyProGlnProAsnTrpGlyLysGlyProProGlnTrp 2100
Db 6172 ACCCCGCCAGCCCTTGGCCCAAGGCCCAAGCACTGGGGCAAGGGCCCTCCAGAGACC 6231
QY 2101 ArgSerSerLeuGlnLeuAspThrGlnLeuSerTrpIleSerGlyAspLeuLeuProPro 2120
Db 6232 AGAAGCAGCTTAGTGTGAACACGAGCTGAGCTGGATTTCAAGAGACCTCTGCCCCCT 6291
QY 2121 GlyGlyGlnGlnGlnProProSerProArgAspLeuLysLysCysTyrrSerValGlnAla 2140
Db 6292 GGGGGCCAGAGAGAGCCCATCCCAAGGACCTGAAGAAAGTCTAAGCGTGAAGGCC 6351
QY 2141 GlnSerCysGlnArgArgProThrSerTrpLeuAspGlnGlnArgArgHisSerIleAla 2160
Db 6352 CAGAGCTGCCAGCGCGGCTTACGTCTGGCTGATGAGACAGAGACACTTATCGCC 6411
QY 2161 ValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGly 2180
Db 6412 GTGAGCTGCCTGAGACGGGGCTCCCAACCCCACTGGGACAGACCCCTTAACCTTGGG 6471

QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrCysValAsnTrpAsnGlnTyrTyr	320
Db	901	GACTATGAGGCCCTAACACAGCTCCAGCAACACCACCTGTGTCAACTGGAACTAGTACTAC	960
QY	321	ThrAsnCySerAlaGlyGluHisAsnProPheGlyAlaIleAsnPheAspAsnIle	340
Db	961	ACCAACTGCTCAGCGGGGAGACACACCCTTCAAGGGCGCCATCACTTGCACAATT	1020
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet	360
Db	1021	GGCTATGCTGTGATGCCATCTTCCAGGTTCATCAGCTGGAGGGCTGGGTGCATCATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle	380
Db	1081	TACTTTGTGATGATGCTCATCTCTTCTACAATTTCATCTTCACTTCCTCATCATC	1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
Db	1141	GTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGATTGCCACGCAGTTCTCAGAG	1200
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1201	ACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGGTGCGGTTCTGTCCAACGCC	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuTyrLeu	440
Db	1261	AGCACCTGGCTAGCTTCTTGAGCCCGCAGCTGCTATGAGAGTGTCTCAAGTACCTG	1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVal	460
Db	1321	GTGTACATCCTTCGTAAAGCAGACCCGCGAGCTGGCTCAGGTCCTCGGGCAGCAGGTGTG	1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
Db	1381	CGGGTGGGCTGCTCAGCAGCCCGCAGCACCCTCGGGGGCCAGAGACCAGCCAGCAGCC	1440
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
Db	1441	AGCTGCTCTCGCTCCACCGCGCCTATCCGTCCACCACTGGTGACCAACCACCAAC	1500
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1501	CATCACCACTACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGCCAGCCCGGAG	1560
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
Db	1561	ATCCAGGACAGGATGCCAATGGGTCCGCGGCTCATGTGCCACCACTTCGACGCTT	1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
Db	1621	GCCCTCTCCGGGCCCCCCTGGTGCGCAGAGTGTGACACAGCTTCTACCATGCCGAC	1680
QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Db	1681	TGCCACTTAGAGCCAGTCCGCTGCCAGGGCGCCCTCCAGGTCCCATCTGAGGCACTCC	1740
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu	600
Db	1741	GGCAGGACTGTGGGCAAGGAAAGGTATCCACCGTGCACACCAAGCCCTCCACCGGAG	1800
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	1801	ACGCTGAAGAGAGGACACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACC	1860
QY	621	SerLeuAsnIleProProGlyProTyrSerSerSerMetHisLysLeuLeuGluThrGlnSer	640
Db	1861	AGCCTCAACATCCACCCGGGCGCTACAGCTCCATGCACACAGCTGTGAGACACAGAGT	1920
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
Db	1921	ACAGGTGCTTGCCTCAAGCTCTTGCAAGATCTCCAGCCCTTGTGAAAGCAGACAGTGA	1980
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680

Db	1981	GCCTGTGCTCAGACAGCTGCCCTACTGTGCCGGCGCGGCGAGGGAGGTGGAGCTC	2040
Qy	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
Db	2041	GCCGACCGGTGAATGCTCTACTCAGACAGCGAGCAGTTTATGAGTTTCACACAGATGCC	2100
Qy	701	GlnHisSerAspLeuArgAspProHisSerArgGlnArgSerLeuGlyProAspAla	720
Db	2101	CAGCAGCGAGCCTCCGGGACCCCCACAGCCGGCAACGAGCCTGGGCCAGATGCA	2160
Qy	721	GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal	740
Db	2161	GAGCCAGCTCTGTGCTGGCCCTTCTGAGGCTAATCTGTGACACCTTCGAAAGATTGTG	2220
Qy	741	AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760
Db	2221	GACAGCAAGTACTTTGGCCGGGAATCATGATCGCCATCCTGTGTCAACACACTCAGCATG	2280
Qy	761	GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle	780
Db	2281	GGCATCGAATACCAAGAGCAGCCGAGAGACTTACCAACGCCCTAGAAATCAGCAATC	2340
Qy	781	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPhe	800
Db	2341	GTCTTCACCAAGCTCTTTTGCCCTGAGATGCTGTGAAGCTGCTGTGTATGTCCTT	2400
Qy	801	GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp	820
Db	2401	GGCTACATCAAGATCCCTACACATCTTCATGTGTGTCATTGTGTATCAGCGTGG	2460
Qy	821	GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg	840
Db	2461	GAGATCGTGGCGCAGAGGGGGCGGCTGTGGTGTGCGGACCTTCCGCTGATGGCT	2520
Qy	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
Db	2521	GTGCTGAAGCTGTGGCTTCTCTGCGCGCTGCAGCGGACAGCTGTGTGCTCATGAAG	2580
Qy	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer	880
Db	2581	ACCATGACCAACGTGGCCACCTTCTGATGCTGCTTATGCTCTTCATCTTCATCTTCAGC	2640
Qy	881	IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu	900
Db	2641	ATCCTGGGATGATCTCTCTCGGCTGCAAGTTTGCTCTGAGCGGATGGGACACCTTG	2700
Qy	901	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920
Db	2701	CCAGACCGGAAGATTGTGACTCTCTGCTCTGGGCCATCGTCACTGTCTTCAGATCCTG	2760
Qy	921	ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla	940
Db	2761	ACCAGAGAGACTGGAACAAGTCTCTACATGATGTAAGCCTCCACGTCTCTGGGCG	2820
Qy	941	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal	960
Db	2821	GCCCTTATTTCATTGCTCATGACCTTCGGCACTACGTGCTCTTCAATTGTGCTGTC	2880
Qy	961	AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly	980
Db	2881	GCCATTCTGTGAGGGCTTCCAGCGGAG-----	2910
Qy	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu	1000
Db	2911	-----GGAGATGCCAACAAAGTCCGAA	2931
Qy	1001	SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu	1020
Db	2932	TCAGAGCCCGATTCTTCTCACACCCAGCCTGATGTGATGGGACAGGAAGAAGTGTG	2991
Qy	1021	AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIle	1040

Db 2992 GCCTGTGTCCTCGGAGAGCACCAGAGCTGCGGAAGACCTGCTGCCGCTTCATC 3051
QY 1041 ILeIsthrAlaIaThrPrometSerLeuProLySerThrSerThrgLyLeuGly 1060
Db 3052 ATCCACACGGCCGACACACCCATGTGCTGCCAAGAGCACAGCAGCGCTGGGCGAG 3111
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3112 GCGGTGGGCCCTGCGTCGCGCCGACAGCAGACGGGGTGCAGAGCCTGGGGGGCC 3171
QY 1081 HisGluMetLySerProProSerSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3172 CACGAGATGAAGTCAACGCCAGCGCCCGCAGCTCTCCGCACAGCCCCCTGGAGCGCTGCA 3231
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3232 AGCAGCTGACCAAGAGCGCGCTCCAGCCGGAACAGCCTCGGCGGTGCACCCAGCCTGAAG 3291
QY 1121 ArgArgSerProSerGlyGlyArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140
Db 3292 CGGAGAAGCCCAAGTGAGAGCGCGGCTCCTGTGTGCGGAGAAAGCCAGAGAGCCAG 3351
QY 1141 AspGlyGlyGlySerSerGlyGlyGlyArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3352 GATGAAGAGAGAGCTCAGAAGAGAGCGGGCCAGCCCTGCGGCGAGTGAACCATGCCAC 3411
QY 1161 ArgGlySerLeuGlyArgGlyAlaAlaLySerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 3412 AGGGGGTCCCTGAGCGGGAGGCCAAGACTTCCTTGACCTGCCAGACACATGCAGGTG 3471
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGlyHisGlnAspCysAsn 1200
Db 3472 CCAGGGCTGCATTCGCACTGCCAGTGGCCGAGGGTCTGCTTCTGAGCACCAAGGACTGCAAT 3531
QY 1201 GlyLySerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
Db 3532 GGCAGGTGGCTTCAAGGCGCGCTGGCCGGGCCCTGCGGCTGATGACCCCCACTGGAT 3591
QY 1221 GlyAspAspAlaAspAspGlyGlyAsnLeuSerLySGlyGlyArgValArgAlaTrpIle 1240
Db 3592 GGGGATGACGCCGATGACGAGGGCAACCTGAGCAAGGGGAACGGGTCCGCGCTGGATC 3651
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGlyArgAspSerTrpSerAlaTyrIlePhePro 1260
Db 3652 CGAGCCCGACTCCCTGCTGCTGCTGCAGAGAGACTCCTGGTCAAGCTACATCTCCCT 3711
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLyMetPheAspHis 1280
Db 3712 CCTCAGTCCAGGTTCCGCCCTCTGTGTCAACGGATCATCACCAAGATGTTCCAGCAC 3771
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGlyArgProLySIle 1300
Db 3772 GTGTCTTGTCAATCATCTTCCTTAAGTGCATCACCATGCCATGGAGCGCCCAAAATT 3831
QY 1301 AspProHisSerAlaGlyArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db 3832 GACCCCCACAGCGCTGAACGCATCTTCGAACCTCTCCAATTACATCTTACCCGAGTC 3891
QY 1321 PheLeuAlaGluMetThrValLyValValAlaLeuGlyTrpCysPheGlyGlnGlnAla 1340
Db 3892 TTTTGTGCTGAATGACAGTGAAGGTGTGGCACTGGGCTGTGCTTGGGAGCAGGCG 3951
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 3952 TACCTGCGGAGAGCTTGGAACGTGTCGAGCGGGCTGTGTCATCTCCGTCAATGCAC 4011
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4012 ATTCTGTGTTCATGTGTTCTTGACAGCGGCAACCAAGATCTGGGGCATGCTGAGGGTGTG 4071
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerAlaGlnGlyLeuLysLeu 1400
Db 4072 CGGCTGTGCGGACCCCTGCGCCGCTCAGGGGTGATCAGCCGGCGCAGGGGCTGAAGCTG 4131

QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420
Db 4132 GTGGTGGAGACGCTGATGTCTCTCACTGAACCCCATCGGCACATTTGTATCATCTGCTGT 4191
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLySGlyLysPhePheVal 1440
Db 4192 GCGTCTTCATCATTTTCCGCAATCTTGGGGGTGCAGCTCTTCAAGGGAAGTTTTCGTG 4251
QY 1441 CysGlnGlyGlyAspThrArgAsnIleThrAsnLySerAspCysAlaGlyAlaSerTyr 1460
Db 4252 TGCCAGGGCGAGATACAGAAACATCACCAATTAATCGGACTGTGCCAGGCCAGTTAC 4311
QY 1461 ArgTrpValArgHisLySerTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db 4312 CGGTGGGTCCGGCACAAAGTACAACCTTGACAACACTTGGCCAGGCCCTGATGTCCCTGTT 4371
QY 1481 ValLeuAlaSerLyAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
Db 4372 GTTTTGCCCTCCAAGGATGTTGGGTGAGACATCATGTACGATGGGCTGATGCTGGGC 4431
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
Db 4432 GTGGACCAAGACCCCATCATGAACCAACACCCCTGAGATGCTGTACTTCATCTCGTT 4491
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
Db 4492 CTGCTCATTTGTGGCTTCTTTGCTTGAACATGTTTGGGTGTGTGTGAGAACTTC 4551
QY 1541 HisLyCysArgGlnHisGlnGlyGlyGlyGlyAlaArgArgGlyGlyLyAspGlyLeu 1560
Db 4552 CACAAGTGTGGCAGACCAAGAGAGAGAGAGGCGCGCGGAGAGAGAAAGCGCCTTA 4611
QY 1561 ArgArgLeuGlyLysLyAspArg-----LysAlaGlnCysLys 1573
Db 4612 CGAAGACTGGAGAAAAAGAGAGAGTAAGAGAGAGAGATGGCTGAAGCCAGTGCAAA 4671
QY 1574 ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHis 1593
Db 4672 CCTTACTACTCCGACTACTCCGCTTCCGGCTCCTCGTCCACCACTTGTGCACAGCCAC 4731
QY 1594 TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu 1613
Db 4732 TACCTGAGCCTTTCATCAGAGTGTCAATCGGGCTGAACGTGTCAACCATGGCCATGGAG 4791
QY 1614 HisTyrGlnGlnProGlnIleLeuAspGlyAlaLeuLysIleCysAsnTyrIlePheThr 1633
Db 4792 CACTACAGCAGCCCCAGATTCGATGAGGCTCTGAAGATCTGCAACTACATCTTCACT 4851
QY 1634 ValIlePheValLeuGlySerValPheLyLeuValAlaPheGlyPheArgPhePhe 1653
Db 4852 GTCATCTTGTCTTGAGTCAAGTTTCAAACTTGTGGCCTTGTGTTCCGTGGTCTTC 4911
QY 1654 GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr 1673
Db 4912 CAGGACGCTGGAACCAAGCTGAGCCTGGCCATGTGCTGTCCATCATGGGCATCAGC 4971
QY 1674 LeuGlyGlyIleGlyValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet 1693
Db 4972 CTGGAGAAATCGAGGTCAAGCCTCGCTGCCCATCAACCCCATCATTCGCATCATG 5031
QY 1694 ArgValLeuArgIleAlaArgValLeuLySLeuLeuLySMeAlaValGlyMetArgAla 1713
Db 5032 AGGGTGTGCGCATTGCCCGAGTCTGAAGCTGTGAAGATGGCTGTGGGCATGCGGGCG 5091
QY 1714 LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet 1733
Db 5092 CTGTGGAACAAGGTGATGAGGCCCTGCCCCAGGTGGGAAACCTGGGACTTCTCTCATG 5151
QY 1734 LeuLeuPhePheIlePheAlaAlaLeuGlyValGlyLeuPheGlyAspLeuGlyCysAsp 1753
Db 5152 TTTGTTTTTTTCATCTTTCAGCTCTGGGCGTGAAGCTTTTGAGAGACCTGGAAGTGTGAC 5211

Qy	1754	GIuThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
Db	5212	GAGACACACCCCTGTGAGGGCCTGGGCCGTGATGCCACCTTTCGGAACCTTGGCAATGGCC	5271
Qy	1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr	1793
Db	5272	TTCCTAACCCCTCTCCGAGTCTCCACAGGTGACATGGCAATTGATGAGACACC	5331
Qy	1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
Db	5332	CTCCGGGACTGTGACCAGGAGTCCACTGTCTACAACACGGTCACTCGCCTAATCTACTTT	5391
Qy	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
Db	5392	GTGTCTTCTGTGCTGACGGGCCAGTTCTGTGTAAGTCAAGTGTGATCGCCGTGTGATG	5451
Qy	1834	LysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeu	1853
Db	5452	AAGCACCTGGAGAGAGCAACAAGAGGCCAAGAGAGGCCGAGCTAGAGGCTGAGCTG	5511
Qy	1854	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873
Db	5512	GAGCTGAGATGAAGACCTTCAGCCCCCAGCCCCCACTGCCACTGGGCAGCCCCCTTCTC	5571
Qy	1874	TrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro	1893
Db	5572	TGGCTGGGGTGAAGGGCCCCGACAGCCCCGACAGCCCCAACCTGGGGCTGTGACCCA	5631
Qy	1894	AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis	1913
Db	5632	GCGGCCACGCGAGATCAGCTCCCACTTTCCCTGGAGCACCCACGATGACAGCCCCAC	5691
Qy	1914	ProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr	1933
Db	5692	CCCAACGAGCTGCCAGGACCACTTACTGACTGTGCGGAAGTCTGGGGTCAAGCCGAACG	5751
Qy	1934	HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu	1953
Db	5752	CACTCTCTGCCAATGACAGCTACATGTGTGCGCATGGAGCACTGCCGAGGGGCCCTG	5811
Qy	1954	GlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSer	1973
Db	5812	GGACACAGGGGCTGGGGGCTCCCAAGCTCAGTCAGGCTCCGTCTGTCCGTTCACTCC	5871
Qy	1974	GlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGln	1993
Db	5872	CAGCCAGCAGATACCAGCTACATCTGCAAGCTTCCCAAGATGCACCTCATCTGCTCAG	5931
Qy	1994	ProHisSerAlaProThrTyrGlyThrIleProLysLeuProProGlyArgSerPro	2013
Db	5932	CCCCACAGCGCCCCAACCTGGGGCACCATCCCCAAACTGCCCCACACGAGAGCTCCCT	5991
Qy	2014	LeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGln	2033
Db	5992	TTGGCTCAGAGGCCACTCAGGCGCCAGGCAGCAATAAGCACTGACTCCTTGACGTTACG	6051
Qy	2034	GlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAla	2053
Db	6052	GGTCTGGGCGAGCCGGGAAGACTGTGGCAGAGGTGAGTGGGCCCTCCCGCCCTGGCC	6111
Qy	2054	ArgAlaTyrSerPheTyrGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis	2073
Db	6112	CGGGCTTACTCTTCTTCTGGGGCGCAAGTCAAGTACCAGGCACAGCACTCCCGCAGCCAC	6171
Qy	2074	SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrp	2093
Db	6172	AGCAGATCTCCAAGCACATGACCCGCCAGCCCCCTTGCCCGAGGCCCAAGACCAACTGG	6231
Qy	2094	GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTyrIle	2113
Db	6232	GGCAAGGGCCCTCCAGAGACCAGAAAGCACTTAGAGTTGACACCGAGCTGAGCTGGAATT	6291
Qy	2114	SerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLys	2133

Db	6292	TCAGGAGACCTCTGCCCCCTGGCGGCCAGGAGAGACCCCATCCCCACGGGACTGAAG	6351
Qy	2134	LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu	2153
Db	6352	AAGTGCTACAGCGGTGAGGCCACAGAGCTGCCAGCGCCGGCTACGTCTGCTGGATGAG	6411
Qy	2154	GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly	2173
Db	6412	CAGAGAGACACTATTCGCCGTCACTGCTGTCAGACGGCTCCCAACCCCACTGGGC	6471
Qy	2174	ThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLys	2193
Db	6472	ACAGACCCCTTAACCTTGGGGGCCAGCCCTTGGGGGGCCCTGGAGCCGGCCAGAA	6531
Qy	2194	LysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro	2213
Db	6532	AAACTCAGCCCGCCTAGTATCACCATAGACCCCCCGAGAGCCAAAGTCTCTGGACCCCG	6591
Qy	2214	ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu	2233
Db	6592	CCCAAGCCCTGTATCTGCCTCCGAGAGAGGGCTCGTCCAGCACTCCAAGATCCCTTG	6651
Qy	2234	AlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSer	2253
Db	6652	GCCTCTGGCCCCCTGACAGCATGGCTGCCTCGCCCTCCCAAGAAGATGTGCTGAGT	6711
Qy	2254	LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266
Db	6712	CTCTCCGGTTATCTCTGACCCAGCAGACCTTGACCC 6750	

RESULT 7
ID AAX83482 standard; cDNA; 6783 BP.
XX AAX83482;
XX AC
XX 07-DEC-1999 (first entry)
XX DT
XX Human T-type voltage-gated Ca channel alpha-1-G (hCav1b) cDNA.
DE
XX
XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
XX Homo sapiens.
OS
XX
XX WO929847-A1.
PN
XX
XX 17-JUN-1999.
PD
XX
XX 30-OCT-1998; 98WO-US023161.
PF
XX
XX 05-DEC-1997; 97US-00985809.
PR
XX
XX (LOYO) UNIV LOYOLA CHICAGO.
PA
XX
XX Perez-Reyes E, Cribbs LL;
PI
XX WPI; 1999-394972/33.
DR P-PSDB; AAY14587.
XX
XX
XX New T-type voltage-gated calcium channels.
PT
XX
XX
PS Disclosure; Page 40-49; 138pp; English.
XX
XX This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCav1b. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type

CC channels include short current time, slow activation kinetics near
CC threshold, fast inactivation kinetics and slow tail current. The
CC sequences AAX83481-X83492 represent novel T-type voltage-gated Ca channel
genes from humans and rats. Each of the novel Ca-channels contains a
CC putative IVS4 region comprising the amino acid sequence AAY14598. Cells
CC expressing the T-type voltage-gated calcium channel proteins can be used
CC to screen for drugs which affect calcium channels. Methods are also
CC disclosed for treating a disease or disorder associated with a deficiency
CC in a native T-type calcium channel nucleic acid, e.g. to treat
CC cardiomyopathy, epilepsy, etc

XX Sequence 6783 BP; 1294 A; 2182 C; 1990 G; 1317 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	6783
Score:	11735.50	Matches:	2241
Percent Similarity:	98.16%	Conservative:	1
Best Local Similarity:	98.12%	Mismatches:	1
Query Match:	98.58%	Indels:	41
DB:	2	Gaps:	2

US-09-611-257A-37 (1-2266) x AAX83482 (1-6783)

QY 1 MetAspGluGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
DB 1 ATGACGAGGAGAGGATGAGCGGCGCCGAGAGTCGGGACAGCCCCGAGCTTCATG 60
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyIYARgProGlyProGlySerAlaGluLysAsp 40
DB 61 CGGCTCAACGACCTGTCGGGGCGCGGGGGCGGCGGGCGGGGTCAAGAAAGAGAC 120
QY 41 ProGlySerAlaaspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
DB 121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGCTGCCGTACCCGGCGCTGCCCCGGTGTT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
DB 181 TTCTTCTACTTGAGCCAGGACAGGACGCCCGCGGAGCTGGTGTCTCCGACCGGTCTAAC 240
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
DB 241 CCCTGGTTGAGCGCATCAGCATGTTGGTCATCTTCTCAACTGCGTGACCTGGGCATG 300
QY 101 PheArgProCysGluAspIleAlaCysaspSerGlnArgCysArgIleLeuGlnAlaPhe 120
DB 301 TTCCGGCCATGCGAGGACATCGCTTGACTCCAGCGCTGCCGATCCTGCAGGCTTT 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGly 140
DB 361 GATGACTTCATCTTGCTTCTTTCGCTGGAGATGGTGAAGATGGTGGCTTGGGC 420
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
DB 421 ATCTTTGGGAAAAAGTTTACCTGGGAGACACTTGGAACCGCTTGACTTTTCATCGTC 480
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
DB 481 ATCGCAGGAGATGCTGAGTACTCGCTGGAACCTGCAGAAACGTCAAGCTTCTCAGCTGTCAAG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
DB 541 ACAGTCCGTGTGTCGACCGCTCAGGGCCATTAAACCGGTGCCCCAGCATGCGCATCTT 600
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
DB 601 GTCAAGTGTGCTGATACGCTGCCCATGCTGGCAACGTCCTGCTGCTCTTCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
DB 661 GTCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCAAGGCTGCTTCGAAACCGA 720
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260

DB 721 TGCTTCTTACCTGAGAAATTTCAGCCTCCCTGAGCGGTGACCTGGAGCGCTATTACCAG 780
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
DB 781 ACAGAGAAACGAGATGAGAGCCCTTCATCTGTCTCCAGCAGCGGAGAACGGCATGCGG 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyIYpProProCysGlyLeu 300
DB 841 TCCTGAGAGAAGCGTGCCCAAGCTGCGGGGAGCGGGGGCGGTGAGCCCACTTGCGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
DB 901 GACTATGAGGCTTACAACAGCTCCAGCAACACCACTGTGTCAACTGGAAACGACTACTAC 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
DB 961 ACCAACTGCTCAGCGGGGAGCACAACCCCTTCAAGGGCGCCATCACTTGACAAACATT 1020
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrPValAspIleMet 360
DB 1021 GGCTATGCTTGATCGCCATCTTCCAGGTATCAACGCTGAGAGGGCTGGGTGACATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
DB 1081 TACTTGTGATGATGATGCTCATCTCTTCTACAATTCTACTTCACTTCTCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
DB 1141 GTGGGCTCTTCTTCATGATCAACCTGTGCTGTGTGATTGCCACGCAAGTCTCAGAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
DB 1201 ACCAAGCAGCGGGAAGCCAGCTGATGCGGAGCAGCGGTGTGCGGTCTGTCCAACGCC 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
DB 1261 AGCACCTGCTAGCTTCTTGTAGCCCGGACGCTGCTATGAGAGCTGTCAAGTACCTG 1320
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
DB 1321 GTGTACATCCTTGTAAGGAGCCCGCAGGCTGCTCAGGTCTTCGGGACGAGGTGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
DB 1381 CGGTTGGGCTGCTCAGAGCCCAAGCACCCTCGGGGGCCAGAGAGCCAGCCAGCAGC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
DB 1441 AGCTGCTCTGCTCCCAACCGCGCCTATCCGTCACCACTGTGTGCACCAACCAACAC 1500
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
DB 1501 CATCACCACTACCTACCTGGGCAATGGAGCTTCAGGGCCCCCGGGCCAGCCCGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
DB 1561 ATCCAGGACAGGATGCAATGGGTCCGCGGCTCATGTGCCACCACTTCAGCGCTT 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
DB 1621 GCCCTCCCGGGCCCCCTGGGTGGCGCAGAGTGTGTGCACACAGCTTCAACATGCCGAC 1680
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
DB 1681 TGCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCTCCAGGTCCCACTGAGGCATCC 1740
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
DB 1741 GGCAGACTGTGGCAGCGGGAAGGTGTATCCACCGTGCAACACAGCCCTCCACCGAG 1800
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
DB 1801 ACGCTGAAGAGAAAGCACTAGTAGAGGTGGCTGCAGCTCTGGGCCCCCAACCTCACC 1860

QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisIleLeuGluThrGlnSer 640
| | | | |
Db 1861 AGCCTCAACATCCACCCGGCCCTACAGCTCCATGCACAGAGCTGTGGAGACAGAGCT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysIleSeriSerProCysIleuIysAlaAspSerGly 660
| | | | |
Db 1921 ACAGGTGCCTGGCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAAGCAGACAGCTGGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyIleValGluLeu 680
| | | | |
Db 1981 GCCTGTGTCCAGACAGCTGCCCTACTGTGCCCGGGCCGGGCGAGGGAGGTGAGCTTC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
| | | | |
Db 2041 GCCGACCGTGAATGCTGACTCAGACAGCGAGGCAATTATGAGTTCAACAGAGATGCC 2100
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
| | | | |
Db 2101 CAGCACAGCGACCTCCGGGACCCCCACAGCCGGCGGCAACGAGCTGGGCCAGATGCA 2160
QY 721 GluProSerSerValLeuAlaPheThrPargLeuIleCysAspThrPheArgIleVal 740
| | | | |
Db 2161 GAGCCCAAGCTCTGTGCTGGCTTCTGGAGGCTTAATCTGTGACACCTTCCGAAAAGATTGTG 2220
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
| | | | |
Db 2221 GACAGCAAGTACTTTGGCCGGGGAATCATGATGCCATCTGTGTCAACACACTCAGCATG 2280
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
| | | | |
Db 2281 GGCATCGAATACCAAGAGAGCCCGAGAGCTTACCAGCCCTAGAAATCAGCAACATC 2340
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800
| | | | |
Db 2341 GTCTTCACCAAGCCTTTGGCCCTTGAGATGCTGTGAAGCTGCTGTGTATGTCCTT 2400
QY 801 GlyTyrIleIysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTyr 820
| | | | |
Db 2401 GGCTACATCAAGAATCCCTACCAACATCTTCGATGGTGTCAATTGTGTCTCAGCGTGTGG 2460
QY 821 GluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
| | | | |
Db 2461 GAGATCGTGGCCAGAGGGGGGGCGGCTGTGCTGTGCGGACCTTCCGCTGATGCGT 2520
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
| | | | |
Db 2521 GTGCTGAAGCTGTGTGCGCTTCTGCGGCGCTGCAGCGGAGCTGTGTGCTCATGAAAG 2580
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
| | | | |
Db 2581 ACCATGGAACAAGTGGCCACTTCTGCATGCTGCTATGCTCTTCATCTCATCTTCAGC 2640
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
| | | | |
Db 2641 ATCCTGGGCATGCATCTTCTGGCTGCAGATTGCTCTGAGCGGATGGGACACCCCTG 2700
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTyrAlaIleValThrValPheGlnIleLeu 920
| | | | |
Db 2701 CCAGACCGGAAGAAATTTGACTTCTGCTCTGGGCCATCGTCACTGTCTTTCAGATCCTG 2760
QY 921 ThrGlnGluAspTyrPAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrAla 940
| | | | |
Db 2761 ACCCAGAGAGACTGGAACAAGTCTCTTACAATGTATGGCTCCACAGTCGTCTGGGCG 2820
QY 941 AlaIleuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
| | | | |
Db 2821 GCCCTTAATTTCATTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTGTGCTC 2880
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
| | | | |
Db 2881 GCCATTCTGTGTGAGGGCTTCCAGCGCGAG----- 2910

QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
| | | | |
Db 2911 -----GGAGATGCCCAACAAGTCCGAA 2931
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysIleCysLeu 1020
| | | | |
Db 2932 TCAGAGCCCGATTCTTCTTCAACCCAGCTTGATGTGTGATGGGACAGAGAAGTCTTG 2991
QY 1021 AlaLeuValSerLeuGlyLysHisProGluLeuArgLysSerLeuLeuProProIle 1040
| | | | |
Db 2992 GCCTGTGTCTCCCTGGAGAGCACCCGAGCTGCGGAAGAGCTTGCTGCCGCTTCTCATC 3051
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
| | | | |
Db 3052 ATCCACACGGCCGCCACACCCATGTGCTGCCCAAGAGCACACACGCGCTGGCGAG 3111
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
| | | | |
Db 3112 GCGGTGGCCCTGCGTCCGCGCCGACAGACAGCGGGTGGCAGAGCTGGGGCGGCC 3171
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSerAlaAla 1100
| | | | |
Db 3172 CACGAGATGAAGTCAACCCCAAGCCGCCGACGCTCTCCGCACAGCCCTGAGCGCTGCA 3231
QY 1101 SerSerTyrPheSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
| | | | |
Db 3232 AGCAGCTGAGCACAGCGCGCTCCAGCCGGAACAGCTCGGCGGTGCAACCAAGCTGTAAG 3291
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnSerGln 1140
| | | | |
Db 3292 CGGAGAAGCCCAAGTGGAGAGCGCGGTCCCTGTGTGCGGAGAAAGCCAGAGAGCCAG 3351
QY 1141 AspGluGluGlnSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
| | | | |
Db 3352 GATGAAGAGAGAGCTCAGAAGAGAGCGGGCCAGCCCTGCGGGCAGTGACCATCGCCAC 3411
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
| | | | |
Db 3412 AGGGGGTCCCTGGAGCGGGAGGCCAAGATTCTTTGACCTGCCACACACTGCAGGTG 3471
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
| | | | |
Db 3472 CCAGGGCTGCATGCACCTGCCAGTGGCGGAGGTCTGCTTGTGAGCACCAAGACTGCAAT 3531
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
| | | | |
Db 3532 GGCAAGTCGGCTTCAAGGGCGCCTGGCCCGGCGCTGCGGCTGATGACCCCACTGGAT 3591
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTyrIle 1240
| | | | |
Db 3592 GGGGATGACGCCGATGACGAGGGCAACCTGAGCAAAAGGGAACGGGTCCGCGTGATC 3651
QY 1241 ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTyrSerAlaTyrIlePhePro 1260
| | | | |
Db 3652 CGAGCCCGACTCCCTGCTTGTGCTGCTGCAGCAGAGACTCCTGTGTCAGCTTATCCCT 3711
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisIleMetPheAspHis 1280
| | | | |
Db 3712 CCTCAGTCCAGGTTCGCGCTCTGTGTACCGGATCATCACCCACAGATGTTGACCAC 3771
QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
| | | | |
Db 3772 GTGTCTCTTGCATCACTTCTCTTAACGTGATCACCATGCGCATGGAGCGCCCAAAATT 3831
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
| | | | |
Db 3832 GACCCCCACAGCGGTGAACGATCTTCTTGACCCCTCCAAATTAATCTTACCGCAGATC 3891
QY 1321 PheLeuAlaGluMetThrValLysValAlaLeuGlyTyrCysPheGlyGluGlnAla 1340
| | | | |
Db 3892 TTCTGTGCTGAATGACAGTGAAGTGTGGCACTGGGCTGTGCTTCCGGGAGCAGCGCG 3951
QY 1341 TyrLeuArgSerSerTyrPAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360

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Db 3952 TACGCGGAGCAGTTGGAAAGCTGCTGACGGGCTGTGGTCTCATCTCCGTCAATCGAC 4011
QY 1361 ILeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4012 ATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCTGGGCATGTGTGAGGGTGTG 4071
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
Db 4072 CGGCTGCTCGGACCCCTGCGCCCGCTCAGAGGTGATCAGCCGGCGCGCAGGGCTGAAGCTG 4131
QY 1401 ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420
Db 4132 GTGGTGAGACGCTGATGTCTCTCACTGAACCCATCGGCACATGTGTAGTCATCTGCTGT 4191
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
Db 4192 GCCTTCTTCATCATTTTCCGCATCTTGGGGGTGCAGCTCTTCAAAGGAAGTTTTCGTG 4251
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
Db 4252 TGCCAGGGCGAGGATACCAGGAACATCAACAATAATCCGACTGTGCCGAGGCCAGTTAC 4311
QY 1461 ArgTTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db 4312 CGGTGGGTCCGGCAAGTACAACTTTGACAACTTGCCAGGCCCTGATGTCCCTGTTC 4371
QY 1481 ValLeuAlaSerLysAspGlyTTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
Db 4372 GTTTTGCCCTCAAGATGGTGGTGACATCATGATGCGGCTGATGCTGTGGGC 4431
QY 1501 ValAspGlnInProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
Db 4432 GTGACACGACGCCCATCATGAACCAACCCCTGATGCTGTACTTCATCTGTCTTC 4491
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
Db 4492 CTGCTCATGTGGCCTTCTTGTCTGTAACATGTTGTGGGTGTGGTGAGAACTTC 4551
QY 1541 HisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeu 1560
Db 4552 CACAAGTGTGGGAGCACCAAGAGGAAGAGGCGCCGGCGGGGAGAGAACGCCCTTA 4611
QY 1561 ArgArgLeuGluLysLysArgArg----- 1568
Db 4612 CGAAGACTGGAAAAAGAGAAGATCTAATGCTGACGATGTAATTGCTTCGGGACG 4671
QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPhe 1582
Db 4672 TCAGCCAGCGCTGCTCAGAAAGCCCGTCAAACTTACTACTCCGACTACTCCGCTTC 4731
QY 1583 ArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThrGlyVal 1602
Db 4732 CGGCTCCTCGTCAACCACTGTGCAACGCACTACTGACTCTTCATCACAGGTGTC 4791
QY 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622
Db 4792 ATCGGGCTGAACGTGTCTACCATGGCCATGGAACACTACCAAGCAAGCCCGAGATTCTGAT 4851
QY 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642
Db 4852 GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTCACTTGTCTTGAGTCAGTTTTC 4911
QY 1643 LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTTrpAsnGlnLeuAspLeu 1662
Db 4912 AAACCTGTGGCCTTGGTTCCGTCGGTCTTCCAGACAGGTGAAACAGCTGGACCTG 4971
QY 1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer 1682
Db 4972 GCCATTGTGCTGTCCATCATGGGCATCAGCTGAGGAATCGAGGTCAACGCTCG 5031
QY 1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702
|||||

Db 5032 CTGCCCATCAACCCACCATCATCCGCATCATGAGGGTCTGCGCATTGCCCGAGTGCTG 5091
QY 1703 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722
Db 5092 AAGCTGTGAAGATGGCTGTGGGCATGCGGGCGCTGTGACACAGGTGATGACAGGCCCTG 5151
QY 1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAlaIleLeu 1742
Db 5152 CCCAGGTGGGGAACCTGGGACTTCTCTTCATGTGTGTTTTCATCTTGGACAGCTCTG 5211
QY 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGlnGlyLeuGly 1762
Db 5212 GGCGTGAGCTCTTGGAGACCTGGAAGTGTGACGACACACACACCCCTGTAGGGCCTGGGC 5271
QY 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782
Db 5272 CGTCATGCACTTTCGGAACCTTGGCATGTGGCTTCTTAACCTCTTCCGAGTCTCCACA 5331
QY 1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802
Db 5332 GGTGACAAATTGGAATGGCATTAAGAAAGACACCCCTCGGGAAGTGTGACCAAGATCCACC 5391
QY 1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822
Db 5392 TGCTACAAACGCTCATCTGCCTATCTACTTGTGTCTTCTGCTGACGGCCAGTTTC 5451
QY 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842
Db 5452 GTGCTAGTCAACGTGTGATGCCGTGTGATGAAGCACCTGGAGAGACAAAGAG 5511
QY 1843 AlaIleGlnGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerPro 1862
Db 5512 GCCAAGAGGAGGCCGAGCTAGAGGCTGAGCTGAGTGAAGATGAAGACCTCAGCCCC 5571
QY 1863 GlnProHisSerProLeuGlySerProPheLeuTTrpProGlyValGluGlyProAspSer 1882
Db 5572 CAGCCCCACTCGCCACTGGGAGACCCCTTCTCTGGCTGGGGTGCAGGGGCCCGACAGC 5631
QY 1883 ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902
Db 5632 CCCGACAGCCCCAAGCCTGGGCTCTGCACCCAGCGGCCACCGGAGATCAGCTCCAC 5691
QY 1903 PheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyProAspLeu 1922
Db 5692 TTTTCCCTGAGACACCCACGATGCAGCCCAACCGAGCTGCCAGGACCAAGACTTA 5751
QY 1923 LeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMet 1942
Db 5752 CTGACTGTCCGGAAGTCTGGGTTCAGCCGAACGCACTCTGCCCAATGACAGTACATG 5811
QY 1943 CysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTTrpGlyLeuProLys 1962
Db 5812 TGTCCGCAATGGGAGCACTGCCGAGGGGCCCTGGGACACAGGGGCTGGGGCTCCCCAAA 5871
QY 1963 AlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeu 1982
Db 5872 GCTCAGTCAAGGCTCCGTCTGTTCCTTCACTCCAGCCAGCAGATACCAGCTACATCCTG 5931
QY 1983 GlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTTrpGlyThr 2002
Db 5932 CAGCTTCCCAAAGATGACACTCATCTGCTCCAGCCCCACAGCGCCCAACCTGGGGCAC 5991
QY 2003 IleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGln 2022
Db 5992 ATCCCAAACTGCCCCACAGGAGCGCTCCCTTGGCTCAGAGGCCACTGAGCGCCAG 6051
QY 2023 AlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeu 2042
Db 6052 GCAGCAATAAGCACTGACTCTCTTGAAGCTTCAAGGCTGGGCAAGCCGGAAGACTGCTG 6111
QY 2043 AlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTTrpGlyGlnSer 2062
Db 6112 GCAGAGGTGAGTGGCCCTCCCGCCCTGCGGCCGCTACTCTTCTGGGGCCAGTCA 6171
|||||

QY 2063 SerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMetThrPro 2082.
DB 6172 AGTACCAGGCGACAGCACTCCCGCAGCCACAGACAGATCTCCAAGCATGACCCCG 6231
QY 2083 ProAlaProCysProGlyProGluProAsnTrpGlyLysGlyProProGluThrArgSer 2102
DB 6232 CCAGCCCCCTTGCCAGGCCCAAGAACCTAGTGGGCAAGGGCCCTCCAGAGACCAGAAC 6291
QY 2103 SerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGly 2122
DB 6292 AGCTTAGAGTTGACACGAGAGCTGAGCTGATTTCAGAGACCTTCTGCCCTGGCGGC 6351
QY 2123 GlnGluGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaGlnSer 2142
DB 6352 CAGGAGAGCCCCCATCCCAAGGAGCTGAAGAAGTGCTACAGCGTGAGGCCAGAGC 6411
QY 2143 CysGlnArgArgProThrSerSerTrpLeuAspGluGlnArgArgHisSerIleAlaValSer 2162
DB 6412 TGCCAGCGCCGCTTACGCTCCTGGCTGATGACAGAGAGACACTATCGCCGTACGC 6471
QY 2163 CysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGlyGln 2182
DB 6472 TGCCTGACACAGCGGCTCCCAACCCCACTGGGACACAGACCCCTTAACCTTGGGGCCAG 6531
QY 2183 ProLeuGlyGlyProGlySerArgProLysLysLeuSerProProSerIleThrIle 2202
DB 6532 CCTCTTGGGGGCGCTGGGAGCCGGCCCAAGAAAACTCAGCCCGCTAGTATCACCAT 6591
QY 2203 AspProProGluSerGlnGlyProArgThrProProSerProGlyIleCysLeuArgArg 2222
DB 6592 GACCCCCCGAGAGCAAGTCTCTCGACCCCGCCAGCCCTGTATCTGCTCCGAGG 6651
QY 2223 ArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSerMetAla 2242
DB 6652 AGGGCTCCGTCAGCACTCCAAGATCCCTTGGCCTCTGACCCCTGACAGCATGGCT 6711
QY 2243 AlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAla 2262
DB 6712 GCCTCGCCCTCCCAAGAAAGATGTGTGTGTCTCTCCGGTTATCTCTGACCCAGCA 6771
QY 2263 AspLeuAspPro 2266
DB 6772 GACCTGAGACCC 6783
RESULT 8
AAx83483
ID AAx83483 standard; cDNA; 6804 BP.
XX
AC AAx83483;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human T-type voltage-gated Ca channel alpha-1-G (hCav1.1) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion; activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Homo sapiens.
XX
PN WO9929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.

DR P-PSDB; AAY14588.
XX
PT New T-type voltage-gated calcium channels.
XX
PS Disclosure; Page 49-58; 138pp; English.
XX
CC This sequence represents the coding region for a human T-type voltage-gated calcium (Ca) channel alpha-1-G designated hCav1.1. Voltage gated channels are membrane bound glycosylated proteins formed of several CC subunits. The large alpha subunits form a pore in the membrane that is CC selective for a given ionic species. Each alpha subunit contains 4 CC domains (I, II, III and IV) and each domain contains 6 putative CC transmembrane helical segments (S1-S6). T-type Ca channels are activated CC at a lower voltage than L- or N-type channels. Characteristics of T-type CC channels include short current time, slow activation kinetics near CC threshold, fast inactivation kinetics and slow tail current. The CC sequences AAx83481-X83492 represent novel T-type voltage-gated Ca channel CC genes from humans and rats. Each of the novel Ca-channels contains a CC putative IVS4 region comprising the amino acid sequence AAY14598. Cells CC expressing the T-type voltage-gated calcium channel proteins can be used CC to screen for drugs which affect calcium channels. Methods are also CC disclosed for treating a disease or disorder associated with a deficiency CC in a native T-type calcium channel nucleic acid, e.g. to treat CC cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6804 BP; 1301 A; 2186 C; 1998 G; 1319 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 6804
Score: 11727.00 Matches: 2240
Percent Similarity: 97.82% Conservative: 1
Best Local Similarity: 97.77% Mismatches: 2
Query Match: 98.51% Indels: 48
DB: 2 Gaps: 2
US-09-611-257A-37 (1-2266) x AAx83483 (1-6804)
QY 1 MetAspGluGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
DB 1 ATGACGAGAGAGAGATGAGCGGGCGCCGAGAGTCCGGACAGCCCGAGACTTATG 60
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyIleArgProGlyProGlySerAlaGluLysAsp 40
DB 61 CGGCTCAACGACTGTCGGGGCGCGGGGGCGGGCGGGGGGTACAGAGAAAGGAC 120
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
DB 121 CCGGGCAGCGCGGACTCCGAGCGCGAGGGGCTGCCGTACCCGCGCTGGCCCCGTGTT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
DB 181 TTCTTCTACTTGACCAAGACAGACCGCGCGGAGCTGGTGTCTCCGACAGGTCTGTAAC 240
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
DB 241 CCTGTGTTGAGCGCATCAGCATGTGTGATCTTCTCAACTGCGTGACCTGGGCAATG 300
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
DB 301 TTCCGGCCATGCGAGACATCGCTGTGACTCCAGCGCTGCCGATCTGCAGAGCCTTT 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
DB 361 GATGACTTCATCTTTCCTTCTTTCGCGTGAGATGTGTGAAGATGTGGCCTTGGGC 420
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
DB 421 ATCTTTGGAAAAAGTGTACTCTGGGAGACATTGAAACCGGCTTGAATTTCATCGTC 480
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
DB 481 ATCGCAGGAGATGTGAGTACTGCTGGAAGCTGACAAAGTACGCTTCTCAGCTGTACAG 540

QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	541	ACAGTCCGTGTGCTGCACCGCTCAGGGCCATTAACTGGGTGCCACGATGCGCATCTT	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetIleuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	601	GTCACGTTGCTGCTGGATACGCTGCCCATGCTGGGCAAGTCCTGCTCTCTTCTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
Db	661	GTCTTCTTCATCTTCGGCATCTGTCGGCTCCAGCTGTGGGCAGGGCTGCTTCGGAACCGA	720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
Db	721	TGCTTCTTACCTGAGAAATTTCAGCCTCCCTCGAGCGTGGAACCTGGAGCGCTATTACCAAG	780
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
Db	781	ACAGAGAACGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGGCATGCCG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
Db	841	TCCTGCAGAACGCTGCCACGCTGCGCGGAGCGGGCGGTGGCCCACTTGCGGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
Db	901	GACTATGAGCCTACACAGCTCCAGCAACACCACTGTGTCAACTGGAACTACTACTAC	960
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheGlyAlaIleAsnPheAspAsnIle	340
Db	961	ACCAACTGCTCAGCGGGGAGCAACAACCCCTTCAGGGCGCCATCAACTTGGACAACATT	1020
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet	360
Db	1021	GGCTATGCTGATCGGCATCTTCCAGGTCACTACGCTGGAGGGCTGGGTGACATCATG	1080
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
Db	1081	TACTTTGTATGATGATGCTCATCTTCTTCAATTTCACTTCACTTCACTTCACTCATC	1140
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
Db	1141	GTGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGTGATTGCCACGAGTTCTCAGAG	1200
QY	401	ThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1201	ACCAAGCAGCGGGAAAGCCAGCTGATGCGGAGCAGCGTGTCTCTGTCCACAGCC	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuYsTyrLeu	440
Db	1261	AGCACCTGTGCTAGCTTCTCTGAGCCCGGCAGCTGTATGAGGAGCTGCTCAAGTAACTTG	1320
QY	441	ValTyrIleLeuArgGlySAlaAlaArgArgLeuAlaGlnValSerArgAlaIaGlyVal	460
Db	1321	GTGTACATCCTTCGTAAAGCAGCCCGCAGAGCTGGTCAAGTCTCTCGGCAGCAGGTGTG	1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
Db	1381	CGGGTTGGGCTGCTCAGCAGCCCAAGCACCCTCGGGGGCCAGGAGACCCAGCCACAGC	1440
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
Db	1441	AGCTGCTCTGCTCCACCGCCGCTATCCGTCCACCACTGTGTGACCAACCAACCAAC	1500
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
Db	1501	CATCACCACTACCACTGGGCAATGGGACGCTCAGGGGCCCCCGGGCCAGCCCGGAG	1560
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
Db	1561	ATCCAGGACAGGGATGCCAATGGGTCCCGCGGCTCATGTGCCACCACTCGACGCTT	1620
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560

Db	1621	GCCTCTCCGGGGCCCCCCTGGTGGCGAGAGTCTGTGCACAGCTTCTACCATGCCGAC	1680
QY	561	CySHiSleuGIuProValArgCysGlnAlaProProProArgSerProSerGIuAlaSer	580
Db	1681	TGCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTGAGGCATCC	1740
QY	581	GIYArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGIu	600
Db	1741	GGCAGACTGTGGGACGCGGAAGGTGTATCCACCCTGCACACCAAGCCTCCACCGGAG	1800
QY	601	ThrLeuLysGIuLysAlaLeuValGIuValAlaAlaSerSerGIuProProThrLeuThr	620
Db	1801	ACGCTGAAGAGAGAAGGCACTAGTAGAGTGGCTGCCAGCTCTGGGCCCAACCTCACC	1860
QY	621	SerLeuAsnIleProProGIuProTyrSerSerMetHisLysLeuGIuThrGlnSer	640
Db	1861	AGCCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAAGCTGCTGGAGACACAGAGT	1920
QY	641	ThrGIuAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGIy	660
Db	1921	ACAGTGCCTGCCAAAGCTCTTGCAAGATCTTCCAGCCCTTGCTTGAAGCAGACAGTGA	1980
QY	661	AlaCysGIyProAspSerCysProTyrCysAlaArgAlaGIyAlaGIyGIuValGIuLeu	680
Db	1981	GCCTGTGGTCCAGACAGCTGCCCTACTGTGCCGGGGCCGGGCGAGGGAGGTGAGCTC	2040
QY	681	AlaAspArgGIuMetProAspSerAspSerGIuAlaValTyrGIuPheThrGlnAspAla	700
Db	2041	GCCGACCGTGAATGCTTGACTCAGACAGCGAGCAAGTTATGAGTTACACAGGATGCC	2100
QY	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGIyProAspAla	720
Db	2101	CAGCACAGCGAAGCTCCGGGACCCCAAGCCGGGCAACGAGAGCTGGGGCCAGATGCA	2160
QY	721	GIuProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal	740
Db	2161	GAGCCAGCTCTGTGCTGGCCTTCTGAGGCTTAATCTGTGACACCTTCGAAAGATTGTG	2220
QY	741	AspSerLysIlePheGlyArgGIyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760
Db	2221	GACAGCAAGTACTTTGGCCGGGAATCATGATGCCATCCTGCTCAACACTCAGCATG	2280
QY	761	GIyIleGIuTyrHisGIuGlnProGIuGIuLeuThrAsnAlaLeuGIuIleSerAsnIle	780
Db	2281	GGCATCGAATACCAAGAGCAGCCCGAGAGCTTACCAACGCCCTAGAAATCAGCAACATC	2340
QY	781	ValPheThrSerLeuPheAlaLeuGIuMetLeuLeuLysLeuLeuValTyrGIyProPhe	800
Db	2341	GTCTTCACCAAGCTCTTTGCCCTGAGATGCTGTGAAGCTGCTGTGTATGTGCCCTTT	2400
QY	801	GIyTyrIleLysAsnProTyrAsnIlePheAspGIyValIleValValIleSerValTrp	820
Db	2401	GGCTACATCAAGATCCCTACACATCTTCGATGCTGTCATTTGTGTCATCAGCGTGTG	2460
QY	821	GIuIleValGIyGlnGlnGIyGIyGIyLeuSerValLeuArgThrPheArgLeuMetArg	840
Db	2461	GAGATCGTGGCCAGCAGGGGGCGGCTGTGCTGCTGCGGACCTTCGGCCTGATGCGT	2520
QY	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
Db	2521	GTGCTGAAGCTGGTGGCTTCTGCGCGCTGCAGCGGAGCTGTGTGTCTCATGAAG	2580
QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer	880
Db	2581	ACCATGGAACAAGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTCAGC	2640
QY	881	IleLeuGIyMetHisLeuPheGIyCysLysPheAlaSerGIuArgAspGIyAspThrLeu	900
Db	2641	ATCTGGGCGATCATCTCTTCGGCTGCAGTTTGCTCTGAGCGGGATGGGACACCCCTG	2700
QY	901	ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu	920

Db 2701 CCAGACCGGAAGATTTTGACTCCTTGCTTGCGCCATCGTCACTGCTTTTCAGATCCTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
|||||
Db 2761 ACCCAGAGAGACTGGAACAAAGTCCCTTACATGATGCGCTCCACGTCGCTCGGCGC 2820
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
|||||
Db 2821 GCCCTTATTTCATGCGCTCATGACCTTCGCAACTACGTGCTCTTCAATTGTGTC 2880
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGlnIleSerLysArgGluAspAlaSerGly 980
|||||
Db 2881 GCCATTCTGTGAGGGCTTCCAGGCGGAG----- 2910
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGlu 1000
|||||
Db 2911 -----GGAGATGCCAACAAAGTCCGAA 2931
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020
|||||
Db 2932 TCAGAGCCCGATTTCTTCTCACCCAGCCTTGATGTGATGGGACAGAGAAGAGTGTG 2991
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
2992 GCCTTGGTGTCCTGGGAGACACCCGAGAGTCGGAAAGACCTGCTCGCTCTCATC 3051
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
|||||
Db 3052 ATCCACACGGCCGCCACACCCATGTGCTGCCAAGACACACAGCGGGCCTGGCGAG 3111
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
|||||
Db 3112 GCGCTGGGCCCTGCTCGCGCCGCCACACAGCAGCGGGTGGCAGAGCCTGGGGCGGCC 3171
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
|||||
Db 3172 CACGAGATGAAGTCAACCGCCAGCGCCGCGAGCTTCCGCACAGCCCCCTGGAGCGCTGCA 3231
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
|||||
Db 3232 AGCAGCTGGACACGAGCGGCTCCAGCCGGAACGCTCGCGCTGCACCCAGCCTGAAG 3291
QY 1121 ArgArgSerProSerGlyGluArgArgSerSerLeuLeuSerGlyGlyGlnGluSerGln 1140
|||||
Db 3292 CGGAGAAGCCCAAGTGAAGCGGCGGTCCCTGTGTCCGGAGAAGGCCAGAGACCAG 3351
QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
|||||
Db 3352 GATGAAGAGAGAGCTCAAGAGAAGAGCGGGCCAGCCTCCGGGCACTGACCATCGCCAC 3411
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
|||||
Db 3412 AGGGGGTCCCTGGAGCGGAGGCCAAGAGTTCCTTTGAACCTGCCAGACACACTGCAGGTG 3471
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
3472 CCAGGGCTGCATCGCACTGCAGTGGCGGAGGGTCTCTTGAGCACCAGACTGCAAT 3531
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeuAsp 1220
3532 GGCAAGTCGGCTTCAGGGCGCTGGCCGGCGGCTGCTGATGACCCCACTGGAT 3591
Db 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
|||||
Db 3592 GGGGATGACCGCCGATGACGAGGGCAACTGAGCAAGGGGAACGGGTCCGGCGGTGATC 3651
QY 1241 ArgAlaArgLeuProAlaCysGlyTrpLeuGluArgAspSerTrpSerAlaTyrIlePhePro 1260
|||||
Db 3652 CGAGCCCGAATCCCTGCTGCTGCTCGAGCGAGACTCCTGTGTCAGCCTACATCTTCCCT 3711
QY 1261 ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis 1280
|||||
Db 3712 CCTCAGTCCAGGTTCCGCTCTGTGTCAACGGATCATCACCAAGAGTTCGACCAC 3771

QY 1281 ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
|||||
Db 3772 GTGTCCTGTTCATCATCTTCTTAAGTGCATCACCATCGCATGAGCGCCCAAAATT 3831
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
|||||
Db 3832 GACCCCAACAGCGCTGAACGCATCTTCTGACCCCTCCCAATTACATCTTACCCGAGTC 3891
QY 1321 PheLeuAlaGluMetThrValLysValAlaAlaLeuGlyTyrCysPheGlyGluGlnAla 1340
|||||
Db 3892 TTTCTGCTGAATGACAGTGAAGTGGTGGCACTGGGCTGTGCTTCGGGAGCAGCGC 3951
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
3952 TACCTCGGAGCAGTTGGAACGTGCTGACCGGCTGTGGTGTCTCATCTCCGTCAATCAGC 4011
Db 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
|||||
Db 4012 ATTCTGTGTCCATGTCTCTGACAGCGGCACCAAGATCTGGGCATGCTGAGGGTGTG 4071
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
4072 CGGCTGCTGGGACCTTGCGCCGCTCAGGGTGATCAGCCGGCGGCAGGGCTGAAGCTG 4131
QY 1401 ValValGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
4132 GTGTGGAGACGCTGATGTCTCTACGTAAACCATCGGCAACATTGTAGTCATCTGTCT 4191
Db 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
4192 GCCTTCTTCATCATTTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAGGAAGTTTTCGTG 4251
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr 1460
4252 TGCCAGGGCGAGGATACAGGAACATCACCAATAAATCGACTGTGCGAGGCCAGTTAC 4311
Db 1461 ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
4312 CGGTGGGTCCGGCAAGTACAACTTTGACAACTTGGCCAGGCCCTGATGTCCCTGTTC 4371
QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly 1500
4372 GTTTTGCCCTCCAGGATGTTGGTGGACATCATGTACGATGGCTGATGCTGTGGC 4431
Db 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe 1520
4432 GTGACCAAGACGCCCATCATGAACCAACACCCCTGATGCTGCTGTAATTCATCTCGTTC 4491
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
4492 CTGCTCATTTGGCTTCTTGTCTCTGAACATGTTGTGGGTGTGCTGTGAGAACTTC 4551
Db 1541 HisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLysArgLeu 1560
4552 CACAAGTGTGGCAGCACAGAGAGAGAGAGGCCCGGCGGAGAGAGAGCGCTTA 4611
QY 1561 ArgArgLeuGluLysLysArgArg----- 1568
4612 CGAAGACTGAGAAAGAAGAGAGTAAAGAGAAGACAGATGCTGATCTAATGCTGAC 4671
Db 1569 -----LysAlaGlnCysLysProTyr 1575
4672 GATGTAATTGCTTCCGGCAGCTCAGCCAGCGCTGCGTCAAGAGCCCAACTTAC 4731
QY 1576 TyrSerAspTyrSerArgPheArgLeuLeuValHisHisLysCysThrSerHisTyrLeu 1595
4732 TACTCCGACTACTCCGCTTCCGGCTCTCTGTCACCACTTGTGACCAAGCACTACTCTG 4791
Db 1596 AspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyr 1615
4792 GACCTTTCATCACAGGTGTATCGGGCTGAACGTGTCAACCATGGCCATGAGACACTAC 4851

QY	1616	GLNGLNPROGLNILEUASPGLUALALEULYSILECYASNTYRILEPHERVALILE	1635
DB	4852	CAGCAGCCCCAGATTCTGATGAGGCTCTGAAGATCTCAACTACATCTTCACTGTCATC	4911
QY	1636	PHEVALLEUGLUSERVALPHELYSLEUVALALAPHEGLYPHEARGARGPHEPHEGINASP	1655
DB	4912	TTTGCTTGAGTCAAGTTTTCAAACTGTGTGGCCTTTGTTTCCGTGGTTCTTCAGGAC	4971
QY	1656	ARGTRPASNGLNLEUASPLEUALALEVALLEULEUSERILEMETGLYILERTHRLEUGLU	1675
DB	4972	AGGTGAACACGACTGCACTGGCCATTGTGTGCTGTGTCATCATGGCATCAGCGTGAG	5031
QY	1676	GLULLEGLUVALASNALASERLEUPROILEASNPROTHRILEILEARGILEMETARGVAL	1695
DB	5032	GAAATCGAGGTCAACGCCCTCGCTGCCCATCAACCCCACTCATCCGCATCATGAGGTTG	5091
QY	1696	LEUARGILEALARGVALLEULYSLEULEULYSMETALAVAGLYMETARGALALEULEU	1715
DB	5092	CTGCGCATTTGCCGAGTGTGAAGCTGCTGAAGATGGCTGTGGCATGCGGGCGCTGCTG	5151
QY	1716	ASPTHRVALMETGLNALALEUPROGLNVALGLYASNLEUGLYLEULEUPHEMETLEULEU	1735
DB	5152	GACACGGTGATGACAGCCCTGCCAGGTGGGAACCTGGGACTTCTTTCATGTTGTTG	5211
QY	1736	PHEPHEILEPHEALALALEUGLYVALGLULEUPHEGLYASPLEUGLUCYASPGJUTHR	1755
DB	5212	TTTTTCATCTTTGACGCTCTGGGCGTGAGCTCTTTGGAGACCTGGAGTGTGACGAGACA	5271
QY	1756	HISPROCYSGULYLYEUGLYARGHISALATHRPHEARGNPHEGLYMETALAPHELEU	1775
DB	5272	CACCCCTGTGAGGGCGCTGGGCCGTATGCCACCTTTCGGAACCTTGGCATGGCCCTCCTA	5331
QY	1776	THRLEUPHEARGVALSERTHRGLYASPASNTRPASNGIYILEMETLYSASPTHREUARG	1795
DB	5332	ACCCCTCTCCGAGTCTCCACAGGTGACAATTGGAATGGCATTATGAAGACACCCCTCCGG	5391
QY	1796	ASPCYSASPGINGLUSERTHRRCYSTYRASNTHRVALILESERPROILETYRPHENVALSER	1815
DB	5392	GACTGTGACCAAGAGTCCACTCTTACAACACCGGTCACTTCTGCCCTACTTGTGTCTC	5451
QY	1816	PHEVALLEUTHRALAGLNPHENVALLEUVALASNVALILEALAVALLEUMETLYSHIS	1835
DB	5452	TTCTGTCTGACGCGCCCACTTCTGTGTAGTCAACGTGTGATCGCCGTGTATGAAGCAC	5511
QY	1836	LEUGLUGLUSERASNLYSGLUALALYSGULUALAGLULEUGLUALAGLULEUGLLEU	1855
DB	5512	CTGGAGGAGAGCAACAGAGAGGCCAAGAGAGAGGCCGAGCTAGAGCTGAGCTGAGCTG	5571
QY	1856	GLUMETLYSTHRLUSERPROGLNPROHISSEPROLEUGLYSERPROPHLEUTHRPRO	1875
DB	5572	GAGATGAGAGACCCCTCAGCCCCCAGCCCCCACTCGCCACTGGGACAGCCCTTCTGTGGCT	5631
QY	1876	GLYVALGLUGLYPROASPSSERPROASPSSERPROLYSPROGLYALALEUHIISPROALALA	1895
DB	5632	GGGGTCGAGGGCCCCCGACAGCCCCGACAGCCCCAAGCTGGGGCTCTGCACCCACGCGCC	5691
QY	1896	HISALARGSERALASERHISPHESERLLEUGLUHIISPROTHRMETGLNPROHIISPROTHR	1915
DB	5692	CACGCGAGATCAGCCTCCCACTTTCTCCTGAGACACCCACGATGACGCCCCACCCACG	5751
QY	1916	GLULEUPROGLYPROASPSSERLEUTHRVALARGLYSERGLYVALSERARGTHRHIISER	1935
DB	5752	GAGCTGCCAGGACCACTTACTGACTGTGCGGAAGTCTGGGGTCAGCCGAACGCACTCT	5811
QY	1936	LEUPROASNASPSERTYRMETCYARGHISGLYSERTHRAJAGLUGLYPROLEUGLYHIS	1955
DB	5812	CTGCCCAATGACAGCTACTGTGTGGCATGAGACACTGCCGAGGGGCCCTGGGACAC	5871
QY	1956	ARGGLYTRPGLYLEUPROLYSALAGLINSERGLYSERVALLEUSERVALHISSERGLNPRO	1975
DB	5872	AGGGGCTGGGGGCTCCCCAAAGCTCAGTCAGGCTCCGCTTGTCCGTTCACTCCACGCCA	5931
QY	1976	ALASPTHRSERTYRILELEUGLNULEUPROLYSASPALAPROHISLEULEUGLNUPROHIS	1995

D	b			GCAGATACCAGCTACATCCTGACGCTTCCCAAGATGACCATTCATCTGTCCAGCCCCAC	5932
O	y			SerAlaProThrTrpGlyThrIleProLysLeuProProProGlyArgSerProLeuAla	1996
D	b			AGCGCCCCAACCTGGGGCACCATCCCACAACTGCCCCACAGACGCTCCCTTTGGCT	5992
O	y			GlnArgProLeuArgArgGlnAlaIleArgThrAspSerLeuAspValGlnGlyLeu	2016
D	b			CAGAGGCCACTCAGCGCCAGCGACGACAATAAGACTGACTCTTGACGTTCAAGGTCTG	6052
O	y			GlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAla	2036
D	b			GGCAGCCGGGAAGACCTGCTGCGACAGGTAGTGGCCCTCCCGCCCTGGCCGGGCC	6112
O	y			TyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLys	2056
D	b			TACTCTTTCTGGGGCCAGTCAAGTACCAGGACAGACAGCAGCAGCAGCAGCAGCAAAG	6172
O	y			IleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLys	2076
D	b			ATCTCCAAGACATGACCCCGCAGCCCTTGCCAGGCCAAGAACCACCTGGGGCAAG	6232
O	y			GlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGly	2096
D	b			GGCCCTCCAGAGACCAAGAAGACGCTTAGCTTGACACGAGCTGAGCTGGATTTCAGGA	6292
O	y			AspLeuLeuProProGlyGlyGlnGlnGluProProSerProArgAspLeuLysCys	2116
D	b			GACCTCTGCCCCCTGGCGGCCAGAGAGACCCCATCCCCACGGGACTGAAGAAGTGC	6352
O	y			TyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArg	2136
D	b			TACAGCGTGAAGGCCACAGAGCTGCCAGCCCGGCTTACGCTCTGGCTGATGACAGAGG	6412
O	y			ArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAsp	2156
D	b			AGACACTCTATCGCCGTGACGTGCTGGACAGCGGCTCCCAACCCCACTGGGCACAGAC	6472
O	y			ProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeu	2176
D	b			CCCTTAACCTTGGGGGCCAGCCTCTTGGGGGGCCTGGAGCGGGCCCAAGAAAAACTC	6532
O	y			SerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSer	2196
D	b			AGCCCGCCTAGTATCACCATAGACCCCCCGAGAGCCAAAGTCTCGGACCCCGCCAGC	6592
O	y			ProGlyIleCysLeuArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSer	2216
D	b			CCTGTATCTGCTCCGAGAGAGGGCTCCTCCAGCAGCTCCAAGATCTCTTGCCCTCT	6652
O	y			GlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSer	2236
D	b			GGCCCCCCTGACAGCATGGCTGCTGCTCCCAAGAAAAGATGTCTGAGTCTCTCC	6712
O	y			GlyLeuSerSerAspProAlaAspLeuAspPro	2256
D	b			GGTTATCTCTGACCCAGACAGACCTGGACCCC	6772
 RESULT 9 AAH98402 standard; cDNA; 8002 BP.					
A	C			AAH98402;	
X	X			12-OCT-2001 (first entry)	
D	E			Human EST-derived coding sequence SEQ ID NO: 259.	
X	X			Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;	
K	M			tomato; monkey; dog; sea urchin; expressed sequence tag; EST;	
K	M			diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;	
K	M			gene therapy; nutrition; ss.	

XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US002687.
XX PR 25-JAN-2000; 2000US-00491404.
XX PR 17-JUL-2000; 2000US-00617746.
XX PR 03-AUG-2000; 2000US-00631451.
XX PR 15-SEP-2000; 2000US-00663870.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX DR WPI; 2001-476164/51.
XX DR P-PSDB; AAM23743.
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX PT antibodies and research use.
XX PS Claim 1, Page 369-371; 1275pp; English.
XX CC The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
XX CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX CC from the organism of interest. They can be used in diagnostics,
XX CC forensics, gene mapping, identification of mutations, to assess
XX CC biodiversity and for nutritional purposes. The present sequence is a cDNA
XX CC of the invention
XX SQ Sequence 8002 BP; 1590 A; 2504 C; 2273 G; 1635 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 8002
Score: 11627.50 Matches: 2238
Percent Similarity: 97.73% Conservative: 1
Best Local Similarity: 97.69% Mismatches: 4
Query Match: 97.68% Indels: 48
DB: 4 Gaps: 2

US-09-611-257A-37 (1-2266) x AAH98402 (1-8002)

QY 1 MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
DB 496 ATGGAACGAGGAGGAGGATGGAGCGGGCCGAGAGTCCGGACAGCCCGAGACTTCATG 555
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
DB 556 CGGCTCAACGACCTGTCGGGGGCCGGGGGCCGGGGGCCGGGGTCCAGCAGAAAAAGGAC 615
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
DB 616 CCGGGCAGCGCGACTCCGAGGCGGAGGGGTGCGCTACCCGGCGGTGCCCCGGTGGTT 675
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
DB 676 TTCTTCTACTTGAGCCAGACAGCCGCCGCGAGCTGTGTCTCCGACGGTCTGTAAAC 735
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
DB 736 CCCTGGTTTGAGCGCATCAGCATGTTGGTCATCTTCTCAACTGCGTGACCCCTGGGCATG 795
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
DB 796 TTCCGGCCATGCGAGGACATCGCTGTGACTCCAGCGCTGCCGATCTTCAGGCGCTTT 855
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140

DB 856 GATGACTTCAATCTTGCCCTTCTTGCCCGTGAGATGTGTGAAGATGTGGCTTGCGGC 915
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
DB 916 ATCTTTGGAAAAAGTGTACCTGGAGACACTTGAAACCGGCTTGACTTTTTCATCTGC 975
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
DB 976 ATCGCAGGAGATGCTGAGTACTCGCTGACCTGCAGAACGTCAGCTTCAAGTGTACAG 1035
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
DB 1036 ACAGTCCGTGTGCGCAGCCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCTT 1095
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
DB 1096 GTCACGTTGCTGCTGGATACTCTGCCCATGCTGGCAACGTCCTGCTGCTTCTTC 1155
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
DB 1156 GTCTTCTTCACTTCGCGCATCGTCGGCGTCCAGCTGTGGCAGGGCTGCTTCGGAACCGA 1215
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
DB 1216 TGCTTCTTACCTGAGAATTTACGCTTCCCTGAGCGTGAAGCTGAGCGCTATTACAG 1275
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
DB 1276 ACAGAGACGAGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGCGATGCGG 1335
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
DB 1336 TCCTGCAGAAAGCTGCCACGCTGCGGGGAGACGGGGCGGTGGCCACCTTGCGGTCTG 1395
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
DB 1396 GACTATGAGGCTTAACAACAGCTCCAGCAACCACTGTGTCAACTGGAACCACTACTAC 1455
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
DB 1456 ACCAACTGCTCAGCGGGGAGACAAACCTTCAAGGGCGCCATCAACTTGACAACATT 1515
QY 341 GlyTyrAlaTriPheAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
DB 1516 GGCTATGCTGATCGCCATCTTCCAGTTCATCAGCTGAGGGCTGGGTGCACATCATG 1575
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
DB 1576 TACTTTGTATGATGATGCTCATCTCTTCAAAATTTCATCTACTTCATCTCCTCATCATC 1635
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGln 400
DB 1636 GTGGGCTCTTCTTCATGATCAACCTGTGCTGTGATGGTCCACGAGTTCTCAGAG 1695
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
DB 1696 ACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTTCCTGCCAACGCC 1755
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440
DB 1756 AGCAACCTGGCTAGCTCTCTGAGCCCGGAGCTGCTATGAGAGCTGCTCAAGTACCTG 1815
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
DB 1816 GTGTACATCTTCGTAAGCAGACCCGCGAGGTGGCTCAGGTCTTCGGGACAGAGTGTG 1875
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
DB 1876 CCGGTTGGGCTGCTCAGACGACCCAGCACCTTCGGGGGCCAGGAGACCCAGCCAGCAGC 1935
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500

Db 1936 AGCTGCTCTCGCTCCACCGCCGCTATCCGTCCACCACTGTGTGCACCAACCACCAACCAC 1995
QY 501 HISHISHISHISTYRHisleuGlyAsnGlyThrleuArgAlaProArgAlaSerProGlu 520
Db 1996 CATCACCACTACCACTGGGCATGGGACGCTCAGGGCCCCCGGGCCAGCCCCGGAG 2055
QY 521 ILeuGlnAspArgAspAlaAsnGlySerArgArgleuMetLeuProProProSerThrPro 540
Db 2056 ATCCAGGACAGGGATGCCAATGGGTCCCCGGCTCATGTGCTCCACCACTCCGACGCCCT 2115
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyHisAlaAsp 560
Db 2116 GCCCTCTCCGGGGCCCCCTGTGGGCGCAGAGTCTGTGCACAGCTTCTACCATGCGGAC 2175
QY 561 CysHisleuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 2176 TGCCACTTAGAGCAGTCCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTGAGGCATCC 2235
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
Db 2236 GGCAGGACTGTGGGACGCGGAGGTGTATCCCACTGCACACCAAGCCCTCCACCGGAG 2295
QY 601 ThrleuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrleuThr 620
Db 2296 ACGTGAAAGAGAAGGACGACTAGTAGAGGTGGCTGCCAGCTCTGGGCCCCCAACCTCACC 2355
QY 621 SerleuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 2356 AGCCTCAACATCCCAACCCGGGCTTACAGCTCCATGCACAAAGCTGTGAGACACAGAGT 2415
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2416 ACAGGTGCTGCCAAAGCTCTTGCAAGATCTCAGCCCTTGCTTGAAAGCAGACAGTGA 2475
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyLysValGluLeu 680
Db 2476 GCCTGTGTCCAGACAGCTGCCCTACTGTGCCCCGGGCGGAGGAGTGAGCTC 2535
QY 681 AlaAspArgGluMetProAspSerAspSerGlyAlaValTyrGluPheThrGlnAspAla 700
Db 2536 GCCGACCGTGAATGCTGACTCAGACAGGACGAGTATGAGTTCACACAGAGATGCC 2595
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2596 CAGCACAGCACTCCGGGACCCCCACAGCCGGCGCAACGAGCCTGGGCCCAGATGCA 2655
QY 721 GluProSerSerValleuAlaPheThrPArgleuIleCysAspThrPheArgLysIleVal 740
Db 2656 GAGCCCACTGTGTGCTGTGCTGTGAGGCTAATCTGTGACACCTTCCGAAGATTGTG 2715
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2716 GACAGCAAGTACTTTGGCCGGGAATCATGATCGCCATCTGTGTCAACACACTCAGCATG 2775
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2776 GGCATCGAATACCAAGAGCAGCCGAGGAGCTTACCACGCCCTAGAAATCAGCAACATC 2835
QY 781 ValPheThrSerleuPheAlaLeuGluMetLeuLeuLysleuLeuValTyrGlyProPhe 800
Db 2836 GTCTTCACCAACCTCTTTGGCCCTGAGATGCTGTGAAGCTCTGTGTATGTGCCCTTT 2895
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrp 820
Db 2896 GGCTACATCAAGAATCCCTACAACATCTTCATGTGTCTGATGTGTCATCAGCGTGTGG 2955
QY 821 GluIleValGlyGlnGlnGlyGlyLysSerValLeuArgThrPheArgleuMetArg 840
Db 2956 GAGATCGTGGCCAGCAGGGGGGCGGCTGTGGTGTGCGGACCTTCCGCTGATGCGT 3015
QY 841 ValLeuLysleuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 3016 GTGCTGAAGCTGTGCGCTTCTGTGCGGCGCTGCAGCGGCACTGTGTGTCTCATGAAG 3075

QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 3076 ACCATGGACAACGTGGCCACTTCTGCATGTCTGTATGCTCTTCACTTTCATCTTCAGC 3135
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrleu 900
Db 3136 ATCTGGGCATGATCTTTCGGCTGCAGATTGCTCTGAGCGGAGTGGGACACCCCTG 3195
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 3196 CCAGACCGGAAGAATTGTGACTCTTGCTGTGGCCATCGTCACTGTCTTTCAGATCTTG 3255
QY 921 ThrGlnGluAspTrpAsnLysValleuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
Db 3256 ACCCAGGAGACTGGAACAAGTCTCTACAAATGGTATGGCTCCACGTCGTCGGCG 3315
QY 941 AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValleuPheAsnLeuLeuVal 960
Db 3316 GCCCTTATTTCATTTGCCCTCATGACCTTCGGCACTACGTGCTCTTCAATTGTGCTG 3375
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
Db 3376 GCCATTCTGTGAGGGCTTCCAGGCGGAG----- 3405
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyLysAlaAsnLysSerGlu 1000
Db 3406 -----GGAGATGCCCAAGTCCGAA 3426
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3427 TCAGAGCCCGATTCTTTCACCCAGCCTGATGTGTATGGGACAGGAAGAATGCTTG 3486
QY 1021 AlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuProProLeuIle 1040
Db 3487 GCCTGTGTCCCTGGGAGAGCACCCGAGCTGGGGAAGACCTGTGCGGCTCTCATC 3546
QY 1041 IleHisThrAlaAlaThrPrometSerleuProLysSerThrSerThrGlyLeuGlyLys 1060
Db 3547 ATCCACACGGCCGCCACCATGTGCTGCCCAAGACACCAAGCAGCGGCTGGGCGAG 3606
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3607 GCGCTGGGCCCTGCGTCCGCCGCCACCAAGCAGACAGCGGGTCCGACAGCCTGGGGCGGC 3666
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 3667 CACGAGATGAAGTCAACGCCCAAGCGCCGACGCTTCCGACAGCCCCCTGAGAGCGTGCA 3726
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerleuGlyArgAlaProSerLeuLys 1120
Db 3727 AGCAGCTGGACCAAGAGCGGCTCCAGCCGAACAGCCTCGGCGTGACCCAGCTGAAG 3786
QY 1121 ArgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140
Db 3787 CGGAGAACCCCAAGTGGAGAGCGGCGGTCCCTGTGTCCGAGAGAAGGCCAGAGACCCAG 3846
QY 1141 AspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
Db 3847 GATGAAGAGGAGAGCTCAGAAGAAGAGCGGCGCCAGCCTGCGGGCAGTGACCATCGCCAC 3906
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrleuGlnVal 1180
Db 3907 AGGGGTCCCTGAGCGGGAGGCCAAGAGTTCCTTGAACCTGCAGACACACTGCAGGTG 3966
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGln-AspCysAs 1200
Db 3967 CCAGGCTGCATCGACTGCGCAGTGGCCGAGGCTGTCTTGAGCACCAAGGAAGTGA 4026
QY 1200 nGlyLysSerAlaSerGlyArgleuAlaArgAlaLeuArgProAspAspProLeuAs 1220
Db 4027 TGGCAAGTGGCTTCAAGGGCGCTGCGGCCCTGCGGCTGTATGACCCCCCACTGA 4086

QY 1220 pGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpI1 1240
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Db 4087 TGGGATGACCGCCGATGACGAGGGCAACTGAGCAAAAGGGGAACGGGTCCGCGCTGGAT 4146
QY 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr 1260
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Db 4147 CCGAGCCCCGACTCCCTGCTGCTGCGAGCAAGACTCCTGGTCAGCCTACATCTTCCC 4206
QY 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
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Db 4207 TCCTCAGTCCAGGTTCCGCTCTGTGTGACCGGATCATCACCACAAGATGTTGACCA 4266
QY 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMet-GluArgProLysI 1300
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Db 4267 CGTGGTCTGTTCATCATCTTCTTACTGCATCACCATCGCCATGGGAGCGCCCAAAA 4326
QY 1300 le-AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAla 1319
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Db 4327 TTTGACCCCCACAGCGTTGAACGCATCTTCTGACCCCTCTCCAATTACATCTTCACCGCA 4386
QY 1320 ValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGln 1339
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Db 4387 GTCTTTCTGGCTGAATGACAGTGAAGGTGTGGCACTGGGCTGTGCTTGGGGAGACAG 4446
QY 1340 AlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIle 1359
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Db 4447 GCCTACCTGCGAGCAGTTGGAACGTGCTGACGGGCTGTGTGCTCATCTCCGTATC 4506
QY 1360 AspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgVal 1379
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Db 4507 GACATTCTGGTGTCCATGTCTCTGACAGCGGCACCAAGATCCTGGGCATGCTGAGGGTG 4566
QY 1380 LeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLys 1399
|||||
Db 4567 CTGCGGCTGCTGCGGGCCCTGCGCCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAG 4626
QY 1400 LeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCys 1419
|||||
Db 4627 CTGGTGTGAGACGCTGATGTCTCTCACTGAAACCCATCGGCAACATTGTAGTCACTTGC 4686
QY 1420 CysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePhe 1439
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Db 4687 TGTGCCCTTCTTCATCATTTTTCGGCATCTTGGGGGTGACAGCTCTTCAAAGGAAGTTTTC 4746
QY 1440 ValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSer 1459
|||||
Db 4747 GTGTGCCAGGGCGGAGATACCAGAACATCAACAATAATCGACTGTGCCGAGGCCAGT 4806
QY 1460 TyrArgTrpValArgHisLysTyrAsnPheAsnLeuGlyGlnAlaLeuMetSerLeu 1479
|||||
Db 4807 TACCGGTGGTCCGGCACAAGTACAACCTTTGACAACCTTGGCCAGGCCCTGATGTCCCTG 4866
QY 1480 PheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaVal 1499
|||||
Db 4867 TTCGTTTTGGCTTCCAAGATGTTGGGTGACATCATGTACGATGGCTGGATGCTGTG 4926
QY 1500 GluValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSer 1519
|||||
Db 4927 GCGGTGACACGAGCCCATCATGAACCAACACCCCTGGATGCTGTACTTCACTTCTCG 4986
QY 1520 PheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsn 1539
|||||
Db 4987 TTCCTGCTCATTTGTGGCTTCTTGTCTGAACATGTTGTGGTGTGGTGAGAAC 5046
QY 1540 PheHisLysCysArgGlnHisGlnGluGluAlaArgArgGluGluLysArg 1559
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Db 5047 TTCACAAGTGTCCGACAGCACAAGAGAGAGAGGCCCCGCGCGGAGAGAGAGCGC 5106
QY 1560 LeuArgArgLeuGluLysLysArgArg----- 1568
|||||
Db 5107 CTACGAGAAGCTGGAAGAAAAGAGAGAAATGTAAATGCTGGACGATGTAAATTGCTTCCGGC 5166
QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArg 1581

Db 5167 AGCTCAGCCACGCTGCTGACGAAGCCAGTGCAAACTTACTACTCCGACTACTCCCGC 5226
QY 1582 PheArgLeuLeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleThrGly 1601
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Db 5227 TTCGGGTCTCTGTCACCACTTGTCACACGACCTACTGACTTTCATCAACAGGT 5286
QY 1602 ValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeu 1621
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Db 5287 GTCATCGGGCTGAACGTGTACCATGGCCATGGAGCAGCTAACAGACGCCAGATTCTG 5346
QY 1622 AspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerVal 1641
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Db 5347 GATGAGGCTTGAAAGATCTGCAACTACATCTTCACTGTCACTTGTCTTGAGTCAGTT 5406
QY 1642 PheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAsp 1661
|||||
Db 5407 TTCAACTTGTGGCTTGTGTTCCGTGGTTCTTCCAGGACAGGTGGAACCAAGCTGGAC 5466
QY 1662 LeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAla 1681
|||||
Db 5467 CTGGCCATTGTGCTGCTGTCCATCATGGGCATCACGCTGAGAGAAATCGAGTCAACGCC 5526
QY 1682 SerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgVal 1701
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Db 5527 TCGCTGCCCATCAACCCCAACCATCATCCGCATCATGAGGGTGCTGCGCATTGCCCGAGTG 5586
QY 1702 LeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAla 1721
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Db 5587 CTGAAGCTGCTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGGACACGGTGATGCAGGCC 5646
QY 1722 LeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAla 1741
|||||
Db 5647 CTGCCCCAGGTGGGGAACCTGGGACTTCTTTCATGTGTGTTTTCATCTTTGCACT 5706
QY 1742 LeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeu 1761
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Db 5707 CTGGCGTGAAGCTCTTGGAGACCTGAGTGTGACGAGACACCCCTGTGAGGGCTG 5766
QY 1762 GluArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSer 1781
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Db 5767 GGGCGTCATGCCACTTTCGAACTTGGCATGGCTTCTTAACCTCTTCCGAGTCTCC 5826
QY 1782 ThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSer 1801
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Db 5827 ACAGGTGACAATTGGAATGGCATTTAAGAAGACACCCTCCGGGACTGTGACCAAGAGTCC 5886
QY 1802 ThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGln 1821
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Db 5887 ACCTGCTACAACGCGTCATCTCGCTTAATCTTGTGTCTTCTGCTGACGGGCCAG 5946
QY 1822 PheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLys 1841
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Db 5947 TTCGTGCTAGTCAACGTGTGATCGCGTGTGATGAAGCACTGGAAGAGAGCAACAG 6006
QY 1842 GluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSer 1861
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Db 6007 GAGGCCAAGAGAGGCCGAGCTAGAGCTGAGCTGAGCTGAGATGAAGACCCTCAGC 6066
QY 1862 ProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAsp 1881
|||||
Db 6067 CCCCAGCCCCACTCGCCACTGGGCGAGCCCTTCTCTGCGCTGGGGTGAAGGCCCGCAG 6126
QY 1882 SerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArg-SerAlaSe 1901
|||||
Db 6127 AGCCCCGACAGCCCCAAGCCTGGGGCTTGCAACCCAGCGGCCACGAGATCAAGCTTC 6186
QY 1901 HisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGlyProAs 1921
|||||
Db 6187 CCACTTTTCCCTGAGCACCCACGATGACGCCCAACCCACGGAAGCTGCCAGGACCAAGA 6246
QY 1921 PheLeuThrValArgLysSerGlyValSerArgThrHisSerLeu-ProAsnAspSerT 1941
|||||

Db	6247	CTTACTGACTGTGCGGAAGTCTGGGGTCAGCCGAA	CGCACTCTCTGCCCCCAATGACAGCT	6306
Qy	1941	YrMetCysargHis-GlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrGlyLeu		1960
Db	6307	ACATGTGTGCGCATGGGAGACACTGCCGAGGGGCCCC	TGGACACAGGGGCTGGGGGCTC	6366
Qy	1961	ProLysAlaGlnSerCylSerValLeuSerValHisSerGlnProAlaAspThrSerTyr		1980
Db	6367	CCCAAGCTCAGTCAGGCTCCGTCTGTCCGTTCACTCC	CAGCCAGCAGATACCACTAC	6426
Qy	1981	IleLeuGlnLeuProLysAspAlaProHisIleLeuGlnProHisSerAlaProThrTyr		2000
Db	6427	ATCTGCAGCTTCCCAAGATGCACCTCATGTGCTCCAG	CCCCCAGCGCCCACTGG	6486
Qy	2001	GlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArg		2020
Db	6487	GGCACCATCCCAACTGCCCCCACCAGAGCGCTCCCC	TTGGCTCAGAGGCCACTCAGG	6546
Qy	2021	ArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAsp		2040
Db	6547	CGCCAGGCAGCAATAGAACTGACTCTTGAGCTTCA	GGGCTGTGGCAGCCGGGAAGAC	6606
Qy	2041	LeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTyrGly		2060
Db	6607	CTGCTGGCAGAGGTGAATGGGCCCTCCCGCCCTGG	CGCCCTACTCTTCTGGGGC	6666
Qy	2061	GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet		2080
Db	6667	CAGTCAAGTACCACGGCACAGCAGCACTCCCGCAG	CCACAGCAAGATCTCCAAGACATG	6726
Qy	2081	ThrProProAlaProCysProGlyProGluProAsnTyr-GlyLysGlyProProGluThr		2100
Db	6727	ACCCCGCCAGCCCTTGCCCCAGGCCACAGACC	CACTGGGGGCAAGGGCCCTCCAGAGAC	6786
Qy	2100	PArgSerSerLeuGluLeuAspThrGluLeuSerTrrPileSerGlyAspLeuLeuProPr		2120
Db	6787	CAGAAGCAGCTTAGAGTTGGACACGAGACTGAGCT	GGAATTTCAGGAGACCTCTCTGCCCCC	6846
Qy	2120	OGlyGlyGlnGluGluProProSerProArgAspLeuLysLysCysTyrSerValGluAl		2140
Db	6847	TGGCGGCCAGAGAGAGCCCCCATCCCA	CGGAGCTGAAGAAGTGCTACAGCGTGAGGCGC	6906
Qy	2140	aglnSerCysGlnArgArgProThrSerTrrPleuAspGluGlnArgArgHisSerIleAl		2160
Db	6907	CCAGAGCTGCCAGCGCGGCCCACTCTGCTGGATG	AGACAGAGACACTCTATCGC	6966
Qy	2160	aValSerCysLeuAspSerGlySerGlnProHisIleLeuGlyThrAspProSerAsnLeuG		2180
Db	6967	CGTCAGCTGCCTGGACAGCGGCTCCCAACCC	CACCTGGGGCACAGACCCCTTAACCTTGG	7026
Qy	2180	YglYglNProLeuGlyYglYProGlySerArgProLysLysLysLeuSerProProSerTrl		2200
Db	7027	GGGCCAGCCTCTTGGGGGGGCTGAGAGCCGGCC	CAAGAAAAAACTCAGCCCGCTAGTAT	7086
Qy	2200	eThrIleAspProProGluSerGlnGlyProArgThrProProSerProGlyIleCysLe		2220
Db	7087	CACCATAGACCCCCCGAGAGCCAAAGGTCTCTCG	AGCCCGCCCACTGTATCTGCTT	7146
Qy	2220	uArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyProProAspSe		2240
Db	7147	CCGGAGGAGGCTCCGTCACGCACTCCAAAGATCC	CTTGGCCTCTGGCCCCCCTGACAG	7206
Qy	2240	rMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAs		2260
Db	7207	CATGGCTGCCTCGCCCTCCCAAGAAAGATGTGT	AGTCTCTCCGGTTATCTCTGA	7266
Qy	2260	pProAlaAspLeuAspPro	2266	
Db	7267	CCCAAGCAGACCTGACCCC	7285	
RESULT 10				
AAZ52309				
standard; cDNA; 7286 BP.				

XX	AAZ52309;	
AC		
XX	18-JUL-2000	(first entry)
DT		
XX		
DE	Rat pancreatic T-type calcium channel cDNA.	
XX		
KM	Rat; pancreatic T-type calcium channel alpha subunit; insulin;	
KM	pancreatic beta cell; alpha1G; low voltage activated Ca2+ channel family;	
KM	antidiabetic; calcium influx; L type calcium channel; NIDDM;	
KM	type II diabetes; non-insulin dependent diabetes mellitus; ss.	
XX		
OS	Rattus sp.	
XX		
FH	Key	Location/Qualifiers
FT	misc_feature	1..157
FT		/*tag= b
FT		/note= "Region upstream to the coding region of
FT		pancreatic T-type calcium channel protein"
FT		2..7285
CDS		/*tag= a
FT		/product= "Pancreatic T-type calcium channel alpha
FT		subunit"
FT		/transl_except= (pos:11..13, aa:Xaa)
FT		/transl_except= (pos:7022..7024, aa:Xaa)
FT		/transl_except= (pos:7112..7114, aa:Xaa)
FT		/note= "Xaa corresponds to in-frame stop codon. This
FT		region includes sequence upstream to the coding region of
FT		pancreatic T-type calcium channel protein. Does not
FT		include stop codon"
FT		/partial
FT	mat_peptide	158..7285
FT		/*tag= c
FT		/product= "Pancreatic T-type calcium channel alpha
FT		subunit"
FT		/note= "This region is claimed as SEQ ID NO: 1"
XX		
PN	WO200015845-A1.	
XX		
PD	23-MAR-2000.	
XX		
PF	26-AUG-1999;	99WO-US019675.
XX		
PR	26-AUG-1998;	98US-0098004P.
PR	27-JAN-1999;	99US-0117399P.
XX		
PA	(SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.	
XX		
PI	L1 M;	
XX		
DR	WPI; 2000-271475/23.	
DR	P-PSDB; AAY70720.	
PT		
XX		
XX		
PS	Example 1; Page 114-119; 124pp; English.	
XX		
CC	The present cDNA encodes a protein that includes pancreatic T-type	
CC	calcium channel alpha subunit derived from rat insulin secreting beta	
CC	cell line, INS-1. The protein shows 96.3 % identity to the neuronal T-	
CC	type calcium channel alpha subunit (alpha1G). The T-type Ca2+ channel	
CC	from INS-1 (alpha1G-INS) and neuronal alpha1G are alternative splice	
CC	isoforms of the same gene. The INS-1 isoform is also expressed in brain,	
CC	neonatal heart and kidney besides pancreatic beta cells. T-type Ca2+	
CC	channel belongs to the family of low voltage activated Ca2+ channels. The	
CC	present sequence is used for treating diseases associated with abnormal	
CC	expression or function of T-type calcium channels. They are especially	
CC	used for treating type II diabetes. Modulators of pancreatic T-type Ca2+	
CC	channel e.g. antisense oligonucleotides, ribozymes and inhibitors are	
CC	used in methods for modifying insulin secretion by pancreatic beta cells,	
CC	basal calcium levels, potential L type calcium channel activity,	
CC	pancreatic cell death, pancreatic beta cell proliferation and calcium	

CC influx through L type calcium channels in cells
XX Sequence 7286 BP, 1467 A, 2224 C, 2064 G, 1531 T, 0 U, 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 7286
Score: 1111.00 Matches: 2135
Percent Similarity: 94.80% Conservative: 35
Best Local Similarity: 93.27% Mismatches: 95
Query Match: 93.34% Indels: 24
DB: 3 Gaps: 5

US-09-611-257A-37 (1-2266) x AA252309 (1-7286)

QY 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
DB 158 ATGACGAGGAGGAGATGGACGGGCGCCCGAGAGTCGGGACAGCCCGTAGCTTCACG 217
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
DB 218 CAGCTCAACGACCTGTCGGGGCCGGGGCCGGCAGGGCCGGGTCGACGGAAAGGAC 277
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
DB 278 CCGGGCAGCGCGACTCCGAGGCGGAGGGGCTGCCGTACCCCGCGCTAGCCCGGTGTT 337
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
DB 338 TTCTTCTACTTGAGCCGACGACAGCCGCCCGGAGCTGGTGTCTCCGACGGTCTGTAAC 397
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
DB 398 CCGTGGTTCGAGCGAGTCAGTATGCTGTCTTCTTCTCACTGTGTACTCTGGGTATG 457
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
DB 458 TTCAGGCCGCTGTGAGCATTTGCTGTGACTCCAGCGCTGCCGGATCTGCAGGCCCTTC 517
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
DB 518 GATGACTTCATCTTTCCTTCTTCTTCTGTAATGTTGTGTAAGATGTGGCCTTGGGC 577
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
DB 578 ATCTTTGGGAAGAATGTTACTGGGAGACACTTGGAACCGGCTTGACTTTTCATTGTC 637
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
DB 638 ATTGCAGGGATGCTGGAGTATTTCGTGGACCTGCAGAACGTCACTTCTCCGACGTACG 697
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
DB 698 ACAGTCCGTGTGCTGCAGCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCAATTCTC 757
QY 201 ValThrLeuLeuLeuAspThrLeuPrometLeuGlyAsnValLeuLeuLeuCysPhePhe 220
DB 758 GTCACTTACTGCTGACACTTGCTATGCTGGCAACGTCTGCTGCTGTTCTTC 817
QY 221 ValPhePheIlePheGlyIleValGlyValGluLeuTrpAlaGlyLeuLeuArgAsnArg 240
DB 818 GTCTTTTTCATCTTTGGCATCTGGGGCTCCAGCTGTGGGCAAGACTGCTCGCAACCGA 877
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
DB 878 TGCCTTCCTCCCGAGAACTTTCAGCTCCCTGAGCGTGGACCTGGAGCCTTATTACCA 937
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
DB 938 ACAGAGATGAGGACGAGAGCCCTTCATCTGCTTCAGCCTCGGGAGATGCGCATGAGA 997
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
DB 998 TCCTGCAGAGAGTGCCACACACTGCGTGGGGAAGGCGGTGTGGCCACCCCTGCAGTCTG 1057

QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
DB 1058 GACTATGAGACCTATTAACAGTTTCAGCAACACCACCTGTGTCAACTGGAACCACTACTAT 1117
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
DB 1118 ACCAACTGCTTGCGGGCGAGCAACACCCCTTCAAAAGGCCCATCACTTGACACATT 1177
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet 360
DB 1178 GGCTATGCTGGATCGCCATCTTCAGGTCACTCACACTGGAGGGCTGGTCGACATCATG 1237
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
DB 1238 TACTTCGTATGACCGCTCACTCCTTCTACAACTTCATCTCATCTTCTTCATCATC 1297
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
DB 1298 GTGGGCTCTTCTTCATGATCAACCTGTGCTGTGTGATTTGCCAGCATTCCTCCAG 1357
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGluGlnArgValArgPheLeuSerAsnAla 420
DB 1358 ACCAAACAGCGGAGAGTCACTGATGCGGAGCAGCGTGTACGATTCTGTCCAATGCT 1417
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
DB 1418 AGCACCTGGCACTTCTCTGAGCCAGGACAGCTGATAGAGAGCTACTCAAGTACTCTG 1477
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
DB 1478 GTGTACATCTCCGAAAGCAGCCCGAAGCTGGCCCAAGTCTTAGGGCTATAGGCGTG 1537
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnIuThrGlnProSerSer 480
DB 1538 CCGGCTGGGCTGTCAGCAGCCAGTGCGCTAGTGGGCGAGAGCCCAAGCTAGTGGC 1597
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis 500
DB 1598 AGCTGACTCGCTCACACCGTGTGTGTGTGTCCACCACTGTGTCCACCATCACAC 1657
QY 501 HisHisHisIleTyrHisIleGluGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
DB 1658 CACCATCACCACTACCACTGGTAAATGGACGCTCAGAGTTCCCGGGCCAGCCAGAG 1717
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
DB 1718 ATCCAGGACAGGATGCCAATGGGTCTGCCGGCTCATGCTACCAACCTCTACACCC 1777
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
DB 1778 ACTCCCTCGGGGCCCTCCGAGGGGTGGAGTCTGTACACAGCTTCTTACCATGCTGAC 1837
QY 561 CysHisIleGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
DB 1838 TGCCACTTGAGCCAGTCCGTTGCCAGGCAACCCCTCCAGATGCCATCGGAGCATCT 1897
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
DB 1898 GGTAAGACTGTGGGTAGTGGGAAGTGTACCCCACTGTGCATACGACCTCCACCAAG 1957
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
DB 1958 ATACTGAAGATTAAGCACTAGTGAGGTGGCCCCAGCCCTGGGGCCCCACCTCACC 2017
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
DB 2018 AGCTTCAACATCCCACTGGGCCCTTCAGTTCATGCACAAAGCTCTCGAGACACAGAGT 2077
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
DB 2078 ACGGAGCCTGCATAGCTCTGCMAAATCTCCAGCCCTTGCTCCAAAGCAGACAGTGA 2137

QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680
Db	2138	GCCTGCGGGCCGAGACAGTTGTCCCTACTGTGCGCCGACAGAGCAGAGAGCCAGAGTCC	2197
QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
Db	2198	GCTGACCATGTGCATGCTGACTCAGACAGCCAGGCTGTGTATGAGTTCAACAGGACGCT	2257
QY	701	GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp	719
Db	2258	CAGCACAGTAGTACCTCCGGGATCCACACAGCCGGCGCGACAGCGAGCCTGGGCCAGAT	2317
QY	720	AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle	739
Db	2318	GCAGAGCCTAGTCTGTGCTGGCTTCTTGAGAGCTGATCTGTGACACATTCCGGAAGATC	2377
QY	740	ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer	759
Db	2378	GTAGATAGCAATACTTTGGCCGGGAATCATGATCCCATCTGTGTCATAACACTCAGC	2437
QY	760	MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn	779
Db	2438	ATGGGCATCGAGTACCAAGACAGACGCCGAGAGACTCAACACGCCCTGGAATCAGCAAC	2497
QY	780	IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPro	799
Db	2498	ATCGTCTTCAACCAGCCTCTCGCCTTGAGATGCTGTGAAACTGCTGTCTACGGTCCC	2557
QY	800	PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal	819
Db	2558	TTTGCTACATTAGAATCCCTACACACATCTTGATGGTGTCAATGTGTCATCAGTGTG	2617
QY	820	TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet	839
Db	2618	TGGAGATTGTGGCCAGCAGGAGGTGGCTGTGGTGTGCGGACCTTCCGCTGATG	2677
QY	840	ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValLeuMet	859
Db	2678	CGGGTCTGAAGCTGTGGCTTCTCGCCGCCCTGCAGCGCCAGCTCGTGGTGCATG	2737
QY	860	LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe	879
Db	2738	AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCTCATGCTGTTCATCTTCACTTC	2797
QY	880	SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr	899
Db	2798	AGCATCCTGGGCATGATCTCTTTGGTTGCAAGTTCCGATCTGAACGGGATGGGACACG	2857
QY	900	LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle	919
Db	2858	TTGCCAGACCGGAAGATTTCGACTCCCTGCTGTGGCCATCGTCACTGCTTTTCAGATT	2917
QY	920	LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp	939
Db	2918	CTGACTCAGGAAGACTGGAATAAGTCCCTTACACAGCGCATGGCCTCCACATCGTCTGG	2977
QY	940	AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu	959
Db	2978	GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCACTATGTGCTCTTAACTTGCTG	3037
QY	960	ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer	979
Db	3038	GTTGCCATTCTTGTGAAGATTCCAGGACAGAGAAATCGCAAAACGGGAAGATGCGAGT	3097
QY	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSer	999
Db	3098	GGACAGTTAAGCTGATTCAGCTGCTGTCAACTCTCAGGGGGAGATGCCACCAAGTCT	3157
QY	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019
Db	3158	GAGTCAGAGCCTGATTTCTTTTCGCCCACTGTGATGTGATGGGGACAGAAAGAACGCGC	3217
QY	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu	1039

Db	3218	TTGGCCCTGTGGCTTTGGAGAAACACGGCGAACTACGAAAGAGCCTTTGGCACCCCTC	3277
QY	1040	ILEILEHIEThraAlaAlaThrPrometSerLeuProlysserThrsThrglyLeugly	1059
Db	3278	ATCATCCATACCGGCTGCCAGACACCAATGTACTACCCAGAGCTCCAGACAGGTGTGGG	3337
QY	1060	GLUAlaleuglyProAlaSerArgArgThrsSerSerglySeralaglProglyAla	1079
Db	3338	GAAGCACTGGCTTGGCTCTCGACGTACAGTAGAGTGGGTCCGCTGAGCCTGAGCT	3397
QY	1080	Ala--HisgluMetlysserProProSeralAargsserProHisserProTrpser	1098
Db	3398	GCCCAACCATGAGATGAATCTCCGCCAAGTCCCGCAGCTCCCGCAGACTCCTGGAGT	3457
QY	1099	AlaAlaSerSerTrpThrsSerArgArgSerSerArgAsnSerLeuglyArgAlaProSer	1118
Db	3458	GCGGCAAGCAGCTGGACCAAGCAGCGCCTCCAGCAGGAACAGCCTGGGCGGCGCCAGC	3517
QY	1119	LeuLySArgArgSerProSerglygluArgArgSerLeuLeuSerglygluGlyGlnlu	1138
Db	3518	CTAAAGCGAGAGACCCGAGCGGGAGCGAGGTCCCTGCTGTCTGAGAGGGCCAGAG	3577
QY	1139	SerglAspgluGluGluSerSergluGluGluArgAlaSerProAlaglSerAspHis	1158
Db	3578	AGTCAGGATGAGAGGAAGTTCAGAGAGAGACCGGGCCAGCCAGCGGCAGTGACCAT	3637
QY	1159	ArgHisArgGlySerLeuGluArgGluAlaIySserSerPheAspLeuProAspThrLeu	1178
Db	3638	CGCCACAGGGGTTCTTGGAACGTGAGGCCCAAGATTCTTGAACCTGACACTCTG	3697
QY	1179	GlnValProGlyLeuHisArgThraAlaSerGlyArgGlySeralaserGluHisGlnasp	1198
Db	3698	CAGGTGCCGGGCTGCCACCGCACAGCAGCGCGGAGCTTGCTCTGAGCACCAAGAC	3757
QY	1199	CysAsnGlyLySserAlaSerGlyArgLeuAlaArgAlaLeuArgProaspProPro	1218
Db	3758	TGTAATGCAAGTCGGCTTCAGGGCGTTGGCCCGCACCTGAGACTGATGACCCCAA	3817
QY	1219	LeuAspGlyAspAspAlaAspAspGluGlyAenLeuSerLySgluArgValArgAla	1238
Db	3818	CTGGATGGGATGATGACATGATGAGGGAATCTGAGCAAGGGGAACGATACAAGCC	3877
QY	1239	TrpIleArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSeralATyrIle	1258
Db	3878	TGGGTCAATCCCGGCTTCTGCTGCTGTGGCCGAGAGGAGATTCTTGTCGGCTATATC	3937
QY	1259	PheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278
Db	3938	TTTCCTCCTCAGTCAAGGTTTCGTCTCCTGTGTCAACCGATCATCACCCACAAGATT	3997
QY	1279	AspHisValValLeuValIleIlePheLeuAancysIleThrIleAlaMetGluArgPro	1298
Db	3998	GACCATGTGTCCTCGTCATCATCTTCCTCACTGTATCACCATCGCTATGAGCGCCCC	4057
QY	1299	LysIleaspProHisSeralaglArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318
Db	4058	AAAATTGACCCCAAGCGCTGAGCGCATCTTCGACCCTCCAACATCACTTTCACG	4117
QY	1319	AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlu	1338
Db	4118	GCACTCTTCTAGCTGAATGACAGTGAAGGTGTGGCACTGGGCTGTGCTTTGGGAG	4177
QY	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358
Db	4178	CAGGCTTACCTGCGCAGCAGCTGGAATGTGTGACGGCTTGCTGTCTCATCTCCGTC	4237
QY	1359	IleAspIleLeuValSerMetValSerAspSerglyThrLysIleLeuGlyMetLeuArg	1378
Db	4238	ATCGACATCCTGGTCTCCATGTGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGG	4297
QY	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398

Db 4298 GTGCTGCGGCTGCTGCGGACCCCTGCTCACTCAGGGTCATCAGCCGGCCAGGACTG 4357
QY 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIle 1418
Db 4358 AAGCTGGTGAGACTGTGATGTCATCCCTCAAAACCATTGGCAACATTGTGTCATT 4417
QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438
Db 4418 TGCTGTGCTCTTCTTCATTCATTTTGGAAATTCGCGGGTGAGCTCTTCAAAAGGAAGTTC 4477
QY 1439 PheValCysGlnGlyIleAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458
Db 4478 TTCGTGTGTCAAGGTGAGACACAGGAACATCACTAACAAATCCGACTGCGTGAGGCC 4537
QY 1459 SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db 4538 AGCTACCGATGGGTCCGGCACAGTACACTTGAACAACCTGGGCCGCTGTGATGTCC 4597
QY 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498
Db 4598 CTGTTTGTGCTGGCTCTCCAGGATGGTTGGGTGACATCATGTATGATGGGCTGATGCT 4657
QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
Db 4658 GTGGGTGTGATCAGCAAGCCCATCATGAACCAACCCCTGATGCTGTACTTACTCATC 4717
QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538
Db 4718 TCCTTCTCTCATCGTGGCTTCTTGTGTCTGAACATGTTTGTGGCGTGTGTGAG 4777
QY 1539 AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluLys 1558
Db 4778 AACTTCATAGTGCAGACAGCACAGGAGGAGGAGGAGGCGGCGTGAAGAGAG 4837
QY 1559 ArgLeuArgArgLeuGluLysLysArgArg----- 1568
Db 4838 CGACTACGGAGGCTGGAGAAAAGAGAAATCTAATGTTGACGATGTAATTGCTTCC 4897
QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580
Db 4898 GGCAGCTCAGCCAGCGCTGCGTCAGAGGCCAGTGCAGGCCCTACTACTCTGACTACTCG 4957
QY 1581 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1600
Db 4958 AGATTCCGGCTCTGTGTCCACCACTGTGTACAGCCACTACCTGAGCCTCTTCATCACT 5017
QY 1601 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620
Db 5018 GGTCATCATCGGCTGAGCGTGGTCACTATGGCCATGGAACATTACAGAGCCCCAGATC 5077
QY 1621 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer 1640
Db 5078 CTGGACGAGGCTCTGAAGATCTGAATTACATTACCGTCATCTTTGTGAGTCA 5137
QY 1641 ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1660
Db 5138 GTTTCAAACTTGTGGCTTTGGCTTCCGCCGTTTCTTCAGAGACAGGTGGAACAGCTG 5197
QY 1661 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsn 1680
Db 5198 GACCTGGCTATTGTGCTTGTCCATCATGGGCATCACACTGAGAGATTGAGGTCAAT 5257
QY 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700
Db 5258 GCTTCGCTGCCCATCAACCCACCATCATCCGATCATGAGGGTGCCTCGCATTTGCTCGA 5317
QY 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720
Db 5318 GTTCTGAAGCTGTGTGAAGATGCTGTGGGCAATGCGGCACTGCTGAGACGGTGATGCAG 5377
QY 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAla 1740
Db 5378 GCCCTGCCCCAGGTGGGGAACCTGGGACTTCTTCATGTTATTGTTTTCATCTTTGCA 5437

QY 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760
Db 5438 GCTCTGGCGGTGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCTTTGTGAGGGC 5497
QY 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780
Db 5498 TTGGGTGGGATGCCACCTTAGAAGCTTTGGTATAGCCCTTTCAGCCCTTCGAGTCC 5557
QY 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800
Db 5558 TCCACTGTGTCACTGGAATGGTATTATGAAGACACCCCTCCGGACTGTGACGAGAG 5617
QY 1801 SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla 1820
Db 5618 TCCACTGTGTCAACACTGTGATCTCCCTATCTACTTGTGTCTTGTGCTGACGGCC 5677
QY 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsn 1840
Db 5678 CAGTTGTGTGTCAACGTGGTCAATGACTGTGTGATGAAGCACCTGGAAGAACCAAC 5737
QY 1841 LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeu 1860
Db 5738 AAAGAGGCCAAGAGAGGCCGAGCTGAGGCCGAGCTGAGCTGAGATGAAGACGCTC 5797
QY 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880
Db 5798 AGCCCGCAGCCCACTCCCGCTGGGAGCCCTTCTGTGGCCCGGGGTGAGGGTGTCC 5857
QY 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900
Db 5858 AACAGTCTGTAGACCCCTAAGCCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCC 5917
QY 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro----- 1918
Db 5918 TCGGGCTTCTCCCTGAGCACCCACGATGTATCCCAACCCGAGGAGGTGCCAGTCCCC 5977
QY 1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937
Db 5978 CTAGAGCAGACCTGCTGACTGTGAGGAAGTGTGTGTCAAGCCGAGCAGCACTCTGCCC 6037
QY 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGly 1957
Db 6038 AATGACAGCTACATGTGCCGCAATGGAGCACTGTGAGAGATCCCTAGAGACAGGGGC 6097
QY 1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977
Db 6098 TGGGGGCTCCCAAAAGCCAGTCAAGGCTCCATCTGTCCGTTCACTCCCAACAGCAGAC 6157
QY 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAla 1997
Db 6158 ACCAGCTGATCTTACAGCTTCCCAAGATGTGACTATGTGCTCCAGCTCATGGGGCC 6217
QY 1998 ProThrTrpGlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArg 2017
Db 6218 CCCACCTGGGGCCCATCCCTAAACTAACCCCACTGGCCGCTCCCTGTGCTCAGAG 6277
QY 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLysGlySer 2037
Db 6278 CCTCTCAGGCGCAGGACGAATAAGACTGACTCCCTGATGTGACAGGCTGGTACC 6337
QY 2038 ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057
Db 6338 CGGGAAGACCTGTGTCAAGAGGTGAGGGCCCTCTGCTGACCCGCTCATATCC 6397
QY 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077
Db 6398 TTCTGGGGCGGGTGAAGCATCCAGGTGACAGCAGCGTTCCGGCATCCAGAGCAAGTCTCC 6457
QY 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097
Db 6458 AAGCACATCCGCTGCCAGCCCTTGCCAGGCTGGAACCAAGCTGGGCCAAGGACCTT 6517

Db 661 GTCTTTTCATCTTTGGCATCGTGGCGCTCCAGCTGTGGGACAGACTGCTTCGCAACCGG 720
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 721 TGCTTCCTCCCGAAGACTTACGCTCCCTTCAGCGCTGAGCGTGACCTGAGCCTTATTACAG 780
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 781 ACAGAGATGAGAGCAGAGACCCCTTCATCTGCTCTCAGCCTCGGAGAAATGCGATGAGA 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 841 TCCTGACGAGAGTGTGCCACACTGCGTGGGAAAGCGGTGGTGCCACCCCTGACGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAAACCACTACTAT 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheGlyAlaIleAsnPheAspAsnIle 340
Db 961 ACCAACTGCTCTGCGGGAGACACAACCCCTTCAAAGCGCCATCACTTTGACCAACATT 1020
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrTrpValAspIleMet 360
Db 1021 GGCTATGCCTGATCGGCATCTTCCAGGTCACTGAGGGGCTGGTGCACATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1081 TACTTCGTAATGACGCTCACTCTTCACTTCACTTCACTTCACTTCTCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCybLeuValValIleAlaThrGlnPheSerGlu 400
Db 1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGGTGATTGCCACGAGTTCTCCGAG 1200
QY 401 ThrLySGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1201 ACCAAACAGCGGAGAGTCACTGATGCGGAGACGCTGATGATTCCTGTTCCAATGCT 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGlyGluLeuLeuLysTyrLeu 440
Db 1261 AGCACCTTGCAAGCTTCTGAGCCAGGACAGCTGCTATGAGAGCTACTCAAGTACCTG 1320
QY 441 ValTyrIleLeuArgLyAlaAlaArgArgLeuAlaGlnValSerArgAlaGlyVal 460
Db 1321 GTGTACATCTCCGAAAGAGACCCGAAAGCTGCGCCAGGTCTTAGGGCTATAGCGGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1381 CGGGCTGGGCTGCTCAGACGCCCAAGTGGCCCGTAGTGGGACAGGCCCCCAAGTGGC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1441 AGCTGACTCGCTCACACCGTCTGTCTGTCCACCACTGTGTCCACCACTATCACCAC 1500
QY 501 HisHisHisHisTyrHisHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1501 CACCATCACCACTACCACTGGGTAATGGAGCGTCAAGATTCCCCGGGCCAGCCAGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 1561 ATCCAGGACAGGAGATGCCAATGGGTCTGCGCGGTCACTGTAACCACTCTTACACCC 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGGGAGTGTGTACACAGCTTCTACCATGTGAC 1680
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1681 TGCACCTTGGAGCCAGTCCGTTGCCAGGCAACCCCTCCAGATGCCCATCGAGGCACTCT 1740
QY 581 GlyArgThrValGlySerGlyLybValTyrProThrValHisThrSerProProProGlu 600
Db 1741 GGTAGAGTGTGGGTAGTGGAAAGTGTACCCCACTGTGATACCAAGCCCTTCCACCAAGAG 1800

QY 601 ThrLeuLySGlyLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1801 ATACTGAAGATAAAGCACTAGTGAGGTGGCCCCCAGCCCTGGGCCCCCACCCTCAC 1860
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLybLeuLeuGluThrGlnSer 640
Db 1861 AGCTTCAACATCCCACTGGGCCCTTCAGCTCCATGACCAAGCTCCTGGAGACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLybIleSerSerProCysLeuLybAlaAspSerGly 660
Db 1921 ACGGAGCCTGCAATAGCTCCTGCAAAATCTCAGCCCTTGCTCCAAGCAGACGTGGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 1981 GCCTGCGGGCGGACAGTTGTCTCCTACTGTGCCCGACAGAGACAGAGCCAGACTCC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGlyAlaValTyrGluPheThrGlnAspAla 700
Db 2041 GCTGACCATGATGCTGACTCAGACAGCGAGCTGTGTATGAGTTCACACAGAGACGCT 2100
QY 701 GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlyProAsp 719
Db 2101 CAGCACAGTACCTCCGGATCCCAAGCCGGCGGACAGCGGAGCCTGGGCCCATGAT 2160
QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLybIle 739
Db 2161 GCAGAGCCTAGTTCTGTGCTGCTTGTGAGAGCTGATCTGTGACACATTCCGGAAGATC 2220
QY 740 ValAspSerLybTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 2221 GTAGATAGCAAAATCTTTGGCCGGGAATCATGATGCCATCTGTGTAATACACTCAGC 2280
QY 760 MetGlyIleGlyTyrHisGlyGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 2281 ATGGGCATGAGTACCAAGAGCAGCCGAGGAGCTCACCAAGCCCTGGAATCAGCAAC 2340
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLybLeuValTyrGlyPro 799
Db 2341 ATGCTCTTACCAGCCTCTTCCGCTTGAAGATGCTGTGAAACTGCTGTCTACGGTCCC 2400
QY 800 PheGlyTyrIleLybAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819
Db 2401 TTTGGCTACATTAAGAATCCCTACAAACATCTTGTATGATGTCTATGTGTCATCAGTGTG 2460
QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
Db 2461 TGGGAGATTGTGGGCCACGAGGAGGTGGCTGTGCTGTCGCGCACTTCCGCGCTGATG 2520
QY 840 ArgValLeuLybLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
Db 2521 CGGGTCTGAAGCTGTGGCTTCTTCCGCGGCCCTGCAAGCGCCAGCTCGTGTGCTCATG 2580
QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879
Db 2581 AAGACCATGACAACTGGCCACCTTGCATGTCTCTCATGTGTCTCATCTTCACTTTC 2640
QY 880 SerIleLeuGlyMetHisLeuPheGlyCysLybPheAlaSerGluArgAspGlyAspThr 899
Db 2641 ACCATCCTGGGCATGATCTTTGGTTCGAAGTTGCGATCTGAACGGGATGGGACACG 2700
QY 900 LeuProAspArgLybAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
Db 2701 TTGCCAGACCGGAAGAAATTTGCACTCCCTGCTCTGGGCCATCGTCACTGTCTTACAGATT 2760
QY 920 LeuThrGlnGluAspTrpAsnLybValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939
Db 2761 CTGACTCAGGAAGACTGGAATAAAGTCTCTTACAAAGGCAATGGCCTCCACATCGTCTTG 2820
QY 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959
Db 2821 GCTGCTCTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTTTTAACTGTCTG 2880

QY	960	ValAlaIleLeuValGluGlyPheGlnAlaGluIleIleSerLysArgGluAspAlaSer	979
Db	2881	GTGGCCATTCTTGGAAGATTCCAGGCAGAG-----	2913
QY	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSer	999
Db	2914	-----GGAGATGCCACCAAGTCT	2931
QY	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019
Db	2932	GAGTCAGAGCCTGATTCTTTCCGCCAGTAGTGATGGGACAGAAAGAACGCC	2991
QY	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeu	1039
Db	2992	TTGGCCCTGTGGCTTTGGCAGAACACGCCGAACTACGAAGAAGCCTTTGGCCACCCCTC	3051
QY	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059
Db	3052	ATCATCCATACGGCTGCGACACCAATGTACACACCCCAAGAGCTCCAGCACAGGTGTGGGG	3111
QY	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySeraIaGluProGlyAla	1079
Db	3112	GAAACACTGGGCTCTGGCTCTCGACGTACCACTAGCAGTGGGTCCGCTGAGCCTGAGCT	3171
QY	1080	Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer	1098
Db	3172	GCCACCATGAGATGAATGTCGCCCAAGTGCCCGCAGCTCCCGCACAGTCCCTGGAGT	3231
QY	1099	AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer	1118
Db	3232	GCGGCAAGCAGCTGACCAAGCAGCGCTCCAGCAGAACAGCCTGGGCCGGGCCCCAGC	3291
QY	1119	LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlu	1138
Db	3292	CTAAAGCGGAGAGCCCGAGCCGGGAGCGGAGTCCCTGTGCTGTGAGAGGGCCAGAG	3351
QY	1139	SerGlnAspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHis	1158
Db	3352	AGTCAGATGAGGAGGAAGTTTCAGAAAGAGACCGGGCCAGCCACAGCAGCAGTACCAT	3411
QY	1159	ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu	1178
Db	3412	CGCCACAGGGGTTCTTGGAACGTAGGCCCAAGAGTTCCTTTGACCTGACCTGACACTTG	3471
QY	1179	GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp	1198
Db	3472	CAGTGCCGGGGCTGCACCGCACAGCCAGCGGCCGAGCTCTGCCTTGAGCACCAAGAC	3531
QY	1199	CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro	1218
Db	3532	TGTAATGGCAAGTCGGCTTCAGCGGCTTTGGCCCCGACCTGAGGACTGATGACCCCAA	3591
QY	1219	LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla	1238
Db	3592	CTGGATGGGATGATGACAAATGAGGGAATCTGAGCAAAAGGGGAACGCAATACAAAGCC	3651
QY	1239	TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSeraIaTyrIle	1258
Db	3652	TGGGTCAATCCCGGCTTCTGCTGTTGCCGAGAGCGAATTCCTGTGGCTATATATC	3711
QY	1259	PheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278
Db	3712	TTTCCTCCTCAGTCAAGGTTTCTCTCTGTGTACCCGATCATCACCCACAAGATGTTT	3771
QY	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298
Db	3772	GACCATGTGTCTCTGTCATCATCTTCTCAACTGATATGACATCGCTATGAGCGCCC	3831
QY	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318
Db	3832	AAAAATTGACCCCAAGCGCTGAGCGCATCTTCTGACCTCTCCAATCATATCTTACG	3891
QY	1319	AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlu	1338

Db	3892	GCAGCTCTTCTAGCTGAATGACAGTGAAGGTGTGGCAGCTGGGCTGTGCTTTGGGAG	3951
QY	1339	GLNALaTYrLeuARgSerSerTrpAsnValLeuAspGlyLeuLeuValleuIleSerVal	1358
Db	3952	CAGGCTTACTCGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTCTCATCTCCGTC	4011
QY	1359	ILeAspIleLeuValSerMetValSerAspSerGlyThrIysIleLeuGlyMetLeuArg	1378
Db	4012	ATCGACATCTGTGCTCTCCATGTGTCTCCACAGCGGCACCAAGATCTTGGCATGTGAGG	4071
QY	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	4072	GTGCTGGCGGTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCACAGGACTG	4131
QY	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle	1418
Db	4132	AAGCTGGTGTAGAGACTCTGATGTCAATCCCTCAAAACCATTGGCAATGTGTGTCATT	4191
QY	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Db	4192	TGCTGTGCTTCTTATCATTTTGGAAATCTCGGGGTGAGCTCTTCAAGGAAGTTTC	4251
QY	1439	PheValCysGlnGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
Db	4252	TTCGTGTGTCAGGGTGAGACACACAGAACATCACTAACAAATCCGACTGCGTGAGGCC	4311
QY	1459	SerTYrArgTrpValArgHisLysSerTYrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	4312	AGCTACCGATGGGTCCGGCACAGTACACTTTGACAACCTGGGGCCAGGCTGTGATGTCC	4371
QY	1479	LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTYrAspGlyLeuAspAla	1498
Db	4372	CTGTTTGTGTGGCTTCCAAGATGTTGGGTGACATCATGTATGATGGCTGGATGCT	4431
QY	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTYrPheIle	1518
Db	4432	GTGGGTGTGATCAGACAGCCCATCATGAACCAACCCCTGGATGTGTATTACTTCATC	4491
QY	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538
Db	4492	TCCTTCCCTCATCGTGGCTTCTTGTCTGAACATGTTGTGGCGTGTGTGGAG	4551
QY	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluLys	1558
Db	4552	AACTTCCATAGTGCAGACAGACACCAGGAGGAGGAGGCGGCGTGAAGAGAAG	4611
QY	1559	ArgLeuArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTYrTYrSerAsp	1578
Db	4612	CGACTACGGAGGCTGGAGAAAAAGAGAGAAAGCCCACTGCAAGCCCTACTACTGTGAC	4671
QY	1579	TYrSerArgPheArgLeuLeuValHisHisLeuCysThrSerHisTYrLeuAspLeuPhe	1598
Db	4672	TACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACTGGAACCTCTTC	4731
QY	1599	IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTYrGlnGlnPro	1618
Db	4732	ATCACTGTGTATCGGGCTGAACGTGTCACTATGGCCATGAACATTACAGCAGCCC	4791
QY	1619	GlnIleLeuAspGluAlaLeuLysIleCysAsnTYrIlePheThrValIlePheValLeu	1638
Db	4792	CAGATCCTGAGCAGGCTCTGAAGATCTGCAATTAATCTTACCGTCACTTGTCTTT	4851
QY	1639	GluSerValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsn	1658
Db	4852	GAGTCAGTTTCAAACTTGTGGCTTGGCTTCCGCCGTTTCTTCCAGGACAGGTGAAC	4911
QY	1659	GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGluIleGlu	1678
Db	4912	CAGCTGAGACCTGGCTATTGTGCTTGTGCCATCATGGGCATCACACTGGAGGAGATTGAG	4971
QY	1679	ValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIle	1698

Db 4972 GTCATCTGTCGCTGCCCATCAACCCCATCATCCGTATCATGAGGGTGCTCCGCAATT 5031
QY 1699 AlArGVaLleuLySleuLeuLySmeLaVaLgLyMeLaRgaLaLeuLeuAspThrVaL 1718
Db 5032 GCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGCATGCGGGCACTGCTGCACACGGTG 5091
QY 1719 MetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIle 1738
Db 5092 ATGCAGGCCCTGCCCAAGTGGGAACCTGGAACTTCTCTTCATGTATGTTTTTCATC 5151
QY 1739 PheAlaAlaLeuGlyValGlyLeuPheGlyAspLeuGlyCysAspGlyThrHisProCys 1758
Db 5152 TTTCAGACTCTGGGCGCTGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTTGT 5211
QY 1759 GluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPhe 1778
Db 5212 GAGGGCTTGGGTCGGCATGCCACCTTAGGAACCTTGATGGCTTTCTGACCCCTCTTC 5271
QY 1779 ArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAsp 1798
Db 5272 CGAGTCTCCACTGGTGCAACCTGAATGGTATATGAAGACACACCTCCGGGACTGTGAC 5331
QY 1799 GlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeu 1818
Db 5332 CAGGAGTCCACCTGCTACAACACTGTCACTCCCTATCTACTTGTGTCTTCGTGCTG 5391
QY 1819 ThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlyIu 1838
Db 5392 ACGGCCCAAGTTGTGTGCTGCTCAACGTGTGCTCATAGCTGTGATGAAGCACTGGAAGAA 5451
QY 1839 SerAsnLySGlyAlaLySGlyGlyIuAlaGlyLeuGlyAlaGlyLeuGlyLeuGlyMetLys 1858
Db 5452 AGCAACAAGAAGAGCCCAAGAGAGAGGCCGAGCTGCAGGCCGAGCTGGAGCTGGAATGAAG 5511
QY 1859 ThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGly 1878
Db 5512 ACGCTCAGCCCGCAGCCCACTCCCGCTGGGCAAGCCCTTCTCTGGCCCCGGGGTGAG 5571
QY 1879 GlyProAspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArg 1898
Db 5572 GGTGTCAACAGTACTGACAGCCCTTAAGCCTGGGCTCCACACACCACTGCCACATTGGA 5631
QY 1899 SerAlaSerHisPheSerLeuGluHisProThrMetGlnProHisProThrGlyLeuPro 1918
Db 5632 GCAGCCTCGGGCTTCTCCCTTGAGCACCCCAAGATGGTAAACCCCAAGAGAGGTGCCA 5691
QY 1919 -----GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSer 1935
Db 5692 GTCCCCCTAGGACCAAGACTGCTGACTGTGAGGAAGTCTGGTGTCAAGCCGAGCACTCT 5751
QY 1936 LeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGlyGlyProLeuGlyHis 1955
Db 5752 CTGCCCAATGACAGCTACATGTGCCGAATGGAGCACTGCTGAGAGATCCCTAGGACAC 5811
QY 1956 ArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnPro 1975
Db 5812 AGGGGCTGGGGCTCCCAAGCCAGTCAAGGCTCCATCTTGTCCGTCACTCCCAACCA 5871
QY 1976 AlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHis 1995
Db 5872 GCAGACACCAAGCTGCATCTTAAGCTTCCCAAGATGTGCACTATCTGTCTCCAGCCTCAT 5931
QY 1996 SerAlaProThrTrpGlyThrIleProLysLeuProProGlyArgSerProLeuAla 2015
Db 5932 GGGGCTCCCACTGGGGCGGCATCCCTAAACTACCCCACTGGCGCTCCCTCTGGCT 5991
QY 2016 GlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeu 2035
Db 5992 CAGAGGCTCTCAGGGCGCCAGGCAATTAAGACTGACTCCCTGGATGTGCAAGGGCTG 6051
QY 2036 GlySerArgGluAspLeuLeuAlaGlyValSerGlyProSerProProLeuAlaArgAla 2055
Db 6052 GTAGCCGGGAAGACCTGTGTGACAGAGGTGAGTGGGCCCTCTGCCCTTGACCCGGTCC 6111

QY 2056 TyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLys 2075
Db 6112 TCATCCTTCTGGGGCGGGTGCAGCATCCAGGTGCAGACGCTTCCGGCATCCAGACAA 6171
QY 2076 IleSerLyHisMetThrProProAlaProCysProGlyProGlyProAsnTrpGlyLys 2095
Db 6172 GTCTCCAGACATCCGCCCTGCAGCCCCCTTGCCAGGCTTGGAACCCAGCTGGGCCAAG 6231
QY 2096 GlyProProGlyuThrArgSerSerLeuGlyLeuAspThrGlyLeuSerTrpIleSerGly 2115
Db 6232 GACCCTCCAGAGACCAGAAAGCAGCTTAGAGCTGCACAGGAGCTGAGCTGATTCAGGA 6291
QY 2116 AspLeuLeuProProGlyGlyGlnGlyGlyuProProSerProArgAspLeuLySlyCys 2135
Db 6292 GACCTCCTT---CCAGCAGCCAGGAAGAACCCCTGTTCCACGGGACCTGAAAGAGTGC 6348
QY 2136 TyrSerValGlyAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlyGlnArg 2155
Db 6349 TACAGTGTAGAGACCAGAGCTGCAGGCGCAGGCTGGGTTCTGGCTAGATGAACAGCGG 6408
QY 2156 ArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAsp 2175
Db 6409 AGACACTCCATGCTGTCAAGTGTGTGACAGCGGCTCCCAACCCCGCTATGTCCAAGC 6468
QY 2176 ProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLySlyLeu 2195
Db 6469 CCCTCAAGCCTCGGGGGCCCACTCTGGGGGTCTGGAGCCGGCCTTAAGAAAAAATC 6528
QY 2196 SerProProSerIleThrIleAspProProGlyuSerGlnGlyProArgThrProProSer 2215
Db 6529 AGCCCAACCAATATCTCTATAGACCCCGGAGAGCCAGGCTCTGGCCCCCATGCACT 6588
QY 2216 ProGlyIleCysLeuArgArgArgAlaProSerSerAspSerLySlyAspProLeuAlaSer 2235
Db 6589 CCTGTGTCTGCTCAGAGAGAGGGCGCCGCGCAGTACTTAAAGATCCCTCGGTCTCC 6648
QY 2236 GlyProProAspSerMetAlaAlaSerProSerProLysLySlyAspValLeuSerLeuSer 2255
Db 6649 AGCCCCCTTGACAGCACGCGTGCCTCAACCTCCCAAGAAAGACACGCTGAGTCTCT 6708
QY 2256 GlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6709 GGTGTGTCTTGACCCCAAGACATGGAACCC 6741
Db
RESULT 12
AAx83485
ID AAX83485 standard; cDNA; 6762 BP.
XX AC AAX83485;
XX AC
DT 07-DEC-1999 (first entry)
XX DE
XX DE Rat T-type voltage-gated Ca channel alpha-1-G (rcav1a) cDNA.
XX KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
XX KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX OS Rattus sp.
XX PN W09929847-A1.
XX PD 17-JUN-1999.
XX PF 30-OCT-1998; 98WO-US023161.
XX PR 05-DEC-1997; 97US-00985809.
XX PA (LOYO) UNIV LOYOLA CHICAGO.
XX PI Perez-Reyes E, Cribbs LL;
XX WPI; 1999-394972/33.

DR P-PSDB; AAY14590.

XX New T-type voltage-gated calcium channels.

PT Disclosure; Page 67-76; 138pp; English.

PS

XX

CC This sequence represents the coding region for a rat T-type voltage-gated
CC calcium (Ca) channel alpha-1-G designated rCav1.1a. Voltage gated channels
CC are membrane bound glycosylated proteins formed of several subunits. The
CC large alpha subunits form a pore in the membrane that is selective for a
CC given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC and IV) and each domain contains 6 putative transmembrane helical
CC segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC than L- or N-type channels. Characteristics of T-type channels include
CC short current time, slow activation kinetics near threshold, fast
CC inactivation kinetics and slow tail current. The sequences AAX83481-
CC X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC voltage-gated calcium channel proteins can be used to screen for drugs
CC which affect calcium channels. Methods are also disclosed for treating a
CC disease or disorder associated with a deficiency in a native T-type
CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6762 BP; 1362 A; 2044 C; 1917 G; 1439 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	6762
Score:	10945.00	Matches:	2107
Percent Similarity:	93.99%	Conservative:	34
Best Local Similarity:	92.49%	Mismatches:	101
Query Match:	91.94%	Indels:	36
DB:	2	Gaps:	6

US-09-611-257A-37 (1-2266) x AAX83485 (1-6762)

QY 1 MetAspGluGluGluAspGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 1 ATGAGCAGAGAGAGATGAGCGGGGCCGAGAGTCCGGACAGCCCCGTAGCTTCACG 60
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGlnLysAsp 40
Db 61 CAGCTCAACGACTCTCCGGGGCCGGGGGCCGAGGGGGCGGCTGCACGGAAGAGAC 120
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGCGCTAGCCCCGGTGTT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 181 TTCTTCTACTTGACCCAGGACAGCCGCCGCGAGCTGGTGTCTCCGACGGTCTTAAC 240
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 241 CCGTGGTTCGAGCGACTCAGTATGTGTCATTCTTCTCACTGTGTAAGTGGTATG 300
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 301 TTCAGGCCGTGTGAGACATTGCCCTGTACTCCAGCGCTGCCGATCCTGCAGGCTTC 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValLysMetValAlaLeuGly 140
Db 361 GATGACTTCATCTTTGCCCTTCTTGTCTGTGGAATGTGTGAAGATGTGGCCTTGGGC 420
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal 160
Db 421 ATCTTTGGGAAGAAATGTACTGTGGAGACACTTGAAACCGGCTTGACTTTTCAATTGTC 480
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 481 ATTCAGAGGATGCTGAGATATTCGTGGACCTGCAGAAACGTCACTTCCGCAATCAGG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200

Db 541 ACAGTCCGTGTGTCGCGACCTCAGGGCCATTAAACGGGTGCCCATGCGCATTTCTC 600
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 601 GTCACTTACTGTGGACACCTTGCCCTATGTGGGCAACGTCCTGCTGTCTGTTCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrPalaGlyLeuLeuArgAsnArg 240
Db 661 GTCTTTTTCATCTTTGGCATGTGGCGCTGCCAGCTGTGGGACAGACTGCTTCGCAACCGG 720
QY 241 CysPheLeuProGluAsnAspSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 721 TGCTTCCTCCCGAGAACTTCAAGCTCCCGCTGAGCGTGAGCTGAGCTTATTACCAG 780
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 781 ACAGGAATGAGGACGAGAGCCCCCTTCATCTGCTTCAGCCTCGGAGATGGCATGAGA 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 841 TCCTGCAGAGGTGTGCCACACTCGTGGGGAAGCGGTGTGTGCCCATCTGCAGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTyrAsnGlnTyrTyr 320
Db 901 GACTATGAGACCTATAACAGTTCCAGCAACACACCTGTGTCAACTGGAAACAGTACTAT 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnAspAsnIle 340
Db 961 ACCAACTGCTCTGCGGGCAGCACAACCCCTTCAAAGCGCCATCACTTGACAAACATT 1020
QY 341 GlyTyrAlaTyrPalaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1021 GGCTATGCCCTGATGCGCACTCTCCAGTCACTACAGAGGAGGCTGGGTCGACATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1081 TACTTCGTAATGAGCGCTCACTCCTTCTACACTTCACTTCACTTCTTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1141 GTGGGCTCTTCTTCAATGATCAACCTGTGCTGTGTGATTGCCACGAGTCTCCGAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1201 ACCAAACAGCGGAGAGTCACTGATGCGGAGCAGCGTGTACGATTCTGTCCAATGCT 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGlnLeuLysTyrLeu 440
Db 1261 AGCACCTGGCAAGCTTCTCTGAGCCAGGACGTGCTATGAGAGCTACTCAAGTACCTG 1320
QY 441 ValTyrIleLeuArgLysAlaIleArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1321 GTGTACTCTCCGAAAGACGCCGAGAGCTGGCCAGGTCTTAGGGCTATAGCGGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1381 CCGGCTGGGCTGCTCAGACGCCCAAGTGCCCGTGTGGGACAGAGCCCCCAGTGGC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1441 AGCTGCACTCGCTCACACCGTCGTGTGTGTCTGCACCACTGTGTCCACCATCACAC 1500
QY 501 HisHisHisIstYrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1501 CACCATCACCACTACCACTGGGTATATGGAGCGCTCAGAGTTCCCGGGCCAGCCAGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1561 ATCCAGAGCAGGATGCGAATGGGTCTCGCGGCTCATGCTACACCACTCTACACCC 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560

Db 1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGAGTCTGTACACAGCTTCTACCATGCTGAC 1680
QY 561 CYSHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1681 TGCCACTTGAGCCAGTCCGTTGCCAGGCACCCCTCCAGATGCCCATCGGAGGCATCT 1740
QY 581 G1yArgThrValG1ySerG1yLysValTyProThrValHisThrSerProProGlu 600
Db 1741 GGTAGGACTGTGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAAGCCCTCCACCAGAG 1800
QY 601 ThrLeuLysG1uLysAlaLeuValG1uValAlaAlaSerSerG1yProProThrLeuThr 620
Db 1801 ATACTGAAGATAAAGCACTAGTGAGGTGGCCCCAGCCCTGGGCCCCCACCCTCACCT 1860
QY 621 SerLeuAsn1leProProG1yProTyrrSerSerMetHisLysLeuLeuG1uThrGlnSer 640
Db 1861 AGCTTCAACATCCCACTGGGCCCTTACGCTCCATGCACAAGCTCCTGGAGACACAGAGT 1920
QY 641 ThrG1yAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerG1y 660
Db 1921 ACCGGAGCCTGCGCATAGCTCTCTGCAAAATCTCCAGCCCTTGCTCCAAGGCACAGAGTGA 1980
QY 661 AlaCysG1yProAspSerCysProTyrrCysAlaArgAlaG1yAlaG1yGluValG1uLeu 680
Db 1981 GCTGCGGGCCGGACAGTGTTCCTACTGTGCCGGAAGAGAGAGAGAGAGAGAGAGAGTCC 2040
QY 681 AlaAspArgG1uMetProAspSerAspSerGluAlaValTyrrGluPheThrGlnAspAla 700
Db 2041 GCTGACCATGTGATGCTGACTCAGACAGCAGAGCTGTGTATGAGTTCAACAGAGAGCT 2100
QY 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuG1yProAsp 719
Db 2101 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGAGCTGGGCCAGAT 2160
QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
Db 2161 GCAGAGCCTAGTTCTGTGCTGGCTTCTGGAAGGTGATCTGTGACACATTCGGGAAGATC 2220
QY 740 ValAspSerLysTyrrPheG1yArgG1yIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 2221 GTAGATAGCAAAATACTTGGCCGGGAATCATGATCGCCATCTGTGTAATACACTCAGC 2280
QY 760 MetG1yIleGluTyrrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrrG1yPro 799
Db 2341 ATGCTCTTCAACAGCCTCTTGCCCTTGAGATGCTGTGAACCTGCTGTCTACGCTCCC 2400
QY 800 PheG1yTyrrIleLysAsnProTyrrAsnIlePheAspG1yValIleValIleSerVal 819
Db 2401 TTTGGCTACATTAGAATCCCTTCAACATCTTTGATGGTGTCAATTGTGTCACTCAGTGTG 2460
QY 820 TrpGluIleValG1yGlnGlnG1yG1yLeuSerValLeuArgThrPheArgLeuMet 839
Db 2461 TGGGAGATTGTGGCCAGAGGAGGTGGCTGTGCTGCGGACCTTCGCGCTGATG 2520
QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
Db 2521 CGGGTGCTGAAGCTGTGCGCTTCTCGCGCCGCTGCAGCGCCAGCTCGTGGTGCCTCATG 2580
QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879
Db 2581 AAGACCATGGACAACGTGGCCACTTCTGCATGCTCTCATGCTGTTCATCTTCATCTTC 2640
QY 880 SerIleLeuG1yMetHisLeuPheG1yCysLysPheAlaSerG1uArgAspG1yAspThr 899
Db 2641 AGCATCTGGGCATGCATCTCTTTGGTTGCAAGTTCCGATCTGAACGGGATGGGAGACAG 2700
QY 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
Db 2701 TTGCCAGACCGGAAGAAATTGCACTCCCTGCTCTGGGCCATGTCACACTGTCTTTCAGATT 2760

QY 920 LeuThrGlnGluAspTrpAsnLysValLeuTyrrAsnG1yMetAlaSerThrSerSerTrp 939
Db 2761 CTGACTCAGGAAGACTGGAATAAAGTCTCTTACAACGGCATGGCCCTCCACATCGTCTTGG 2820
QY 940 AlaAlaLeuTyrrPheIleAlaLeuMetThrPheG1yAsnTyrrValLeuPheAsnLeuLeu 959
Db 2821 GCTGCTCTTACTTTCATCGCCCTCAATGACTTTTGGCAACTTATGTGCTCTTAACTGTCTG 2880
QY 960 ValAlaIleLeuValG1uG1yPheGlnAlaG1uGluIleSerLysArgGluAspAlaSer 979
Db 2881 GTGGCCATTCTTGGAAGGATTCAGGCGACAG----- 2913
QY 980 G1yGlnLeuSerCysIleGlnLeuProValAspSerGlnG1yAspAlaAsnLysSer 999
Db 2914 -----GAGATGCCACCAAGTCT 2931
QY 1000 GluSerGluProAspPhePheSerProSerLeuAspG1yAspG1yAspArgLysLysCys 1019
Db 2932 GAGTCAGAGCCTGATTTCTTTCCGCAAGTGTGATGTGATGGGACAGAAAGAACGCC 2991
QY 1020 LeuAlaLeuValSerLeuG1yGluHisProGluLeuArgLysSerLeuLeuProProLeu 1039
Db 2992 TTGGCCCTGTGGCTTTGGGAAGACAGCGGAACCTACGAAGAGCCTTTTGCCACCCTC 3051
QY 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrG1yLeuG1y 1059
Db 3052 ATCATCCATACGGCTGCAGACCAATGTCAACCCCAAGAGCTCCAGACAGAGTGTGGG 3111
QY 1060 GluAlaLeuG1yProAlaSerArgArgThrSerSerSerG1ySerAlaGluProG1yAla 1079
Db 3112 GAAGCACTGGGCTCTGGCTCTCGACGTACCAAGTAGAGTGGTCCGCTGAGCCTGAGCT 3171
QY 1080 Ala--HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098
Db 3172 GCCCACCATGAGATGAATGTCCGCCAAGTGCCCGCAGCTCCCGCAAGTCCCTGGAGT 3231
QY 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuG1yArgAlaProSer 1118
Db 3232 GCGGCAAGCAGCTGGACCAAGCAGCGCTCCAGCAGAAACAGCTGGGCCGCCCCAGC 3291
QY 1119 LeuLysArgArgSerProSerG1yGluArgArgSerLeuLeuSerG1yGluG1yGlnGlu 1138
Db 3292 CTAAGCGGAGAGGCCCGAGCGGAGGAGGTCCCTGCTGTGAGAGGCGCAGAG 3351
QY 1139 SerGlnAspGluGluSerSerG1uGluArgAlaSerProAlaG1ySerAspHis 1158
Db 3352 AGTCAGGATGAGAGGAAGTTCAAGAGAGAACCGGCCAGCCCAAGCAGAGTACCAT 3411
QY 1159 ArgHisArgG1ySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178
Db 3412 CGCCACAGGGGTCTCTTGAACGTGAGGCCAAGATTCTTTGACTGCTGCACACTCTG 3471
QY 1179 GlnValProG1yLeuHisArgThrAlaSerG1yArgG1ySerAlaSerGluHisGlnAsp 1198
Db 3472 CAGGTCCGGGCTGCACCGCACAGCGCGCCGAGCTGTGCTTGAGCACCAGAC 3531
QY 1199 CysAsnG1yLysSerAlaSerG1yArgLeuAlaArgAlaLeuArgProAspAspProPro 1218
Db 3532 TGTAATGGCAAGTCGCTTCAAGCGCGTTGGCCCGCACCCCTGAGACTGATGACCCCAA 3591
QY 1219 LeuAspG1yAspAspAlaAspAspG1uG1yAsnLeuSerLysG1yGluArgValArgAla 1238
Db 3592 CTGGATGGGATGATGACAATGATGAGGAAATCTGAGCAAGGGGAACGATACAGACC 3651
QY 1239 TrpIleArgAlaArgLeuProAlaCysTyrrLeuGluArgAspSerTrpSerAlaTyrrIle 1258
Db 3652 TGGGTCAATCCCGCTTCTGCTGTGCGCGGAGAGCGAGATTCTGTCGGCTATATC 3711
QY 1259 PheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278
Db 3712 TTTCCTCCTCAGTCAAGGTTTGTCTGTGTACCCGAGATCATCACCAAGAGATT 3771

QY	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298
Db	3772	GACCATGTGTCCTCGTCATCATCTTCTCAACTGTATCAACCATCGTATGAGCGCCC	3831
QY	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318
Db	3832	AAATATGACCCCCACAGCGCTGAGCGCATCTTCTGACCCCTCCAACTACATCTTCACG	3891
QY	1319	AlaValPheLeuAlaGluMetThrValLysValAlaIleGluIYTrpCysPheGlyGlu	1338
Db	3892	GCAGTCTTCTAGCTGAATAAGACAGTGAAGGTGTGTGCACCTGGGCTGTGCTTTGGGAG	3951
QY	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleSerVal	1358
Db	3952	CAGGCTACCTGGCGACAGCTGGAATGTGTGAGCGGCTTCTGTGTCTCATCTCCGTC	4011
QY	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
Db	4012	ATCGACATCCTGTCTCATGTGTCTCCGACAGCGGCACCAAGATCCTTGCGATGTGAGG	4071
QY	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	4072	GTGCTGGCGCTGCTGCGGACCCCTGCGTCCACTCAGGGTATCAGCCGGGCCAGGGACTG	4131
QY	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIle	1418
Db	4132	AAGCTGGTGTAGAGACTCTGATGTATCCTCCAACCATTGGCAACATTGTGTCAATT	4191
QY	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Db	4192	TGCTGTGCCTTCTTCATCATTTTGGAAATTCTCGGGTGACGCTCTTCAAGGGAAGTTC	4251
QY	1439	PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
Db	4252	TTCGTGTGTACAGGCTGAGGACACCAGAACATCACTAACAAATCCGACTCGCGTGAGGCC	4311
QY	1459	SerTyrArgTrpValArgHisLysLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	4312	AGCTACCGATGGGTCGGGCAAGTACAACTTGACAACTGGGCCAGGCTCTGATGTCC	4371
QY	1479	LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla	1498
Db	4372	CTGTTTGTGCTGCGCTCCAGGATGGTTGGTTGACATCATGTATGATGGGCTGATGCT	4431
QY	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle	1518
Db	4432	GTGGGTGTGATCAGCAGCCCATCATGAACCAACCCCTGGATGCTGTATCTTCACTC	4491
QY	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu	1538
Db	4492	TCCTTCCTCCTCATCGGCTTCTTTGTCTGAACATGTTTGTGGGCGTGTGTGGAG	4551
QY	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLys	1558
Db	4552	AACTTCCATTAAGTCAGACAGCAACAGAGAGAGAGAGCGGCGGTGAGGAGAAAG	4611
QY	1559	ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln	1571
Db	4612	CGACTACGGAGGCTGGAGAAAAGAGAAGAGTAAGAGAGACAGATGGCCGAAGCCAG	4671
QY	1572	CysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThr	1591
Db	4672	TGCAAGCCCTACTACTGTACTGAGATTCCGGCTCTTGTCTCCACCACCTGTGTACC	4731
QY	1592	SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAla	1611
Db	4732	AGCCACTACCTGGAACCTTTCATCACTGTGTCACTGGGCTGAACGTGTCTACTATGGCC	4791
QY	1612	MetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle	1631
Db	4792	ATGGAACATTACAGCAGCCCGAGATCCTTGACGAGGCTCTGAAGATCTGCAATTACATC	4851
QY	1632	PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg	1651

Db	4852	TTTACCCTCACTTTGTCTTGTAGATCAAGTTTCAAACTTGTGGCTTTGGCTTCCGCCGT	4911
QY	1652	PhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuSerIleMetGly	1671
Db	4912	TTCTTCCAGACAGGTGGAAACCAGCTGACCTGGCTATTGTGCTTCTGTGCCATCATGGGC	4971
QY	1672	IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg	1691
Db	4972	ATCACACTGGAGGAGATTGAGGTCAATCTGTCTGCTGCCATCAACCCCACTCATCCGT	5031
QY	1692	IleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMet	1711
Db	5032	ATCATGAGGGTCTCCGCAATTGCTCGAGTTCTGAAGCTGTTGAAGATGCTGTGGGCATG	5091
QY	1712	ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeu	1731
Db	5092	CGGGCACTGCTGCACACGGTGATGCAGGCCCTGCCCAAGTGGGGAACCTGGACTTCTC	5151
QY	1732	PheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGlu	1751
Db	5152	TTCATGTTATTGTTTTCATCTTTCACGCTCTGGCGGTGAGCTCTTTGGAGACCTGGAG	5211
QY	1752	CysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGly	1771
Db	5212	TGTATGAGACACACCTTGTGAGGGCTGGGTCCGATGCCACCTTAGGAACCTTGGT	5271
QY	1772	MetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLys	1791
Db	5272	ATGGCCTTTCGACCCCTCTCCGAGTCTCACTGTTGACAACTGGAATGTTATTATGAAG	5331
QY	1792	AspThrLeuArgAspCysAspGlnGlnSerThrCysTyrAsnThrValIleSerProIle	1811
Db	5332	GACACCCCTCCGGGACTGTGACCAAGAGTCCACTGCTACACACTGTCTCCCTATC	5391
QY	1812	TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValIleAlaVal	1831
Db	5392	TACTTGTGTCCTTGTGCTGACGGCCAGTTTGTGCTGTTCAACGTGTCTATAGCTGTG	5451
QY	1832	LeuMetLysHisLeuGluGlnGlnSerAsnLysGlnAlaLysGluGluAlaGluLeuAla	1851
Db	5452	CTGATGAAGCACCCTGGAAGAAGCAACAAGAGGCCAAGAGAGGCCGAGCTCGAGGCC	5511
QY	1852	GluLeuGluLeuGlnMetLysThrLeuSerProGlnProHisSerProLeuGlySerPro	1871
Db	5512	GAGCTGAGCTGGAGATGAAGACGCTCAGCCCGCAGCCCACTCCCGCTGGCGACGCC	5571
QY	1872	PheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeu	1891
Db	5572	TTCTCTGGCCCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTTAAGCTTGGGGCTCA	5631
QY	1892	HisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGln	1911
Db	5632	CACACCACTGCCCAATTGAGACAGCTCGGCGCTTCTCCCTTGAGCACCCCAAGATGTA	5691
QY	1912	ProHisProThrGluLeuPro-----GlyProAspLeuLeuThrValArgLysSer	1928
Db	5692	CCCCACCCCGAGAGAGGTGCCAGTCCCCCCTAGACCAAGACCTGCTGACTGTAGGAAGTCT	5751
QY	1929	GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr	1948
Db	5752	GGTGTACGCCGACGCACTCTCTGCCCAATGACAGCTACATGTGCTCCGCAATGGGAGCACT	5811
QY	1949	AlaGluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerVal	1968
Db	5812	GCTGAGAGATCCCTAGGACACAGGGCTGGGGCTCCCAAAAGCCAGTCAAGCTCCATC	5871
QY	1969	LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla	1988
Db	5872	TTGTCCGTTCACTCCCAACGACGACACCACTGCATCCTACAGCTTCCCAAGAATGTG	5931
QY	1989	ProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProPro	2008

Db 5932 CACTATCTGCTCCAGCCTCATGgggCTCCACCTGGGGCCCATCCCTAACTACCCCA 5991
QY 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThrAsp 2028
Db 5992 CCTGGCCGCTCCCTCTGCTCAGAGGCTCTCAAGCGCCAGGCAATTAAGACTGAC 6051
QY 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuAlaGluValSerGlyPro 2048
Db 6052 TCCCTGGATGTGACGGGCTGGGTAGCCGGGAAGACCTGTTGTCAAGAGTGAGTGGGCC 6111
QY 2049 SerProProLeuAlaArgAlaTyrSerPheThrGlyGlnSerSerThrGlnAlaGln 2068
Db 6112 TCCTGCCCTCTGACCCGGTCTCATCTCTGGGGCGGGTCGAGCATCCAGGTGACAGAG 6171
QY 2069 HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly 2088
Db 6172 CGTTCGGGCATCCAGACAAAGTCTCCAGGACATCCGCCCTGACGCCCTTGCCAGGC 6231
QY 2089 ProGluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThr 2108
Db 6232 CTGGAACCCAGCTGGGCCAAGGACCCCTCCAGAGCCAGAAAGCAGCTTGAAGCTGACAG 6291
QY 2109 GluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGlnGlnGluProProSer 2128
Db 6292 GAGCTGAGCTGATTTCAAGAGACCTCCTT---CCAGACAGCCAGAGAACCCTGTTC 6348
QY 2129 ProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr 2148
Db 6349 CCACGGGACCTGAAGAAGTGTACAGTGTAGAGACCAGAGCTGACGGCGCAGGCTGGG 6408
QY 2149 SerTrpLeuAspGlnGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySer 2168
Db 6409 TTCTGGCTAGATGAACAGCGGAGACACTCCATTGCTGTCAAGTGTGTGACAGCGGCTCC 6468
QY 2169 GlnProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGly 2188
Db 6469 CAACCCCGCCTATGTCCAAAGCCCTCAAGCCTCGGGGGCCAACTTTGGGGGCTCTGGG 6528
QY 2189 SerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGln 2208
Db 6529 AGCCGGCCTAAGAAAAAATCAGCCACCCAGATATCTTATAGACCCCGGAGAGCCAG 6588
QY 2209 GlyProArgThrProProSerProGlyIleCysLeuArgArgArgAlaProSerSerAsp 2228
Db 6589 GGCTCTCGGCCCCCATGCACTCCTGTGTCTGCTCAGAGAGAGGGCGCGCCAGTGAAC 6648
QY 2229 SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248
Db 6649 TCTTAAGATCCCTCGGTTCTCCAGCCCTTGACAGACAGGCTGCCTCACCCTCCCAAG 6708
QY 2249 LysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6709 AAAGACACGCTGAGTCTCTGTGTTGTTGTGACCCCAACAGACATGACCCC 6762

RESULT 13
ADSI6295
ID ADSI6295 standard; DNA; 6942 BP.

AC ADSI6295;
XX
DT 02-DEC-2004 (first entry)
XX
DE Rat voltage-dependent T type alpha 1G subunit calcium channel DNA.
XX
KW Voltage-dependent ion channel; drug candidate;
KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;
KW anticonvulsant; antiarrhythmic; rat; alpha 1G subunit; ds.
XX
OS Rattus norvegicus.
XX
PN US2004175761-A1.
XX
PD 09-SEP-2004.

XX PF 01-MAR-2003; 2003US-00377139.
XX PR 01-MAR-2003; 2003US-00377139.
XX PA (MACK/) MACKINNON R.
PA (MACK/) MACKINNON A L.
PA (JIAN/) JIANG Y.
PA (RUTA/) RUTA V.
PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;
XX WPI; 2004-642122/62.
DR REFSEQ; NM_031601.
XX
PT Screening drug candidates that target voltage dependent ion channel
PT protein, involves contacting screening protein with chemical compound,
PT which is drug candidate and determining whether chemical compound binds
PT to screening protein.
XX
PS Disclosure; SEQ ID NO 7; 61pp; English.
XX
CC The invention relates to the composition of matter suitable for use in
CC identifying chemical compounds that bind to voltage-dependent ion channel
CC proteins. The composition comprises a screening protein that consists of
CC an ion channel voltage sensor domain of the ion channel protein
CC immobilised on a solid support. The invention is useful for identifying
CC chemical compounds (drug candidate) that bind to voltage-dependent ion
CC channel proteins. The drug candidate of the invention is utilised for
CC treating a condition mediated by aberrant electrical activity that
CC initiates uptake or release of neurotransmitters and contraction of
CC muscles. The drug candidate of the invention is also utilised for
CC treating epilepsy and arrhythmia. The present sequence is a voltage-
CC dependent calcium channel DNA.
XX
SQ Sequence 6942 BP; 1383 A; 2126 C; 1961 G; 1472 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 6942
Score: 10945.00 Matches: 2107
Percent Similarity: 93.99% Conservative: 34
Best Local Similarity: 92.49% Mismatches: 101
Query Match: 91.94% Indels: 36
DB: 13 Gaps: 6
US-09-611-257A-37 (1-2266) x ADSI6295 (1-6942)
QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 114 ATGACGAGGAGGAGATGAGCGGGCCCGAGAGTCCGGACAGACCCCGTAGCTTCACG 173
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 174 CAGCTCAACGACCTGTCCGGGGCCGGGGCCGCGAGGGGCCGGGGTGCACGAAAGGAC 233
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 234 CCGGGCAGCGCGGACTCCGAGGCGGAGGCTGCCGTACCCGGCGCTAGCCCGGTGTT 293
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 294 TTCTTCTACTTGACCAAGACAGACGCCCGCGGAGAGTGTGTCTCCGACAGGTGTAAAC 353
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 354 CCGTGTTCAGCGAGTCAATATGCTGTCACTTCTTCAACTGTGTGACTCTGGGTATG 413
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 414 TTCAGCGCGTGTGAGACATTGCTGTGACTCCAGCGCTCCGAGATCTGACAGGCTTC 473
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140

Db 474 GATGACTTCATCTTTGCCCTTCTTGTGCTGTGGAATGTGGTGAAGATGTGGCCCTTGGGC 533
QY 141 IlePheGlyLysLysCysTyrIleuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 534 ATCTTTGGGAAGAATGTATACCTGGGAGACACTTGAAACCGGCTTGACTTTTCATTGTGC 593
QY 161 IleAlaGlyMetIleuGluTyrSerIleuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 594 ATTGCAGGGAATGCTGGAGTATTCGCTGGAACCTGCAGAACGTCAGCTTCTCCGCGATCAGG 653
QY 181 ThrValArgValIleuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 654 ACAGTCCGTGTGCTGCAGACCGCTCAGGGCCATTAAACGGGTGCCCAAGCATGCCGATTCTC 713
QY 201 ValThrIleuLeuLeuAspThrIleuProMetLeuGlyAsnValIleuLeuCysPhePhe 220
Db 714 GTCACATTAATGCTGCAGACACCTTGCTTATGCTGGCAACGTCCTGCTGCTGTTTCTTC 773
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 774 GTCTTTTTCATCTTTGGCATCGTGGCGGTCCAGCTGTGGGCAAGAACTGCTTCGCAACCGG 833
QY 241 CysPheIleuProGluAsnPheSerIleuProIleuSerValAspLeuGluArgTyrTyrGln 260
Db 834 TGCTTCCTCCCGAGAACTTCAAGCTCCCTGAGCGTGACCTGGAACCTTATTAACAG 893
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 894 ACAGAGAATGAGAGACGAGACCCCTTCACTGCTCTCAGCTCCGGAGAATGGCATGAGA 953
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 954 TCCTGCAGAGTGTGCCACACACTGCTGGGGGAAGCGGTGTGGCCACCCCTGCAGTCTG 1013
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 1014 GACTATGAGACCTATAACAGTTCACAGAACACACCTGTGTCAACTGGAACCACTATAT 1073
QY 321 ThrAsnCysSerAlaGlyGlyHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
Db 1074 ACCAACTGCTGTGGGGCGAGACAAACCTTCAAAGGCGGCATCAACTTGACAACATT 1133
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrIleuGluGlyTrpValAspIleMet 360
Db 1134 GGCTATGCCCTGGATCGCCATCTTCCAGTCATCACACTGAGGGCTGGTGCACTCATG 1193
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle 380
Db 1194 TACTTCGTAAATGAGCGCTCACTCCTTCTTACAACCTTCACTTCACTTCTTCTCATC 1253
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1254 GTGGGCTCCTTCTTCAATGATCAACCTGTGCTGTGTGATGTCACGAGTTCGCCAG 1313
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1314 ACCAAACAGCGGAGAGTCAAGTGAAGCGGAGCAGCGTGAAGATTCTGTCCAATGCT 1373
QY 421 SerThrIleuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuIleTyrLeu 440
Db 1374 AGCACCCCTGGCAAGCTTCTCTGAGCCAGGCAAGCTGATGAGAGCTACTCAAGTAACTG 1433
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1434 GTGTACATCTCTCCGAAAAGCAAGCCCAAGGCTGGCCCAAGTCTTAGGGCTATAGCGGTG 1493
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1494 CGGGCTGGGCTGCTCAGCAGCCCAAGTGGCCCGTAGTGGGCAAGAGCCCAAGCCAGTGGC 1553
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1554 AGCTGCACTCGCTCAACACCGTGTGTGTCTGTCCACCACCACTGTGTCCACCACCATCAC 1613

QY 501 HisHisHisHisTyrHisIleuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1614 CACCATCACCACTACCACCTGGGTAATGGGAGCGCTCAGAGTTCCCGGGCCAGCCAGAG 1673
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 1674 ATCCAGGACAGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCTCTACACCC 1733
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1734 ACTCCCTCTGGGGCCCTCCGAGGGGTGCGGAGTGTGTACACAGCTTCTTACCATGTGAC 1793
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1794 TGCCACTTGAGCCAGTCCGTTGCCAGGACACCCCTCCAGATGCCCATCGAGGATCT 1853
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
Db 1854 GGTAGCACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACAGAG 1913
QY 601 ThrIleuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1914 ATACTGAAGATAAAGCACTAGTGAAGTGTGCCCCCAAGCCCTGGGGCCCCCACTCACC 1973
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 1974 AGCTTCAACATCCACCTGGGCCCTTCAGCTCATGACAAAGCTCCTGAGACACAGAGT 2033
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2034 ACGGAGCCTGCCATAGCTCCTGCAAAATCTCAGACCTTGCTCCAAGGACAGACAGTGA 2093
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2094 GCTGGGGGGCCGACAGTGTCCCTACTGTGCCCGGACAGAGCAGAGACCAAGAGTCC 2153
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2154 GCTGACCATGTCAATGCCCTGACTCAGACAGCGAGCTGTATGAGTTCAACAGAGCGCT 2213
QY 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719
Db 2214 CAGCAGAGTACCTCCGGGATCCACAGCCGGCGGCGACAGCGAGCCTGGGCCAGAT 2273
QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
Db 2274 GCAGAGCTTAGTCTGTGTGCTGCTTCTTGAGGCTGATGTGACACATTCGGAAGATC 2333
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 2334 GTAGATAGCAATACTTTGGCGGGGAATCATGATCGCCATCCTGTGTAATACACTCAGC 2393
QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 2394 ATGGGATCGAGTACCACGACGAGCCCGAGGAGCTCAACCAAGCCCTGGAATCAGCAAC 2453
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799
Db 2454 ATGCTTTCACCAAGCCTTTCGCCCTTGAGAGTGTGCTGAAACTGCTTGTCTTACGGTCCC 2513
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerVal 819
Db 2514 TTTGGTACATTAAAGATCCCTTACAACATCTTGTATGTGTGTCATGTGTCAGTGTG 2573
QY 820 TrpGluIleValGlyGlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
Db 2574 TGGGAGATTGTGGCCAGCAGGAGGTGGCTGTGGTGTCTGCGGACTTCCGCTGATG 2633
QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValIleuMet 859
Db 2634 CGGTGTGAAGCTGTGTGCTTCTGCGCGCCCTGCAGCGCCAGCTGTGTGCTCATG 2693

QY	860	LysThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePhe	879
Db	2694	AAGACCATGACAAAGTGGCACCTTCTGCATGCTCTTCATCTTCACTTCTTC	2753
QY	880	SerIleLeuGlyMethIleuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr	899
Db	2754	AGCATCTCTGGCATGCATCTTTGGTTGGACAGTTCCGACTGGAACGGGATGGGACACG	2813
QY	900	LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle	919
Db	2814	TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATGCTCACTGCTTTGAGATT	2873
QY	920	LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp	939
Db	2874	CTGACTCAGGAAGACTGGAATAAGTCTCTACAACGGCATGGCTCCACATCGTCTTGG	2933
QY	940	AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValIleuPheAsnLeuLeu	959
Db	2934	GCTGCTCTTACTTCATCGCCCTCATGACTTTTGGCACTATGTGCTCTTAAACCTGCTG	2993
QY	960	ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer	979
Db	2994	GTTGCCATTCTTGTGAAGATTCCAGGCAGAG-----	3026
QY	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer	999
Db	3027	-----GGAGATGCCACCAAGTCT	3044
QY	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019
Db	3045	GAGTCAGAGCCTGATTTCTTTCCGCCCACTGTGATGTGATGGGACAGAAAGAAGCC	3104
QY	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeuLeu	1039
Db	3105	TTGGCCCTGTGTGCTTTGGAGAACACGGGAACTAAGAAAGACCTTTTGCCACCCTTC	3164
QY	1040	IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly	1059
Db	3165	ATCATCCATACGGCTGCGACACCAATGTCAACCCCAAGAGCTCCAGCACAGAGTGTGGG	3224
QY	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla	1079
Db	3225	GAAGCACTGGGCTCTGGCTCTCGACGTACCACTAGACAGTGGTCCGCTGAGCCTGAGCT	3284
QY	1080	Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSer	1098
Db	3285	GCCCAACATGATGAATGTCCGCCAAGTGCCCGCAGCTCCCGCACAGTCCCTGAGCT	3344
QY	1099	AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer	1118
Db	3345	GCGGCAGCAGCTGGACACGACGCGCTCCAGCAGAACAGCTGGGCGGGCCCCCAGC	3404
QY	1119	LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlu	1138
Db	3405	CTTAAACGGAGAGAGCCCGAGCGGGAGCGGAGGTCCCTGCTGTCTGGAAGAGGCCAGAG	3464
QY	1139	SerGlnAspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHis	1158
Db	3465	AGTCAGGATGAGGAGGAAGTTCAAGAAGAGACCGGGCCAGCCACAGGACAGTGAACAT	3524
QY	1159	ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAsnLeuProAspThrLeu	1178
Db	3525	CGCCACAGGGGTCTCTTGAACGTGAGGCCAAGAGTCTTTGACCTGCTGACACTCTG	3584
QY	1179	GluValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp	1198
Db	3585	CAGGTGCGGGGCTGCACCGCACAGCGCGGCGGAGCTTGCTCTGAGCACCAAGAC	3644
QY	1199	CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro	1218
Db	3645	TGTAATGGCAAGTCCGCTTCAGGGCGTTTGGCCCGCACCCCTGAGGACTGATGACCCCAA	3704
QY	1219	LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla	1238

Db	3705	CTGATGGGATGATGACATGATGAGGGAATCTGAGCAAAAGGGAGACCGCATACAAGCC	3764
Qy	1239	TriPLeArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle	1258
Db	3765	TGGGTCAATCCCGGCTTCCTGCTGTCGCCGAGAGCAAGATTCTTGTCGGCTATATC	3824
Qy	1259	PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278
Db	3825	TTTCCTCCTCAGTCAAGGTTTGGTCTCCTGTGTACCGGATCATCACCCACAGATGTTT	3884
Qy	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298
Db	3885	GACCATGTGTCCTCGTCATCATCTTCTCACTGTATCACCATCGCTATGAGCGCCC	3944
Qy	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318
Db	3945	AAATTGACCCCAAGCGCTGAGCGCATCTTCTGACCCTTCCAACATCATCTTCACG	4004
Qy	1319	AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGlu	1338
Db	4005	GCACTCTTCTAGCTGAATGACAGTGAAGTGTGGCACTGGCTGTGCTTTGGGAG	4064
Qy	1339	GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358
Db	4065	CAGGCTAACCTGCGCAGCACTGGAATGTGCTGAGCGGCTGTGCTCATCTCCGTC	4124
Qy	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
Db	4125	ATGCATCTCTGTCATGCTGTCTCCGACAGCGGCAACAAGATCTTGCGATGCTGAGG	4184
Qy	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	4185	GTGCTGGGCTGCTGCGGACCTGCGTCCACTCAGGGTCATCAGCGGCCACAGGACTG	4244
Qy	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle	1418
Db	4245	AAGCTGGTGTAGAGACTCTGATGTATCTCCCTCAACCATTTGGCAACATTTGTGTCATT	4304
Qy	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Db	4305	TGCTGTGCTCTTCATCATTTTGGAAATTCGGGGTGACCTCTTCAAGGGAAGTTT	4364
Qy	1439	PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
Db	4365	TTGCTGTGTCAAGGTGAGACACCAAGAACATCATTAACAATCCGACTGCGCTGAGCC	4424
Qy	1459	SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	4425	AGCTAACGATGGGTCCGGCACAAGTACAACCTTTGACACCTGGGCCAGGCTGTATGTC	4484
Qy	1479	LeuPheValLeuAlaSerLysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAla	1498
Db	4485	CTGTTTGTGCTGCTCCCAAGGATGTTGGTTGACATCATGTATGATGGCGTGGATGCT	4544
Qy	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle	1518
Db	4545	GTTGGTGTGATCAGACGCCATCATGAACACCAACCCCTGATGCTGTATACTTCATC	4604
Qy	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538
Db	4605	TTCTTCTCTCATCTGTCGCTTCTTGTCTGAACATGTTTGTGGCGTGTGTGGAG	4664
Qy	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLys	1558
Db	4665	AACTTCCATTAAGTCAGACAGCACCAAGAGAGAGAGGCGGCGGTGAGGAGAG	4724
Qy	1559	ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln	1571
Db	4725	CGACTACGAGGCTGAGAAAGAGAGAGAGTAAGAGAGAGATGCGCGAAGCCAG	4784
Qy	1572	CysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThr	1591

Db 4785 TGCAGCCCTACTACTGTGACTACTGAGATTCCGGCTCCTGTGCCACCACCTGTGTACC 4844
QY 1592 SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAla 1611
Db 4845 AGCCACTACTGGAACCTCTTCATCATCTGGTGTGCATCGGGCTGAACGTGTGCATATGGCC 4904
QY 1612 MetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle 1631
Db 4905 ATGGAACATTACCAAGACGCCCAAGATCTTGGACGAGGCTTGAAGATCTGCAATTACATC 4964
QY 1632 PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg 1651
Db 4965 TTATCCGTCACTTTGTCTTGTGAGTCAGTTTCAAACCTTGCGCTTTGGCTTCCGCCGT 5024
QY 1652 PhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGly 1671
Db 5025 TTCTTCCAGACAGGTGGAACCAAGCTGGAACCTGCTATTGTGCTTCTGTCCATCATGGGC 5084
QY 1672 IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg 1691
Db 5085 ATCACACTGGAGAGATTGAGGTCAATCTGTGCTGCCCAATCAACCCCAACCATCATCCGT 5144
QY 1692 IleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMet 1711
Db 5145 ATCATGAGGGTGTCCGCATTCGCAGTCTTGAAGCTGTGAAGATGGCTGTGGGCATG 5204
QY 1712 ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeu 1731
Db 5205 CGGGCACTGCTGCACACGGTGATGCAGGCCCTGCCCCAAGTGGGGAACCTGGGACTTCTC 5264
QY 1732 PheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGlu 1751
Db 5265 TTCAATGTTATTGTTTTCATCTTTGACACTGTGGCGTGAAGCTCTTTGAGACCTGGAG 5324
QY 1752 CysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGly 1771
Db 5325 TGTGATGAGACACACCTTGTGAGGGCTGGGTGGCATGCCACTTTAGGAACTTTGGT 5384
QY 1772 MetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLys 1791
Db 5385 ATGGCTTTTTCGACCTCTTCCGAGTCTCCACTGTGACAACTGGAATGTATTATGAAG 5444
QY 1792 AspThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIle 1811
Db 5445 GACACCCCTCCGGGACTGTGACCAGAGTCCACCTGCTACACACTGTCATCTCCCTATC 5504
QY 1812 TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaVal 1831
Db 5505 TACTTTGTGTCTTCTGCTGTGACGGCCAGTTTGTGCTGTGTCAACGTGTGCTAGCTGTG 5564
QY 1832 LeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAla 1851
Db 5565 CTGATGAAGCACTGGAAGAAAGCAAAAGAGGCCAAGGAGAGGCCGAGCTCGAGGCC 5624
QY 1852 GluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerPro 1871
Db 5625 GAGCTGAGCTGAGATGAAGACGCTCAAGCCCGCAGCCCACTCCCGCTGGGCGAGCCCC 5684
QY 1872 PheLeuTrpProGlyValGlyGlyProAspSerProAspSerProLysProGlyAlaLeu 1891
Db 5685 TTCTCTGGGCGGGGTGAGGGGTCAACAGTACTGACAGCCCTAAGCCTGGGGTCCA 5744
QY 1892 HisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGln 1911
Db 5745 CACACCACTGCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCAAGATGGTA 5804
QY 1912 ProHisProThrGluLeuPro-----GlyProAspLeuLeuThrValArgLysSer 1928
Db 5805 CCCCAACCCCGAGAGAGGTGCCAGTCCCTTAGGACCAAGACTGTGACTGAGGAAGTCT 5864
QY 1929 GlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThr 1948
Db 5865 GGTGTACGGCGGACGCACTCTCTGCCCAATGACAGCTACATGTGCGCAATGGGAGCACT 5924

QY 1949 AlaGluGlyProLeuGlyHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerVal 1968
Db 5925 GCTGAGAGATCCCTTAGGACACAGGGGCTGGGGGCTTCCCCAAAGCCCAAGTCAAGCTCCATC 5984
QY 1969 LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla 1988
Db 5985 TTGTCCGTTCACTCCCAACACAGACACACAGCAGCTGCATCTACAGCTTCCCAAGATGTG 6044
QY 1989 ProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProPro 2008
Db 6045 CACTATCTGCTCCAGCCTCATGGGGCTCCCACTGGGGCGCCATCCCTAAACTAACCCCA 6104
QY 2009 ProGlyArgSerProLeuAlaGlnArgProLeuArgGlnAlaAlaIleArgThrAsp 2028
Db 6105 CCTGGCCGCTCCCTCTGGCTCAGAGGCTCTCAGGCGCCAGCAGCAATAAGACTGAC 6164
QY 2029 SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyPro 2048
Db 6165 TCCCTGCATGTGCAGGGCTGGGTAGCCGGGAAGACTGTTGTCAAGAGTGAAGTGGGCC 6224
QY 2049 SerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGln 2068
Db 6225 TCCTGCTCTTGACCCCGGTCTCATCTCTTCTGGGCGGGTCAAGCATCCAGTGCAGCAG 6284
QY 2069 HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly 2088
Db 6285 CGTTCGGCATCCAGAGCAAGTCTCCAAAGCACATCCGCTGCAGCCCTTGCCAGGC 6344
QY 2089 ProGluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThr 2108
Db 6345 CTGGAACCCAGCTGGGCCAAGACCTCCAGAGACCAAGACAGCTTAGAGCTGGAACAG 6404
QY 2109 GluLeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSer 2128
Db 6405 GAGCTGAGCTGATTTCAGAGACCTCCTT--CCAGACAGCCAGAGAACCCCTGTTCC 6461
QY 2129 ProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr 2148
Db 6462 CCACGGGACCTGAAGAAGTGTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCTGGG 6521
QY 2149 SerTrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySer 2168
Db 6522 TTCTGCTAAGATGAACAGCGAGACACTCCATGTCTGTCACTGTCTGTGACAGCGGCTCC 6581
QY 2169 GlnProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGly 2188
Db 6582 CAACCCGCTATGTCCAAGCCCTCAAGCCTCGGGGGCCAACTTGGGGGTCTGCGG 6641
QY 2189 SerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGln 2208
Db 6642 AGCCGGCCTAAGAAAAAACTCAGCCACCCAGTATCTATAGACCCCGGAGAGCCAG 6701
QY 2209 GlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAsp 2228
Db 6702 GGCTCTGGCCCCCATGCAGTCCCTGTGTCTGCTCAGAGAGAGGGCGGCGCACTGAC 6761
QY 2229 SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248
Db 6762 TCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACAGCACGGCTGCTCACCTCCCAAG 6821
QY 2249 LysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6822 AAAGACACGCTGAGTCTCTGTGTTGTCTTGACCCCAACAGACATGACCCC 6875

RESULT 14

AAX83486
ID AAX83486 standard; cDNA; 6795 BP.
XX AAX83486;
AC AAX83486;
XX
DT 07-DEC-1999 (first entry)
XX

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav1b) cDNA.
XX
KW Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS Rattus sp.
XX
PN WO929847-A1.
XX
PD 17-JUN-1999.
XX
PF 30-OCT-1998; 98WO-US023161.
XX
PR 05-DEC-1997; 97US-00985809.
XX
PA (LOYO) UNIV LOYOLA CHICAGO.
XX
PI Perez-Reyes E, Cribbs LL;
XX
DR WPI; 1999-394972/33.
DR P-PSDB; AAY14591.
XX
PT New T-type voltage-gated calcium channels.
PS Disclosure; Page 76-85; 138pp; English.
XX
XX This sequence represents the coding region for a rat T-type voltage-gated calcium (Ca) channel alpha-1-G designated rCav1b. Voltage gated channels are membrane bound glycosylated proteins formed of several subunits. The large alpha subunits form a pore in the membrane that is selective for a given ionic species. Each alpha subunit contains 4 domains (I, II, III and IV) and each domain contains 6 putative transmembrane helical segments (S1-S6). T-type Ca channels are activated at a lower voltage than L- or N-type channels. Characteristics of T-type channels include short current time, slow activation kinetics near threshold, fast inactivation kinetics and slow tail current. The sequences AAX83481-CC X83492 represent novel T-type voltage-gated Ca channel genes from humans and rats. Each of the novel Ca-channels contains a putative IVS4 region comprising the amino acid sequence AAY14598. Cells expressing the T-type voltage-gated calcium channel proteins can be used to screen for drugs which affect calcium channels. Methods are also disclosed for treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ Sequence 6795 BP; 1366 A; 2055 C; 1923 G; 1451 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 6795
Score: 10939.50 Matches: 2107
Percent Similarity: 93.53% Conservative: 34
Best Local Similarity: 92.05% Mismatches: 101
Query Match: 91.90% Indels: 47
DB: 2 Gaps: 6

US-09-611-257A-37 (1-2266) x AAX83486 (1-6795)
QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 1 ATGGAAGAGGAGGAGGATGGAGCGGGCCGAGAGTGGGAGACAGCCCCGTAGCTTCACG 60
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 61 CAGTCAACGACCTGTCCGGGGCCGGGGCCGGCAGGGGCCGGGTGCAGCGAAAAGAC 120
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 121 CCGGGCAGCGCGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGTT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgGlnValCysAsn 80
Db 181 TTCTTCACTTGAGCCAGAGACGCCCGCGGAGCTGTGTCTCCGACGGTCTGTAAAC 240
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100

Db 241 CCGTGGTTCGAGCGAGTCAAGTATGCTGTCATTTCTCACTGTGTGACTCTGGGATG 300
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 301 TTCAGGCCGTGTGAGACATTGCTGTACTCCAGCGCTGCCGATCTGCAGGCTTC 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 361 GATGACTTCATCTTGCCCTTCTTGCTGTGAAATGTGTGAAGATGTGGCTTGCGGC 420
QY 141 IlePheGlyIleSlybCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 421 ATCTTGGGAAGAATGTTACCTGGAGACACTTGAAACCGCCTTGACTTTTCATTGTC 480
QY 161 IleAlaGlyMetLeuGluTyrSerIleuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 481 ATTGAGGGATGCTGAGTATTCCGTGACCTGCAGAACGTCACTTCTCCGACGTGAG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 541 ACAGTCCGTGTGTCGACCGCTCAGGGCCATTAAACCGGGTCCAGCATGCGCATTTTC 600
QY 201 ValThrLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 601 GTACATTACTGCTGGACACACCTTGCTATGCTGGGCAACGCTCTGCTGTTCCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 661 GTCTTTTTCATCTTTGGCATCGTGGGCTCCAGCTGTGGGAGAGACTGTGCAACCGG 720
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 721 TGCTTCTCCCGAGAACTTCAGCCTCCCTGAGCGGTGAGCTGAGACCTTATTACGAG 780
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 781 ACAGAGATGAGAGAGAGAGCCCTTCACTGTCTCTCAGCTCGGAGAAATGGCATGAGA 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 841 TCCTGCAGAGTGTGCCACACTGCGTGGGAAAGCGGTGTGGCCACCCCTGCAGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 901 GACTATGAGACCTATTAACAGTTCCAGCACACCACTGTGTCACTGGAACCACTACTAT 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
Db 961 ACCAACTGCTGTGGCGGAGACACAAACCCCTTCAAGGGCGCCATCACTTGACAACATT 1020
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1021 GGCTATGCTGATCGCATCTTCCAGGTCAACACTGGAGGGCTGGGTGCACATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1081 TACTTCGTAATGAGCGCTCACTCTTCAACACTTCATCTACTTCATCTTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1141 GTGGGCTCCTTTCATGATCAACCTGTGCTGTGTGTGATGTCACGACGAGTTCTCCGAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1201 ACCAAACAGCGGAGAGTCACTGATGCGGAGACAGCGTGTACGATTCTCTCAATGCT 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1261 AGCAACCTGGCAAGCTTCTCTGAGCCAGGAGCTGTATGAGGAGCTACTCAAGTACCTG 1320
QY 441 ValTyrIleLeuArgIleAlaIleArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460

Db 1321 GTGTACATCCTCCGAAAGACGCCGAAAGGCTGGCCCAAGTCTCTAGGGCTATAGGCGGTG 1380
Qy 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1381 CGGAGCTGGGCTGCTCAGCAGCCCAAGTGGCCCGTAGTGGGCAAGAGCCCCAGCCAGTGGC 1440
Qy 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1441 AGCTGCACCTCGCTCACACCCGTCGTGTCTGTCCACCACCTGGTCCACCACCATCACAC 1500
Qy 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1501 CACCATCACCACTAACCACTGGGTAATGGGACGCTCAGAGTTCCCGGGCCAGCCCAAG 1560
Qy 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1561 ATCCAGGACAGGAGATGCCAATGGGTCTCGCCGGCTCATGCTAACACACCTCTACACCC 1620
Qy 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1621 ACTCCCTCTGGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCACTGTAC 1680
Qy 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGCAACCCCTCCAGATGCCCATCGAGGCACTCT 1740
Qy 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
Db 1741 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAAGCCCTCCACCAAG 1800
Qy 601 ThrLeuGlyGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1801 ATACTGAAGGATTAAGCACTAGTGAAGGTGGCCCCCAGCCCTGGGGCCCCCACCTCAC 1860
Qy 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 1861 AGCTTCAACATCCCACTGGGCCCTTTCAGCTCCATGCACAGCTCCTGGAGACAGAGT 1920
Qy 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 1921 ACGGAGCCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTGTCTCCAAGCAGACAGTGA 1980
Qy 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyValGluLeu 680
Db 1981 GCCTGCGGGCCGACAGTTGTCTCTACTGTGCCCGGACAGAGCAAGAGCCAGAGTCC 2040
Qy 681 AlaAspArgGluMetProAspSerAspSerGlyAlaValTyrGluPheThrGlnAspAla 700
Db 2041 GCTGACCATGTCATGCTGACTCAGACAGCGAGGCTGTGTATGAGTTACACACAGGACGCT 2100
Qy 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719
Db 2101 CAGCACAGTGAACCTCCGGATCCCAACGCCGGCGGACAGCGAGCCCTGGGCCAGAT 2160
Qy 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
Db 2161 GCAGAGCCTAGTCTGTGCTGCTTCTGGAAGGCTGATCTGTGACACATTCGGGAAGATC 2220
Qy 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 2221 GTAGATAGCAATACTTTGGCCGGGGAATCATGATCGCCATCCTGTCAATACACTCAGC 2280
Qy 760 MetGlyIleGluTyrHisGlyGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 2281 ATGGGCATCGAGTACCAAGAGCAGCCCGAGGAGCTCACCAAGCCCTGGAAATCAGCAAC 2340
Qy 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799
Db 2341 ATCGTCTTACCAGCCTCTTGGCTTGGAGATGTGCTGAACCTGCTGTACGGTCCC 2400
Qy 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerVal 819
Db 2401 TTGGCTACATTAGAATCCCTACAAACATCTTTGATGTGTCAATTGTGTCACTAGTGTG 2460

Qy 820 TrpGluIleValGlyGlnGlnGlyGlyLysLeuSerValLeuArgThrPheArgLeuMet 839
Db 2461 TGGGAGATTGTGGGCCAGAGGAGGTGGCCCTGTGGTGTGCTGCGGACCTTCCGCTGATG 2520
Qy 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValLeuMet 859
Db 2521 CGGGTGTGAAGCTGTGGCTTCTCTGCCGGCCCTGCAGCGCCAGCTCGTGTGCTCATG 2580
Qy 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879
Db 2581 AAGACCATGACAACGTTGCCACCTTCTGCATGCTCTCATGTGTTCATCTTCACTTTC 2640
Qy 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899
Db 2641 AGCATCCTGGGCATGCATCTTTGGTTGCAAGTTCCGATCTGAACGGGATGGGACACAG 2700
Qy 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
Db 2701 TTGCCAGACCGGAAGAATTCCACTCCCTGCTGGGCCATCGTCACTGTCTTCAGATT 2760
Qy 920 LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939
Db 2761 CTGACTCAGGAAGACTGGAAATAAAGTCCCTCTACACGGCATGGCCCTCCACATCGCTTGG 2820
Qy 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959
Db 2821 GTGCTCTTACTTCACTGATGCCCTCATGACTTTGGCAACTATGTGTCTTTTAACCTGCTG 2880
Qy 960 ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer 979
Db 2881 GTGGCATTTCTTGTGAAGGATTCAGGCAGAG----- 2913
Qy 980 GlyIleLeuSerCysIleGlnLeuProValAspSerGlnGlyLysAspAlaAsnLysSer 999
Db 2914 -----GGAGATGCCCAAGTCT 2931
Qy 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019
Db 2932 GAGTCAGAGCCTGATTTCTTTCCGCCAGTGTGATGGGAGACAGAAAGAGCGC 2991
Qy 1020 LeuAlaLeuValSerLeuGlyGlnHisProGluLeuArgLysSerLeuLeuProProLeu 1039
Db 2992 TTGGCCCTGTGGCTTTGGAGAAACAGCGGAATTAAGAAAGACCTTTTGCCACCCCTC 3051
Qy 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059
Db 3052 ATCATCATACGCGCTGCAGACCAATGTACACCCCAAGAGCTCCAGCAGAGTGTGGGG 3111
Qy 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079
Db 3112 GAAGCATGGGCTCTGGCTCTCGACGTACAGTAGCAGTGGGTCCGCTGAGCTTGAGCT 3171
Qy 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098
Db 3172 GCCCACCATGAGATGAATATGCCCAAGTAGCTCCCGCAGCTCCCGCAGATCCCTGAGT 3231
Qy 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118
Db 3232 GCGGCAAGCAGCTGGAACCAAGCGGCTCCAGCAGGAACAGCTGGGGCCGGCCCCCAGC 3291
Qy 1119 LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlu 1138
Db 3292 CTAAGCGGAGAGCCCGAGGGGAGCGGAGGTCCCTGTGTGAGAGGGCCAGGAG 3351
Qy 1139 SerGlnAspGlyGluGluSerSerGlyGluArgArgAlaSerProAlaGlySerAspHis 1158
Db 3352 AGTCAGATGAGAGGAAGTTCAAGAAGAGACCGGGCCAGCCAGCAGGCAGTGACCAT 3411
Qy 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178
Db 3412 CGCCACAGGGGTCTCTTGAACGTGAGGCCAAGATTCTTTGACCTGCTGACACTCTG 3471

QY 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198
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Db 3472 CAGGTGCCGGGGCTGCACCGCACAGCCGCGGAGCTTGCTCTGAGCACCAAGAC 3531

QY 1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro 1218
|||||
Db 3532 TGTATGCAAGTCGGCTTCAGGGCGTTGGCCCCGACCCTGAGGACTGATGACCCCAA 3591

QY 1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238
|||||
Db 3592 CTGGATGGGGATGATGACAATGATGAGGGAATCTGAGCAAGGGGAACGCATACAAGCC 3651

QY 1239 TrpIleArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTyrIle 1258
|||:::|||||
Db 3652 TGGGTACAGATCCCGCTTCTGCTGTTGGCCGAGAGCGAGATTCTTGCTCGGCTATATC 3711

QY 1259 PheProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278
|||||
Db 3712 TTTCCTCCTCAGTCAAGGTTTGTCTCTGTTGTCACCGGATCATCAACCACAAGATGTTT 3771

QY 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298
|||||
Db 3772 GACCATGTGTCCTGTCATCATCTCTCACTGTATCACCATCGCTATGAGCGCCCC 3831

QY 1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr 1318
|||||
Db 3832 AAAATTGACCCCAACGCGCTGAGCGCATCTTCGACCCTCTCCAATAATCATCTTCACG 3891

QY 1319 AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrPysPheGlyGlu 1338
|||||
Db 3892 GCAGTCTTCTAGCTGAATAACAGAGTGAAGGTGTGGCACTGGGCTGTGCTTGGGGAG 3951

QY 1339 GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerVal 1358
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Db 3952 CAGGCTACCTCGCGCAGCGCTGAATGTGTGACGGCTTGCTGTGCTCATCTCCGTC 4011

QY 1359 IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378
|||||
Db 4012 ATCGACATCCTGTCCTCATGTGTCTCCGACAGCGGCACCAAGATCCTTGGCATGTGAGG 4071

QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398
|||||
Db 4072 GTGTCGGGCTGCTCGGACCCCTGCTCCACTCAGGGTTCATCAGCGGCCCCAGGACTG 4131

QY 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle 1418
|||||
Db 4132 AAGCTGGTGTAGAGACTTGTATGTATCCTCCTAACCCATTGGCAACATTGTGTCAATT 4191

QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438
|||||
Db 4192 TGCCTGCTCTTCATCATTTTGGAAATTCGCGGGTGACGCTTTCAAGGGGAAGTTTC 4251

QY 1439 PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458
|||||
Db 4252 TTCGTGTGTACAGGTGAGGACACAGGAACATCACTAACAATCCGACTCGCTGAGGCC 4311

QY 1459 SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
|||||
Db 4312 AGCTAACCGATGGGTCCGGCAACAATCAACTTGAACAACCTGGGCCAGGCTGTGATGTCC 4371

QY 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498
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Db 4372 CTGTTTGTGCTGGCTCCAAAGATGTTGGGTGACATCATGTATGATGGGCTGATGCT 4431

QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
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Db 4432 GTGGGTGTGATCAGCAGCCCATCATGAACCAACAACCCCTGGATGCTGCTATACTTCATC 4491

QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538
|||||
Db 4492 TCTTCTCTCATGTGTGGCTTCTTGTCTGAACATGTTGTGTGGCGGTGTGTGGAG 4551

QY 1539 AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLys 1558

Db 4552 AACTTCATAGTGCAGACAGACCAAGAGAGAGAGGCGGAGCGGCTGAGAGAAG 4611

QY 1559 ArgLeuArgArgLeuGluLysLysArgArg----- 1568

Db 4612 CGACTACGGAGGCTGGAGAAAAAGAAAGAAATCTAATGTTGACGATGTAATGCTTCC 4671

QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580
|||:::|||||
Db 4672 GGCAGCTCAGCCAGCGCTGCGTCAGAAAGCCAGTGCAAGCCCTACTACTGTGACTACTCG 4731

QY 1581 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1600
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Db 4732 AGATTCCGGCTCTTGTCCACCACCTGTGTATCCAGCCACTACCTGGACCTTTCATCACT 4791

QY 1601 GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle 1620
|||||
Db 4792 GGTGCATCGGGCTGAACGTGTGCTACTATGCGCATGGAACATTACAGACAGCCCGCAGATC 4851

QY 1621 LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGlnSer 1640
|||||
Db 4852 CTGACAGAGGCTGTGAAGATCTGCAATTACATCTTACCGTCACTTTGTTGTGATGCA 4911

QY 1641 ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeu 1660
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Db 4912 GTTTTCAACTGTGGCTTGGCTTCCGCCGCTTCTTCCAGACAGGTGAACCAAGCTG 4971

QY 1661 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGluIleGluValAsn 1680
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Db 4972 GACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGAGAGAGATTGAGGTCAAT 5031

QY 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700
|||||
Db 5032 CTGTGCTGCGCCATCAACCCACCATCATCCGATCATGAGGTGCTCCGCAATTGCTCGA 5091

QY 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720
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Db 5092 GTTCTGAAGCTGTGAAGATGCTGTGGCATGCGGCACGTGCTGCACACAGGTGATGACG 5151

QY 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAla 1740
|||||
Db 5152 GCCCTGCCCCAGGTGGGGAACCTGGGACTTCTTCATGTTATGTTTTCATCTTGCA 5211

QY 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760
|||||
Db 5212 GCTCTGGCGGTGAGCTCTTGGAGACTGGAAGTGTGATGAGACACACCCTGTGAGGGC 5271

QY 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780
|||||
Db 5272 TTGGGTGGCATGCCACTTGTAGAACTTTGGTATGGCTTTCGAACCTCTCCGAGTC 5331

QY 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800
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Db 5332 TCCACTGTGACAACTGGAATGTATGTAAAGACACCCTCCGGGACTGTGACCAAGAG 5391

QY 1801 SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla 1820
|||||
Db 5392 TCCACCTGCTACAACTGTCATCTCCCTATCTACTTGTGTCTTCTGCTGACGCGC 5451

QY 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsn 1840
|||||
Db 5452 CAGTTTGTGCTGTCAACGTGTGTCATAGCTGTGCTGATGAAGACCTGGAAGAAAGCAAC 5511

QY 1841 LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuMetLysThrLeu 1860
|||||
Db 5512 AAAGAGGCCAAGAGAGGCGCGAGCTCGAGCCGAGCTGGAGCTGAGATGAAGACGCTC 5571

QY 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880
|||||
Db 5572 AGCCCGCAGCCCACTTCCCGCTGGGACGCCCTTCTCTGCCCCGGGTGGAGGCTGTC 5631

QY 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900
|||:::|||||

Db 5632 AACAGTACTGCACCCCTTAAGCCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCC 5691
QY 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro----- 1918
Db 5692 TCGGGCTTCTCCCTTGAGCACCACGATGGTACCCCAACCCCGAGGAGGTGCCACTCC 5751
QY 1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937
Db 5752 CTAGGACCAAGACTGTGAGTGTGAGAGTCTGTGTCTGACGGCGGACGCACTCTGTGCC 5811
QY 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGly 1957
Db 5812 AATGACAGCTACATGTGCCCGCAATGGAGCACTGCTGAGAGATCCCTAGGACACAGGGGC 5871
QY 1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977
Db 5872 TGGGGGCTCCCAAAAGCCAGTCAGGCTCATCTGTCCGTTCACTCCCAACCAAGCAGAC 5931
QY 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisleuLeuGlnProHisSerAla 1997
Db 5932 ACCAGCTGCATCCTACAGCTTCCCAAGATGTGCACTATCTGCTCCAGCCTCATGGGCT 5991
QY 1998 ProThrTrpGlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArg 2017
Db 5992 CCCACCTGGGGGCCCATCCCTAAACTACCCCACTGGCCGCTCCCTCTGGCTCAGAGG 6051
QY 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037
Db 6052 CCTCTAGGGCCGCAAGGCAATAGGACTGACTCCCTGGATGTGCAAGGGCCTGGTAGC 6111
QY 2038 ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057
Db 6112 CGGGAAGACTGTGTTCAGAGGTGAGTGGGCCCTCTCTGCCCTCTGACCCGGTCTCATCC 6171
QY 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077
Db 6172 TTCTGGGGCGGGTCAGCATCCAGGTGACAGCGTCCGGCATCCAGAGCAAAAGTCTCC 6231
QY 2078 LysHisMetThrProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097
Db 6232 AAGCACATCCGCTCCAGCCCTTGCCCAAGCCTGGAACCACTGGGCCAAGCACCT 6291
QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db 6292 CCAGAGACCAAGACAGCTTAGAGCTGACACGAGCTGAGCTGATTCAGAGACCTC 6351
QY 2118 LeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLysCysTyrSer 2137
Db 6352 CTT---CCCAGCAGCCAGGAAGAACCTCTTCCACGGGACTGAAAGAGTGTACTAGT 6408
QY 2138 ValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHis 2157
Db 6409 GTAGAGACCCAGAGCTGCAGGCGCAGGCTGGGTTCTGGCTAGATGAACAGCGGAGAC 6468
QY 2158 SerIleAlaValSerCysLeuAspSerGlySerGlnProHisleuGlyThrAspProSer 2177
Db 6469 TCCATTGCTGTCACTGTGACAGAGGGCTCCCAACCCCGCCTATGTCCAAGCCCTCA 6528
QY 2178 AsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerPro 2197
Db 6529 AGCCTCGGGGCCAACCTCTTGGGGGTCTGGGAGCCGCGCTAAGAAAAAACACTCAGCCA 6588
QY 2198 ProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSerProGly 2217
Db 6589 CCCAGTATCTTAAGACCCCGGAGAGCCAGGGCTCTCGGCCCCCATGACAGTCTGTGT 6648
QY 2218 IleCysLeuArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyPro 2237
Db 6649 GTCTGCCTCAGAGGAGGGCGCGCGCACTGACTTAAGATCCCTCGGTCTCAGCCCC 6708
QY 2238 ProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu 2257
Db 6709 CTTGACAGCAGCGCTGCTCACCCTCCCAAAAGAAAGACACGCTGAGTCTCTGTGTTTG 6768

QY 2258 SerSerAspProAlaAspLeuAspPro 2266
Db 6769 TCTTGTGACCCCAACAGACATGACCCCC 6795

RESULT 15

AAx83487

ID AAX83487 standard; cDNA; 6816 BP.

XX AAX83487;

AC AAX83487;

DT 07-DEC-1999 (first entry)

XX 07-DEC-1999 (first entry)

DE Rat T-type voltage-gated Ca channel alpha-1-G (rCav1.1c) cDNA.

XX Human; T-type voltage-gated calcium channel; membrane; pore; ion;

KW activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.

XX Rattus sp.

OS Rattus sp.

XX WO9929847-A1.

PN 17-JUN-1999.

PD 30-OCT-1998; 98WO-US023161.

XX 05-DEC-1997; 97US-00985809.

XX (LOYO) UNIV LOYOLA CHICAGO.

PA Perez-Reyes E, Cribbs LL;

XX WPI; 1999-394972/33.

DR P-PSDB; AAY14592.

XX New T-type voltage-gated calcium channels.

PT Disclosure; Page 85-94; 138pp; English.

XX This sequence represents the coding region for a rat T-type voltage-gated

CC calcium (Ca) channel alpha-1-G designated rCav1.1c. Voltage gated channels

CC are membrane bound glycosylated proteins formed of several subunits. The

CC large alpha subunits form a pore in the membrane that is selective for a

CC given ionic species. Each alpha subunit contains 4 domains (I, II, III

CC and IV) and each domain contains 6 putative transmembrane helical

CC segments (S1-S6). T-type Ca channels are activated at a lower voltage

CC than L- or N-type channels. Characteristics of T-type channels include

CC short current time, slow activation kinetics near threshold, fast

CC inactivation kinetics and slow tail current. The sequences AAX83481-

CC X83492 represent novel T-type voltage-gated Ca channel genes from humans

CC and rats. Each of the novel Ca-channels contains a putative IVS4 region

CC comprising the amino acid sequence AAY14598. Cells expressing the T-type

CC voltage-gated calcium channel proteins can be used to screen for drugs

CC which affect calcium channels. Methods are also disclosed for treating a

CC disease or disorder associated with a deficiency in a native T-type

CC calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc

CC XX

SQ Sequence 6816 BP; 1373 A; 2058 C; 1932 G; 1453 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0

Score: 10925.00

Percent Similarity: 93.16%

Best Local Similarity: 91.72%

Query Match: 91.78%

DB: 2

Gaps: 6

US-09-611-257A-37 (1-2266) x AAX83487 (1-6816)

QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGlnSerGlyGlnProArgSerPheMet 20
Db 1 ATGACAGAGAGAGAGATGAGCGGGCGCGGAGAGTGGGACAGACCCCGTACCTTACAG 60

QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGlyLysAsp 40
:::|||||
Db 61 CAGCTCAACGACCTGTCGGGGCCGGGGCCGAGGGGCCGGGGTTCGACGGAAGAAGAC 120
QY 41 ProGlySerAlaAspSerGlyAlaGlyGlyLeuProTyrProAlaLeuAlaProValVal 60
|||||
Db 121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGTGCGTACC CGCGCTAGCCCCGGTGGTT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
|||||
Db 181 TTCTTCTACTGTAGCCAGACAGCCGCCCGGAGCTGTGTCTCCGACAGGTCTGTAAc 240
QY 81 ProTrpPheGlnArgLieserMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
|||||
Db 241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCACTTCTTCTCACTGTGTGACTCTGGGTATG 300
QY 101 PheArgProCysGlnAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
|||||
Db 301 TTCAGGCCGCTGTAGGACATTGCTGTGACTTCCAGCGCTGCCGATCTGCAGGCGCTTC 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGlnMetValValLysMetValAlaLeuGly 140
|||||
Db 361 GATGACTTCATCTTGCTCTTCTTCTTGCTGTGAAATGTTGGTGAAGATGGTGGCTTGGGC 420
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
|||||
Db 421 ATCTTTGGGAAGAAATGTTACTCTGGAGACACTTGGAACCGGCTGACTTTTTCATTGTCT 480
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
|||||
Db 481 ATTGCAGGGATGCTGAGATATTCGCTGACCTGCAGAACGTACAGCTTCTCCGAGTCAGG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
|||||
Db 541 ACAGTCCGTGTGCTGCACCGCTCAGGGCCATTAAcCGGGTGCCACGATCGGCATTCTC 600
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
|||||
Db 601 GTCAcATTACTGTGACACCTTGcCTATGCTGGcCAACGTCTGCTGCTGTTCTTCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
|||||
Db 661 GTCTTTTTCATCTTGcCATGCTGGGCGTCCAGCTGTGGGcAGAGACTGCTTCGCAACCGG 720
QY 241 CysPheLeuProGlnAsnPheSerLeuProLeuSerValAspLeuGlnArgTyrTyrGln 260
|||||
Db 721 TGCCTTCTCCCGAGAACTTCAGcCTCCcCTGAGCGTGAGcCTGATTAACCAG 780
QY 261 ThrGlnAsnGlnAspGluSerProPheIleCysSerGlnProArgGlnAsnGlyMetArg 280
|||||
Db 781 ACAGAGAATGAGGACGAGAGCCCTTCACTGTCTCTCAcCTCGGGAGAAATGGCATGAGA 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
|||||
Db 841 TCCTGCAGGAGTGTGCCACACTGCGTGGGAAcGGGTGGTGGCCcCACTGCAGTCTG 900
QY 301 AspTyrGlnAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
|||||
Db 901 GACTATGAGACCTATAcAGTTCAGCAACACCAcCTGTGTCAACTGGAACCAcTACTAT 960
QY 321 ThrAsnCysSerAlaGlyGlnHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
|||||
Db 961 ACCAACTGCTCTGCGGGCGAGCAACAcCCCTTCAAGGCGCCATCAACTTGACAACAATT 1020
QY 341 GlyTyrAlaIleAlaIlePheGlnValIleThrLeuGlnGlyTyrTrpValAspIleMet 360
|||||
Db 1021 GGCTATGcCTGGATCGcCATCTTCCAGGTCACTCAcTGGAGGGcTGcGATCATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
|||||
Db 1081 TACTTCGTAATGAGCGCTCACTCTTCTACAACTTCATCTACTTCACTTCTTCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400

Db 1141 GTGGcCTCTTCTTCATGATCAACCTGTGTGCTGTGGTGAATTGCCAGCAGTTCTCCGAG 1200
QY 401 ThrLysGlnArgGlnSerGlnLeuMetArgGlnArgValArgPheLeuSerAsnAla 420
|||||
Db 1201 ACCAAcAGCGGAGAGTCAcTGAATGCGGAGCAGCGGTGTACATTCCTGTCCAATGCT 1260
QY 421 SerThrLeuAlaSerPheSerGlnProGlySerCysTyrGlnGlnLeuLeuLysTyrLeu 440
|||||
Db 1261 AGTACCCTGGCAAGCTTCTCTGAGCCAGGcAGCTGTATGAGGAGCTACTCAAGTACCTG 1320
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
|||||
Db 1321 GTGTACATCTCTCCGAAAGCAcGCCGAAcGCTGGCCcAGGTCTTAGGGCTATAGCGGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
|||||
Db 1381 CCGGCTGGCTGTCTCAGCAGCCcAGTGGCCGTAGTGGGcAGAGCCcCAcCGCCAGTGGC 1440
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis 500
|||||
Db 1441 AGCTGCACTCGCTCACACCGTGTGTGTCTGTCCACCAcCTGTGTCCACCAcCATCAcCAC 1500
QY 501 HisHisHisIleTyrHisIleGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
|||||
Db 1501 CACCATCAcCACTAACCAcCTGGGTATGGGACGTCAcAGATTCCCGGGCCAGCCcAGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
|||||
Db 1561 ATCCAGGACAGGAGATGCCAATGGGTCTCGCCGGCTCATGTACCAcCAcCTTACACCC 1620
QY 541 AlaLeuSerGlyAlaProProGlyAlaGlnSerValHisSerPheTyrHisAlaAsp 560
|||||
Db 1621 ACTCCCTCTGGGGcCCCTCCGAGGGGTGGGAGTCTGTACACAGCTTCTTACCATGTCTGAC 1680
QY 561 CysHisLeuGlnProValArgCysGlnAlaProProProArgSerProSerGlnAlaSer 580
|||||
Db 1681 TGCCACTTGAGCGAGTCCGTTGCCAGGCAcCCCTCCAGATGCCATCGGAGGcCATCT 1740
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
|||||
Db 1741 GGTAGACTGTGGTGTAGTGGAGGTGTACCCCAcTGTGATACCAcCTCCACCAcAGAG 1800
QY 601 ThrLeuLysGlnLysAlaLeuValGlnValAlaAlaSerSerGlyProProThrLeuThr 620
|||||
Db 1801 ATACTGAAGATTAAGCACTAGTGGAGTGGCCcCCCAcCGcCTGGGcCCcCAcCTCAcCC 1860
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
|||||
Db 1861 AGCTTCAACATCCACCTGGGcCTTCAcCTCATGCAACAAGCTCTTGAGACACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
|||||
Db 1921 ACGGGAGcCTGCATAGCTCTGCAAAATCTCCAGCCCTTGCTTCCAAGGCAAGACAGTGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGlnValGlnLeu 680
|||||
Db 1981 GCCTGCGGGCGGAGAGTGTCTCCTACTGTGCCCGACAGAGAGAGAGcCAGAGTCC 2040
QY 681 AlaAspArgGlnMetProAspSerAspSerGlnAlaValTyrGlnPheThrGlnAspAla 700
|||||
Db 2041 GCTGACCATGTGATGCTGACTCAcAGACAGGAGcGTGTATGTAGTTCACACAGAGcGCT 2100
QY 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719
|||||
Db 2101 CAGCACAGTACTCCGGGATCCcCAcAGCCGGCGGcCGACAGCGGAGcCTGGGcCCcAGAT 2160
QY 720 AlaGlnProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
|||||
Db 2161 GCAGAGcCTAGTTCGTGTGCTGTGCTTCTGAGGcGTGATCTGTGACACATTCcGGAAGATC 2220
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
|||||

Db 2221 GTAGATAGCAATACTTTGGCCGGGGAATCATGATCCGCATCCTGGTCAATACACTCAGC 2280
QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPro 799
Db 2341 ATCGTCTTCAACCACTCTTCGCCCTTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2400
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819
Db 2401 TTTGGCTACATTAAGAATCCCTACACATCTTGATGGTTCATTGTGTCATCAGTGTG 2460
QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
Db 2461 TGGAGATTGTGGCCACGACGAGGAGGTGGCCTGTCCGTGTGCGGACCTTCCGCTGATG 2520
QY 840 ArgValLeuLysLeuValArgPheIeuProAlaLeuGlnArgGlnLeuValIleLeuMet 859
Db 2521 CGGGTGCTGAAGCTGGTGGCTTCTCGCCGGCCCTGCAGCCACAGCTCGTGTGTCATG 2580
QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe 879
Db 2581 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCACTTTC 2640
QY 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899
Db 2641 AGCATCCTGGGCATGCATCTCTTGGTTGCAAGTTCCGATCTGAACGGGATGGGACACG 2700
QY 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
Db 2701 TTGCCAGACCCGAAGAATTCGACTCCCTGCTGTGGCCATCGCTCACTGTCTTTCAGATT 2760
QY 920 LeuThrGlnGluAspTrpAsnLysValIleuTyrAsnGlyMetAlaSerThrSerSerTrp 939
Db 2761 CTGACTCAGGAAGACTGGAATAAGTCTCTACACGCGCATGGCCTCCACATCGTCTTGG 2820
QY 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeu 959
Db 2821 GCTGCTCTTACTTTCATCGCCCTCATGACTTTGGCACTATGTGCTCTTAACTGCTG 2880
QY 960 ValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer 979
Db 2881 GTGGCCATTCTTGTGAAGGATTCCAGCGACAG----- 2913
QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer 999
Db 2914 -----GGAGATGCCACCAAGTCT 2931
QY 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019
Db 2932 GAGTCAGAGCCCTGATTCTTTCCGCCAGTGTGATGGGAGCAGAAAGAACGCC 2991
QY 1020 LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu 1039
Db 2992 TTGGCCCTGTGGCTTTGGGAGAACGCGGAACACGAAGACCTTTTGCCACCCCTC 3051
QY 1040 IleIleHisThrAlaAlaThrPrometSerLeuProLysSerThrSerThrGlyLeuGly 1059
Db 3052 ATCATCCATACGGCTCGCACACCAATGTCAACACCCCAAGAGCTCCAGACAGGTGTGGG 3111
QY 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079
Db 3112 GAAGCACTGGGCTCTGGCTCTCGACGTACAGTAGCAGTGGGTCCGTGAGCCTGGAGCT 3171
QY 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098
Db 3172 GCCCACCATGATGAATGTCCGCCAAGTGCCCGCAGCTCCCGCACAGTCCCTGGAAGT 3231
QY 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118
Db 3232 GCGGCAAGCACTGGACCAAGCAGCGGCTCCAAGCAGAAACAGCCTGGGCGCGCCCAAGC 3291

QY 1119 LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlu 1138
Db 3292 CTAAAGCGAGAGACCCGACCGGGAGCGGAGGTCCCTGCTGTGTGAGAGGGCCAGAGAG 3351
QY 1139 SerGlnAspGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHis 1158
Db 3352 AGTCAGATGAGAGGAAGTTCAGAAAGAGACCGGGCCAGCCACAGCAGCAGTACCAT 3411
QY 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178
Db 3412 CGCCACAGGGGTTCTTGAACGTGAGCGCAAGAGTTCCTTGAACCTGCTGACACTCTG 3471
QY 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198
Db 3472 CAGTGCCGGGGCTGCACCGCACAGCCAGCGCGGAGCTCTGCCCTGACCAACCAAGAC 3531
QY 1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro 1218
Db 3532 TGTAAATGGCAAGTCGGCTTCAGGGCGTTTGGCCCGCACCCCTGAGGACTGATGACCCCAA 3591
QY 1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238
Db 3592 CTGATGGGGATGATGACATGATGAGGAATCTGAGCAAAAGGGGAGCAGACCAAGCC 3651
QY 1239 TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle 1258
Db 3652 TGGGTCAGATCCCGGCTTCTGCTGTGCGCAGACGAGATTCTGTGTGGCCTATATC 3711
QY 1259 PheProGlnInSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278
Db 3712 TTTCTCTCAGTCAAGGTTTCGTCTCTGTGTCACCGATCATCACCAAGATGTTT 3771
QY 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298
Db 3772 GACCATGTGTCCTCGTCATCATCTTCTCAACTGTATCACCATCGCTATGAGCGCCC 3831
QY 1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr 1318
Db 3832 AAAATTGACCCCCACAGCGCTGAGCGCATCTTCTGACCCCTCTCCAACATCACTTCAAG 3891
QY 1319 AlaValPheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGlu 1338
Db 3892 GCAGTCTTTAGCTGAATGACAGTGAAGGTGTGGCACTGGGCTGTGCTTGGGAG 3951
QY 1339 GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleSerVal 1358
Db 3952 CAGGCCTACCTGCGCAGACGCTGGAATGTGTGACGGCTTGCTGTGCATCTCCGTC 4011
QY 1359 IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378
Db 4012 ATGCATCCTGTGTCCTCAATGTCTCCGACAGCGGCAACCAAGATCCTTGECATGTGAGG 4071
QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398
Db 4072 GTGCTGCGGCTGCTGCCGACCTCGCTCCACTCAGCGTCAATCAGCCGGGCCAGGACTG 4131
QY 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIle 1418
Db 4132 AAGCTGTGTAGAGACTGTGATGTATCCTCAAAACCATTTGGCAACATTTGTGTCAATT 4191
QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438
Db 4192 TGCTGTGCCCTTCTTCATCATTTTGGAAATTCGCGGTGCAGCTCTTCAAGGAAGTTT 4251
QY 1439 PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458
Db 4252 TTCGTGTCAAGGTGAGGACACCAAGACATCACTAACAAATCCGACTGCGCTGAGGCC 4311
QY 1459 SerTyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db 4312 AGCTACCATGGGTCCGGCACAAAGTACAACTTTGACAACTTGCGCCAGGCTCTGATGTCC 4371

QY	1479	LeupheValLeuAlaSerLyAspGlyTyrValAspIleMetTyrAspGlyLeuAspAla	1498
Db	4372	CTGTTGTGCTGGCCCTCCAAGATGTTGGTTGACATCATGATGATGGCTGGATGCT	4431
QY	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTyrMetLeuTyrPheIle	1518
Db	4432	GTGGGTGTGATCAGACGCCATCATGAACCAACACCCCTGGATGCTGTAATTCATC	4491
QY	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu	1538
Db	4492	TCCTTCCTCCTCATCGTGCCCTTCTTGTCTGTAAACATGTTGTGGCGGTGGTGAG	4551
QY	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLys	1558
Db	4552	AACTTCATAGTGCAGACAGCACAGAGAGAGAGAGCGAGCGCGGTGAGAGAAAG	4611
QY	1559	ArgLeuArgArgLeuGluLysLysArgArg-----	1568
Db	4612	CGACTACGAGGCTGGAGAAAAGAGAAGAGTAAGAGAAGCAGATGGCCGATCTAATG	4671
QY	1569	-----LySAlaGlnCysLys	1573
Db	4672	TTGGACGATGTAATTGCTTCCGGCAGCTCAGCCAGCGCTGCGTCAGAAAGCCAGTGAAG	4731
QY	1574	ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisLysLeuCythrSerHis	1593
Db	4732	CCCTACTACTGTGACTACTCGAGATTCCGGCTCCCTTGTCCACCACTGTGTACAGCCAC	4791
QY	1594	TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThreMetAlaMetGlu	1613
Db	4792	TACCTGAGACCTTTCATCACTGGTGTATCGGGCTGAACGTGTCACTATGGCCATGAA	4851
QY	1614	HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr	1633
Db	4852	CATTACAGACAGCCCGACAGATCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTAAC	4911
QY	1634	ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe	1653
Db	4912	GTCATCTTGTCTTGTGAGTCAGTTTCAAACTGTGTGCTTGGCTTCCGCCGTTTCTTC	4971
QY	1654	GlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	4972	CAGGACAGGTGAACACAGCTGGAACCTGGCTATTGTGCTTCTGCATCATGGGCATCACA	5031
QY	1674	LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
Db	5032	CTGGAGGAGATTGAGGTCAATCTGTCCGCTGCCCATCAACCCCATCATCCGTAATCATG	5091
QY	1694	ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla	1713
Db	5092	AGGGTGCTCCGCATGTCTGAGTTCTGAACTGTGGAAGTGGCTGTGGGCATGCGGCA	5151
QY	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
Db	5152	CTGCTGCACACGGGTGATGCAAGGCCCTGCCACAGTGGGGAACCTGGGACTTCTTCAATG	5211
QY	1734	LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp	1753
Db	5212	TTATGTTTTCATCTTTGACGCTCTGGGCGGTGAGGCTCTTTGGAGACCTGGAGTGTGAT	5271
QY	1754	GluThrHisProCysGluGlyLeuGlyArgHisAlaIleThrPheArgAsnPheGlyMetAla	1773
Db	5272	GAGACACACCCCTGTGAGGCTTGGGTGGCATGCCACCTTAAGAACTTGGTATGGCC	5331
QY	1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTyrAsnGlyIleMetLysAspThr	1793
Db	5332	TTTCTGACCCCTTCTCGAGTCTCCACTGGTGACAACACTGGAATGTATTAAGAAGACACC	5391
QY	1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
Db	5392	CTCCGGGACTGTGACCAAGAGTCCACTGCTACACACTGTTCATCTCCCTATCTACTTT	5451
QY	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833

Db	5452	GTGTCTCTTCGTGCTGACGGCCAGTTTGTGTGCTCAACGTGGTCAATAGCTGTGTGATG	5511
Qy	1834	LYSHSLLEUGLUGLUSERASNLYSGLVALALYSGLUGLVALAGLULEUGLVALAGLULEU	1853
Db	5512	AAGCACTCGAAGAACAACAAGAGGCCAAGAGAGGCCGAGCTCGAGGCCGAGCTG	5571
Qy	1854	GLULEUGLUMETLYSTHRLUSERPROGLNPROHISSEPROLEUGLYSERPROPHLEU	1873
Db	5572	GAGCTGAGATGAAGACCTCAGCCCCGACGCCCACTCCCCGTGGGACGCCCTTCCTC	5631
Qy	1874	TRPProGLYValGLUGLYProASPserProASPserProLYSProGLYAlaLeuHisPro	1893
Db	5632	TGGCCCGGGGTGAGGGGTETCAACAGTACTGACAGCCCTAAGCTTGGGGCTCCACACACC	5691
Qy	1894	ALAAlaHisAlaArgSerAlaSerHisPheSerLeuGLUHisProThrmMetGLNProHis	1913
Db	5692	ACTGCCACATTTGAGCAGCCTCGGGCTTCTCCTTGAGCACCCCGATGTATCCCCAC	5751
Qy	1914	ProThrGLUleuPro-----GLYProASPleuLeuThrValArgLYSserGLYVal	1930
Db	5752	CCCCGAGAGGTGCGACAGTCCCCCTAGACCAAGACTGTGACTGTGAGGAAGTCTGTGTC	5811
Qy	1931	SerArgThrHisSerLeuProASPserTYrMetCysArgHisGLYSerThrAlaGLU	1950
Db	5812	AGCCGGACGCACTCTCTGCCAATGACAGCTACATGTGCCGAATGGAGCACTGCTGAG	5871
Qy	1951	GLYProLeuGLYHisArgGLYTrpGLYLeuProLYSAlaGLNserGLYserValLeuSer	1970
Db	5872	AGATCCCTAGACACAGGGGTGGGGGTCCCCAAAGCCAGTCAGGCTCCATCTGTGTC	5931
Qy	1971	ValHisSerGLNProAlaASPThrSerTYrIleLeuGLNleuProLYSASPAlaProHis	1990
Db	5932	GTTCACTCCCAACAGCAGACCACTGATCCTACAGCTTCCCAAGATGTGCATAT	5991
Qy	1991	LeuLeuGLNProHisSerAlaProThrTrpGLYThrIleProLYSleuProProProGLY	2010
Db	5992	CTGCTCAGCCTCATGGGGTCCACCTGGGGGCCATCCCTAACTACCCCACTGGC	6051
Qy	2011	ArgSerProLeuAlaGLNArgProLeuArgArgGLNAlaAlaIleArgThrasPserLeu	2030
Db	6052	CGCTCCCTCTGGCTCAGAGGCTCTCAGGCGCCAGGCAATGAAGATGACTCCCTG	6111
Qy	2031	ASPValGLNGLYleuGLYserArgGLUASPleuLeuAlaGLUValSerGLYProSerPro	2050
Db	6112	GATGTGACGGCCTGGGTAGCCGGGAAGACCTGTGTCAAGGTGAGTGGGCCCTCTGC	6171
Qy	2051	ProLeuAlaArgAlaTYrSerPheTrpGLYGLNserSerThrGLNAlaGLNHisSer	2070
Db	6172	CCTTGACCCGGTCTCATCTTCTGGGGGGGTGAGCATCCAGGTGCAGACGCTTCC	6231
Qy	2071	ArgSerHisSerLYSILeserLYSHismetThrProProAlaProCysProGLYProGLU	2090
Db	6232	GGCATCCAGCAAGAGTCTCCAGACATCCGCTGCCAGCCCTTGCCCAAGGCTTGAA	6291
Qy	2091	ProASPTrpGLYLYSGLYProProGLUThrArgSerSerLeuGLULEuASPThrGLULEU	2110
Db	6292	CCAGCTGGGCCAAGGACCTCTCCAGACCAAGAACACTTAGAGCTGAGCACGAGCTG	6351
Qy	2111	SerTrpIleSerGLYASPleuLeuProProGLYGLYGLNGLUGLUProProSerProArg	2130
Db	6352	AGCTGATTTACAGAGACCTCTT--CCAGACGACGAAGAACCCTGTTCCTCCACGG	6408
Qy	2131	ASPleuLYSLeuCysTYrSerValGLUAlaGLNserCysGLNArgArgProThrSerTrp	2150
Db	6409	GACCTGAAGAACTGTACAGTGTAGAGACCAGAGCTGCAGGCGCAGGCTTGGTCTGG	6468
Qy	2151	LeuASPGLUlnArgArgHisSerIleAlaValSerCysLeuASPserGLYserGLNPro	2170
Db	6469	CTAGATGAACAGCGGAGACACTTCATGTGTCAAGCTGTGACAGCGGCTCCCAACC	6528
Qy	2171	HisLeuGLYThrASPProSerASPleuGLYGLYGLNProLeuGLYGLYProGLYSerArg	2190

Db 6529 CGCCTATGTCCAAGCCCCCTCAAGCCTCGGGGGCCAACTCTTGGGGTCTGGAGCCGG 6588

Qy 2191 ProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyPro 2210
|||||
6589 CCTAAGAAAAAACTCAGCCCCCAGTATCTATAGACCCCCCGAGAGCCAGGGCTCT 6648

Qy 2211 ArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLys 2230
|||||
6649 CGGCCCCCATGCACTCCTGTGTCTGCTCAGAGAGAGGGCGCGCCAGTGACTTAAG 6708

Qy 2231 AspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAsp 2250
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6709 GATCCCTCGGTCTCCAGCCCCCTTGACAGCACGGCTGCTCACTCCCAAGAAAGAC 6768

Qy 2251 ValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
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6769 ACGCTGAGTCTCTGTGTTGTCTTGACCCCAACAGACATGACCC 6816

Search completed: September 18, 2005, 20:05:17
Job time : 3051.82 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2005, 18:10:57 ; Search time 714.688 Seconds
(without alignments)
5188.000 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEBSGQPRSFM.....PKDVLSLSGISDPADLDP 2266

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=fascap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO MMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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Database : Issued Patents_NA: *
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5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11877.5	99.8	6822	3	US-09-426-998-3 Sequence 3, Appli
2	11877.5	99.8	7741	3	US-09-426-998-4 Sequence 4, Appli
3	11241	94.4	7405	4	US-09-949-016-3859 Sequence 3859, Ap
4	6315.5	53.1	3993	4	US-09-398-522-51 Sequence 51, Appli
5	6214.5	52.2	7898	3	US-08-984-709A-49 Sequence 49, Appli
6	5492.5	46.1	6816	3	US-09-404-650-1 Sequence 1, Appli
7	5492.5	46.1	6816	4	US-09-935-541-1 Sequence 1, Appli
8	5484	46.1	6855	3	US-09-404-650-3 Sequence 3, Appli
9	5484	46.1	6855	4	US-09-935-541-3 Sequence 3, Appli
10	5418.5	45.5	6503	3	US-09-404-650-12 Sequence 12, Appli
11	5418.5	45.5	6503	4	US-09-935-541-12 Sequence 12, Appli
12	2237	18.8	70308	4	US-09-949-016-15601 Sequence 15601, A

13	1971.5	16.6	1669	3	US-08-984-709A-51	Sequence 51, Appli
14	1786.5	15.0	7376	3	US-09-268-163-3	Sequence 3, Appli
15	1784.5	15.0	7362	1	US-08-455-543A-7	Sequence 7, Appli
16	1784.5	15.0	7362	2	US-08-193-078B-7	Sequence 7, Appli
17	1784.5	15.0	7362	2	US-08-223-305C-7	Sequence 7, Appli
18	1784.5	15.0	7362	2	US-08-149-097D-7	Sequence 7, Appli
19	1784.5	15.0	7362	3	US-08-949-386-7	Sequence 7, Appli
20	1784.5	15.0	7362	3	US-08-450-562-7	Sequence 7, Appli
21	1784.5	15.0	7362	3	US-08-984-709A-7	Sequence 7, Appli
22	1784.5	15.0	7362	3	US-08-450-272-7	Sequence 7, Appli
23	1784.5	15.0	7362	4	US-08-450-273-7	Sequence 7, Appli
24	1784	15.0	7266	3	US-08-713-118-1	Sequence 1, Appli
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26	1782.5	15.0	7364	3	US-09-268-163-5	Sequence 5, Appli
27	1778	14.9	7175	1	US-08-455-543A-8	Sequence 8, Appli
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36	1776	14.9	7177	3	US-09-268-163-7	Sequence 7, Appli
37	1728.5	14.5	7011	3	US-09-268-163-9	Sequence 9, Appli
38	1711.5	14.4	5975	1	US-08-314-083B-1	Sequence 1, Appli
39	1711.5	14.4	5975	1	US-08-435-675B-1	Sequence 1, Appli
40	1711.5	14.4	5975	1	US-08-884-599-1	Sequence 1, Appli
41	1711.5	14.4	5975	3	US-08-884-599-1	Sequence 1, Appli
42	1701.5	14.3	5975	1	US-08-336-257A-3	Sequence 3, Appli
43	1691	14.2	6112	4	US-09-495-714C-3	Sequence 5, Appli
44	1690	14.2	6114	4	US-09-495-714C-5	Sequence 5, Appli
45	1690	14.2	7089	3	US-08-949-386-25	Sequence 25, Appli

ALIGNMENTS

RESULT 1
US-09-426-998-3
; Sequence 3, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426, 998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 3
; LENGTH: 6822
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-3

Alignment Scores:
Pred. No.: 0
Score: 11877.50
Percent Similarity: 99.65%
Best local Similarity: 99.60%
Query Match: 99.78%
DB: 3
Length: 6822
Matches: 2264
Conservative: 1
Mismatch: 1
Indels: 7
Gaps: 1

US-09-611-257A-37 (1-2266) x US-09-426-998-3 (1-6822)
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Db 1 ATGACGAGGAGGAGGATGAGCGCGCGCGAGAGAGTGGGACAGCCCGAGCTTCAATG 60

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QY	41	ProGlySerAlaAspSerGluAlaGlyLeuProTyrProAlaLeuAlaProValVal	60
Db	121	CCGGGAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACC GGCGCTGACCCCGGTGTT	180
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80
Db	181	TTCTTCTACTTGAGCCAGACAGACCGCCCGGAGCTGGTCTCCGCACGGTCTGTAAAC	240
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
Db	241	CCCTGGTTGAGCGCATCAGCATGTTGGTCACTCTTCAACTGCGTGACCCCTGGGCATG	300
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	301	TTCCGGCCATGCGAGCATCGCTGTGACTCCACGCGCTGCCGATCCTGCAGGCTTT	360
QY	121	AspAspPheIlePheAlaPhePheAlaValAluMetValValLysMetValAlaLeuGly	140
Db	361	GATGACTTCATCTTGCCCTCTTGCCGTGAGATGGTGTGAAGATGTGGCCCTGGGC	420
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
Db	421	ATCTTTGGAAAAAGTGTTAACCTGGAGACACTTGGAACCGGCTTGACTTTTCAATCGTC	480
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
Db	481	ATCGCAGGATGCTGGAGTACTCGCTGACCTGCAGACGTCAAGCTTCTCAGCTGTCAAG	540
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
Db	541	ACAGTCCGCTGCTGCGACCGCTCAGGGCCATTACCGGGGTGCCACGATGCGCATTCCTT	600
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
Db	601	GTCACGTTGCTGCTGATACGCTGCCCATGCTGGGCAAGTCCCTGCTCTGCTTCTTC	660
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
Db	661	GTCTTCTTCATCTTCGGCATCTGCGCGTCCAGCTGTGGGCAAGGGCTGCTTCGGAACCA	720
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
Db	721	TGCTTCCTACCTGAGAAATTTCAGCCTCCCTGAGCGTGAACCTGAGCGCTATTACAG	780
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
Db	781	ACAGAGAACGAGATGAGAGCCCTTCATCTGCTCCACGCCACGCGAAGCGCATGCGG	840
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
Db	841	TCCTGCAGAAAGCTGCCACGCTGCGGGGACGGGGGGCGGTGGCCACCTTGGCGTCTG	900
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
Db	901	GACTATGAGGCTTACACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTAC	960
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
Db	961	ACCAACTGCTCAGCGGGGAGCAACAACCCCTTCAAGGGGGCCATCAACTTTGACACATT	1020
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlnGlyTrpValAspIleMet	360
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QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
Db	1081	TACTTTGTGATGATGATCTATCTCTTCTACAAATTTCACTTCACTTCACTCTCTCATCATC	1140

QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
Db	1141	GTGGGCTCTTCTTCATGATCAACCTGTGCTGGTGGTATGTCCACGACGTTCTCAGAG	1200
QY	401	ThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
Db	1201	ACCAAGCAGCGGGAAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTTCTCTCCAACGCC	1260
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440
Db	1261	AGCACCTGGCTAGCTTCTCTGAGCCCGGACGCTGCTATGAGAGCTGCTCAAGTACCTG	1320
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
Db	1321	GTGTACATCTTCTGTAAGGCACCCCGCAGGCTGGCTCAGGTCCTCCGGCAGCAGGTGTG	1380
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
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QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
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QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
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QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
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QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
Db	1681	TGCCACTTAGAGCCAGTCCGCTGCCAGCGCCCCCTCCCAAGTCCCATCTGAGGCATCC	1740
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
Db	1741	GGCAGGACTGTGGCAGCGGGAAGGTGTATCCCAACGTGCACACACGACCTTCCACCGAG	1800
QY	601	ThrLeuysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	1801	ACGTGAAGAGAAGGACACTAGTAGAGGTGGCTGCCAGCTCTGGCCCCCAACCTCACCC	1860
QY	621	SerLeuAsnIleProProGlyProTyrSerSerSerMetHisLysLeuLeuGluThrGlnSer	640
Db	1861	AGCCTCAACATCCCAACCCGGGCCCTACAGCTCCATGCACAAGCTGCTGGAGACACAGAGT	1920
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
Db	1921	ACAGGTGCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAAGCAGACAGTGA	1980
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680
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QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
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QY	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla	720
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QY	721	GluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIleVal	740
Db	2161	GAGCCAGCTCTGTGCTGGCTTCTTGAGGCTAATCTGTGACACCTTCCGAAAAGATTGTG	2220
QY	741	AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760

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QY 761 GYLILEGLUTYRHISGLUGLNPROGLUGLULEUThrAsnAlaLeuGluILESerAsnILE 780
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QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTYRGLYProPhe 800
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Db 2401 GGCTACATCAAGAAATCCCTACAAACATCTTCGATGGTGTCATGTGTCATCAGCGTGTGG 2460
QY 821 GUILLeValGLYGLNGLNGLYGLYGLYLeuSerValLeuArgThrPheArgLeuMetArg 840
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Db 2461 GAGATCGTGGCCAGAGGGGGGGCGGCTGTGGTGCTGGCGACCTTCCGCTGATGCGT 2520
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
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Db 2521 GTGCTGAAGCTGGTGGCCTTCTCCGCGCGCTGCAGCGGACGCTGGTGCTCATGAAG 2580
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheILEPheILEPheSer 880
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Db 2581 ACCATGGAACAAGTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTTCAGC 2640
QY 881 ILELeuGLYMetHISLeuPheGLYCysLysPheAlaSerGluArgAspGLYAspThrLeu 900
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Db 2641 ATCTGGGCATGATCTCTTCGGCTGCAAGTTTGCTCTGAGCGGGATGGGACACCCCTG 2700
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaILEValThrValPheGlnILELeu 920
Db 2701 CCAGACCGGAAGAAATTGACTCCTGTGCTGTGGCCATCGTCACTGTCTTCAGATCCTG 2760
QY 921 ThrGlnGluAspTrpAsnLysValLeuTYRAsnGLYMetAlaSerThrSerSerTrpAla 940
Db 2761 ACCCAGAGAGACTGGAACAAGTCCCTCAATGTATGGCCTCCACGTGCTCCTGGCG 2820
QY 941 AlaLeuTYRPhelLeaLeuMetThrPheGLYAsnTYRValLeuPheAsnLeuLeuVal 960
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QY 961 AlaILELeuValGLUGLYPheGlnAlaGLUGLILESerLysArgGluAspAlaSerGLY 980
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QY 981 GlnLeuSerCysILEGlnLeuProValAspSerGlnGLYAspAlaAsnLysSerGlu 1000
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Db 3001 TCAGAGCCCGATTTCTTCCACCACCGCTGATGGATGGGACAGAGAAGAGTGTG 3060
QY 1021 AlaLeuValSerLeuGLYGLHISProGluLeuArgLysSerLeuLeuProProLeuILE 1040
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Db 3061 GCCTTGGTGTCCCTGGGAGAGCACCCGGAGCTGCGGAAGAAGCCTGCTGCCCTCATC 3120
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Db 3121 ATCCACACGGCCGCACACCATGTGCTGCCAAGAGCACACAGCAGGGGCTGGGGGAG 3180
QY 1061 AlaLeuGLYProAlaSerArgArgThrSerSerSerGLYSerAlaGluProGLYAlaAla 1080
Db 3181 GCGCTGGGGCCCTGCTGCGCGCCAGCACAGCAGCGGGTGGCAGAGCTGGGGCGGCG 3240
QY 1081 HISGluMetLysSerProProSerAlaArgSerSerProHISerProTrpSerAlaAla 1100
Db 3241 CACGAGATGAAGTACCGCGCCAGCGCCGACAGCTCTCCGACACAGCCCTGGAGCGCTGA 3300
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Db 3361 CGGAGAAGCCCAAGTGGAGAGCGCGGTCCCTGTGTGGGAGAAGGCCAGAGAGGCCAG 3420
QY 1141 AspGluGLUGluSerSerSerGLUGLUGluArgAlaSerProAlaGLYSerAspHISArgHIS 1160
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QY 1181 ProGLYLeuHISArgThrAlaSerGLYArgGLYSerAlaSerGluHISGlnAspCysAsn 1200
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Db 3541 CCAGGGCTGCATCGCACTGCAGTGGCCGAGGTCGTGCTTGAGACACAGACTGCAT 3600
QY 1201 GLYLysSerAlaSerGLYArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
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QY 1221 GLYAspAspAlaAspAspGLUGLYAsnLeuSerLysGLYGLuArgValArgAlaTrpILE 1240
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Db 3961 TTTCTGCTGAATTGACAGTGAAGGTGTGGCACTGGGCTGTGCTTCGGGGAGCAGGCG 4020
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Db 4021 TACCTCGGAGCAGTTGGAACGTGTGACGGGCTGTTGGTGTCTCATCTCCGTCATCGAC 4080
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Db 4081 ATTCTGTGTCCATGTCTCTGACAGCGGCACCAAGATCCTGGGCATGTGAGGCTGCTG 4140
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Db 4141 CGGCTGCTGCGGACCTGCGCCCGCTCAGGGTGAATCAGCCGGGCGCAGGGGCTGAAGCTG 4200
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Db 4201 GTGGTGAGAGCGTGAATGTCTCTCACTGAACCCATCGGCAACATTGTAGTATCTGCTGT 4260
QY 1421 AlaPhePheILEILEPheGLYILELeuGLYValGlnLeuPheLysGLYLysPhePheVal 1440
|||||
Db 4261 GCCTTCTTCATCATTTTTCGGCATCTTGGGGGTGCAGCTCTTCAAGGGAAGTTTTCGTG 4320
QY 1441 CysGlnGLYGLuAspThrArgAsnILEThrAsnLysSerAspCysAlaGluAlaSerTYR 1460
Db 4321 TGCCAGGGCGAGGATACAGGAACATACCAATAATCGACTGTGCCAGGCCAGTTAC 4380
QY 1461 ArgTrpValArgHISLysTYRAsnPheAspAsnLeuGLYAlaAlaLeuMetSerLeuPhe 1480
|||||
Db 4381 CGGTGGGTCCGGCAACAAGTACAACATTGACAACCTTGCCAGGCGCTGATGTCCCTGTTTC 4440

QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4441	GTTTTGGCCTCCAAGATGTTGGTGACATCATATGACATGGGCTGGATGCTGTGGC	4500
QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	4501	GTGGACCAAGACCCCATCATGAACCAACACCCCTGGATGCTGTACTTCATCTCGTTT	4560
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe	1540
Db	4561	CTGCTCATTTGGCCTTCTTTGTCTTGAACATGTTTGTGGGTGTGGTGTGAGAACTTC	4620
QY	1541	HisLysCysArgGlnHisGlnGlnGluGluGluAlaArgArgGluGluLysArgLeu	1560
Db	4621	CACAAGTGTGGCAGCACCAAGAGAGAGAGGCCCGCGCGGAGAGAGAACCGCTTA	4680
QY	1561	ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys	1573
Db	4681	CGAAGACTGGAGAAAAGAGAGAGAGTAAGAGAGACAGATGGCTGAAGCCCACTGCAAA	4740
QY	1574	ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLysCysThrSerHis	1593
Db	4741	CCTTACTACTCCGACTACTCCCGCTTCCGGCTCTCTGTCCACCACCTGTGTGCACCA	4800
QY	1594	TyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGlu	1613
Db	4801	TACCTGACCTCTTCATCAAGGTGTATCGGGCTGAACGTGTGTACCATGGCCATGGAG	4860
QY	1614	HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr	1633
Db	4861	CACCTACCAAGACCCCAAGATTCTGGATGAGGCTGTGAAGATCTGCAACTACATCTTCA	4920
QY	1634	ValIlePheValLeuGlnSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe	1653
Db	4921	GTCATCTTTGTCTTGAGTCAGTTTTCAAACTGTGTGCTTTGGTTCCGTGGTCTTTC	4980
QY	1654	GlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	4981	CAGGACAGGTGGAAACCACTGGACCTGGCCATTGTGTCTGCTCCATCATGGGCACTACG	5040
QY	1674	LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
Db	5041	CTGGAGAAATCGAGTCAACGCTCGCTGCCATCAACCCACCATCATCCGATCATG	5100
QY	1694	ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla	1713
Db	5101	AGGCTGCTGCGCATTGCCCGAAGTGTGAAGCTGTGAAGATGGCTGTGGCGATGCCGCG	5160
QY	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
Db	5161	CTGCTGGACACCGGTGATGACAGCCCTGCCCAAGTGGGGAACCTGGACTTCTCTTCATG	5220
QY	1734	LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp	1753
Db	5221	TTGTGTTTTCATCTTTGACAGCTCTGGGCGGTGAGCTCTTTGGAGACCTGGAGTGTGAC	5280
QY	1754	GluThrHisProCysGlnGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
Db	5281	GAGACACACCCCTGTGAGGGCTGGGCCGTCAATGCCACTTTCCGAACCTTTGGCATGGCC	5340
QY	1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr	1793
Db	5341	TTCCTAACCTCTTCCGAGTCTCCACAGGTGACAAATTGGAATGGCATTAAGAAGACACC	5400
QY	1794	LeuArgAspCysAspGlnGlnSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
Db	5401	CTCCGGGACTGTGACCAAGAGTCCACCTGCTACAACACGGTCACTCGCCATCTACTTT	5460
QY	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
Db	5461	GTTGCTCTTGCTGACGGGCCAGTTGCTGTAGTCAACGTGTGATCGCCGTGTGATG	5520

QY	1834	LYSHI	LEUGLUGLUSER	ANLYSG	LALALYSGLUGLUALAGLULEUGLUALGLULEU	1853											
Db	5521	AAGCA	CTGGAGAGAGACA	CAAGAGG	CCAAAGAGAGCCGAGCTAGAGCTGAGCTG	5580											
QY	1854	GLULEUGL	METLysThr	LEUSERPROGLN	PROHISERPROLEUGLYSERPROPHLEU	1873											
Db	5581	GAGCTG	GAGATGAAGAC	CCCTCAGC	CCCCCAGCCCCCACTCGCCACTGGGCGAGCCCTTCCTC	5640											
QY	1874	TRP	PROGLYVALGLUGL	PROASP	SERPROASP	SERPROLYS	PROGLYVAL	LEUHI	SPRO	1893							
Db	5641	TGGCCT	TGGGGT	CGAGGG	CCCCCAGAC	CCCCCGCAAGCCTGGGGCT	GTGCAC	CCCA	5700								
QY	1894	ALA	ALA	HIS	ALAARGSER	ALASER	HISPHESER	LEUGL	UHI	SPROTHRMETGLN	PROHIS	1913					
Db	5701	GCGGCC	CA	CGAGAT	CAGCTCCCACTTTCCCT	TGGAGCA	CCCCCAGATG	CAGCCCCAC	5760								
QY	1914	PRO	THRGLULEU	PROGLY	PROASP	LEULEUTHR	VALARGLY	SERGLY	VALSER	ARGTHR	1933						
Db	5761	CCCACG	GAGCTCCAG	AGACCA	CTTACTG	ACTGTGCG	GAAGTCTGGG	GTCA	CGGA	CG	5820						
QY	1934	HIS	SERLEU	PROASN	ASPSERTYMET	CYS	ARGHISGLY	SERTHRA	LAGLUGLY	PROLEU	1953						
Db	5821	CAC	TCTGTGCC	CAATG	ACAGCTA	TGTGTGCG	CA	TGGAG	CACTGCCG	GAGGGCC	CTG	5880					
QY	1954	GLY	HIS	ARGGLY	TRPGLY	LEUPROLYS	ALAGLNSER	GLYSER	VALLEUSER	VALHIS	SER	1973					
Db	5881	GGACA	CAGGGG	CTGGGG	CTCCCCAA	AGCTCAG	TCA	GGCTCCG	TCTGTCC	GTCACTCC	5940						
QY	1974	GLN	PROALA	ASPTHR	SERTYRILE	LEUGL	NLEUPROLYS	ASPA	LA	PROHIS	LEULEUGLN	1993					
Db	5941	CAGCC	AGCAGAT	ACCAGCT	ACATCCTG	CAGCTTCCCA	AAGATG	CACCTCA	CTGCTC	CAG	6000						
QY	1994	PRO	HISER	ALA	PROTHR	TRTPGLY	THRILE	PROLYS	LEUPRO	PRO	PROGLY	ARGSER	PRO	2013			
Db	6001	CCCC	CACAGCG	CCCCCA	CTGGGG	CACCATCC	CCAA	ACTGCC	CCCCCA	CCAG	AG	CGCTCC	CT	6060			
QY	2014	LEU	ALAGL	ARGPRO	LEUARG	ARGGLNAL	ALALAL	ARGTHR	ASPSER	LEUASP	VALGLN	2033					
Db	6061	TTGG	CTAGAG	GGCCACT	CAGCGCC	CAGGCA	CAAT	AAG	ACTG	ACTCTT	GGA	CGTT	CAG	6120			
QY	2034	GLY	LEUGLY	SER	ARGGLU	ASP	LEU	ALAGL	VALSER	GLYPRO	SERPRO	PROLEU	ALA	2053			
Db	6121	GGT	CTGG	CAGCCG	GGA	AGACTG	CTG	CAGAG	GTG	AGCCCT	CCCC	CGCTG	CGC	6180			
QY	2054	ARG	ALATYR	SER	PHETRPGLY	GLNSER	SERTHR	GLNALAGL	NHISER	ARGSER	HIS	2073					
Db	6181	CGG	CCCTACT	CTTCTG	GGGCC	AGTCA	AGTAC	CCAG	GCACAG	CACATC	CCG	CAG	CCAC	6240			
QY	2074	SER	LYSILE	SERLYSHIS	METTHR	PRO	PROALA	PRO	CYS	PROGLY	PROGLN	PROASN	TRP	2093			
Db	6241	AGCA	AGATCT	CCAAG	CACATG	ACCCCG	CAGCCCTT	GGCC	AGG	CCCA	CACTGG	6300					
QY	2094	GLY	LYSGLY	PRO	PROGLU	THR	ARGSER	SERLEUGL	LEU	ASP	THRGLULE	SERTRIPLE	2113				
Db	6301	GGCA	AGG	CCCTCC	AGAG	ACAG	AGCAGCTT	AGATTG	GACAC	CGAG	CTG	AGATT	6360				
QY	2114	SER	GLY	ASP	LEULEU	PRO	PROGLY	GLYGLN	GLUGL	PRO	PROSER	PRO	ARG	ASP	LEULYS	2133	
Db	6361	TCAG	GAG	AGACTCT	CGCCCC	CTGG	CGCC	CAGAG	AGG	CCCCCAT	CC	CAC	GGG	AGCT	GAG	6420	
QY	2134	LYS	CYS	TYR	SER	VALGLU	ALAGLNSER	CYSGLN	ARG	PRO	THR	SERTRIPLE	ASP	GLU	2153		
Db	6421	AAGT	GTCT	ACAG	CGTG	GAGGCC	AGAGCTG	CCAG	CGCG	GGCTT	ACGTCT	GTG	GAT	GAG	6480		
QY	2154	GLN	ARG	ARGHIS	SERILE	ALAVALSER	CYS	LEU	ASP	SERGLY	SERGLN	PROHIS	LEUGLY	2173			
Db	6481	CAG	AGG	AGAC	ACTCTAT	CGCC	CTCAG	CTG	CTG	CA	CGGCTCC	CA	CCCA	CCCA	CTG	GGC	6540
QY	2174	THR	ASPTRO	SERASN	LEUGLY	GLN	PRO	LEUGL	YGLY	PRO	GLY	SER	ARG	PROLYS	LYS	2193	
Db	6541	ACA	GAC	CCCTCT	TAACTT	GGGG	CCAG	CCCTCTT	GGGG	GGCC	CGG	GAG	CCG	CCCA	AGAAA	6600	
QY	2194	LYS	LEUSER	PRO	PROSER	ILETHRILE	ASP	PRO	PROGLN	SERGLN	GLYPRO	ARGTHR	PRO	2213			

|||||
Db 6601 AACTCAGCCCGCTAGTATCACCATAGACCCCGAGAGCCAAAGTCTCGAACCCCG 6660
QY 2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233
Db 6661 CCCAGCCCTGATCTGCTCCGAGAGGGGCTCCGTCAGCAGCTCCAAGATCCCTTG 6720
QY 2234 AlaSerGlyProProAspSerMetalAlaLaserProSerProLysLysAspValLeuSer 2253
Db 6721 GCCTCTGGCCCCCTGACAGCATGGCTGCCCTCCCTCCCAAGAAGATGTGTAGT 6780
QY 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6781 CTCTCCGTTTATCTCTGACCCAGCAGACCTGGAACCC 6819

RESULT 2
US-09-426-998-4
; Sequence 4, Application US/09426998
; Patent No. 6358706
; GENERAL INFORMATION:
; APPLICANT: DUBIN, ADRIENNE E.
; APPLICANT: PYATI, JAYASHREE
; APPLICANT: ZHU, JESSICA Y
; APPLICANT: ERLANDER, MARK G
; APPLICANT: GALINDO, JOSE E
; TITLE OF INVENTION: DNA ENCODING HUMAN ALPHA1G T-TYPE CALCIUM
; TITLE OF INVENTION: CHANNEL (ALPHA1G-C)
; FILE REFERENCE: ORT-1057
; CURRENT APPLICATION NUMBER: US/09/426, 998
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VER. 2.0
; SEQ ID NO 4
; LENGTH: 7741
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-426-998-4

Alignment Scores:
pred. No.: 0 Length: 7741
Score: 11877.50 Matches: 2264
Percent Similarity: 99.65% Conservative: 1
Best Local Similarity: 99.60% Mismatches: 1
Query Match: 99.78% Indels: 7
DB: 3 Gaps: 1

US-09-611-257a-37 (1-2266) x US-09-426-998-4 (1-7741)

QY 1 MetAspGluGluAspGlyAlaGlyAlaGluSerGlyGlnProArgSerPheMet 20
Db 523 ATGAGCAGAGAGGATGAGCGGCGCCGAGAGTCCGGACAGCCCGAGCTTCATG 582
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 583 CGGCTCAACGACCTGTGGGGGCGGGGGCGGGCGGGGTCCAGCAAGAAAAAGAC 642
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal 60
Db 643 CCGGGCAGCGGACTCCGAGCGGAGGGGTGCTGCTACCGCGCTGGCCCCGTGTT 702
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 703 TTCTTCTACTTGAGCCAGACAGCCGCCGCGAGCTGTGTCTCCGACGGTCTGTAAC 762
QY 81 ProTirPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 763 CCCTGTTTGAAGCGCATCAGCATGTTGTCTTCTCAACTGCGTGACCTGGGCATG 822
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 823 TTCCGGCCATGCGAGGACATCGCTGTGACTCCAGCGCTGCGGATCTTGACAGGCCCTT 882
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140

|||||
Db 883 GATGACTTATCTTTCCTTCTTTTGGCGTGAGATGTGTGAAGATGTGGCTTGGCC 942
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPheIleVal 160
Db 943 ATCTTTGGAAAAAGTGTACCTGGAGACACTTGAACCGGCTTGACTTTTTCATCGTC 1002
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 1003 ATCGCAGGAGTGTGAGTACTCGCTGGACCTGCAGAACGTCACTTCTCAGCTGTACG 1062
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 1063 ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCATCTT 1122
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhe 220
Db 1123 GTCACGTTGCTGTGATACGCTGCCCATGTGGCAACGTCCTGCTGCTTCTTTC 1182
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240
Db 1183 GTCTTCTTCACTTCGCGCATCGTCGGCTCCAGCTGTGGCAGGGCTGCTTGGAACCGA 1242
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 1243 TGCTTCTTACCTGAGATTTTCAAGCTCCCTGAGCGTGAAGCTGGAAGCTATTACAG 1302
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 1303 ACAGAGAACGAGATGAGAGCCCTTATCTGCTCCAGCCAGCAGAGACGCGCATGCGG 1362
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 1363 TCCTGCAGAACGTGCCACAGCTGCGGGGAGCGGGGGCGGTGCCACCTTGCGGTCTG 1422
QY 301 AspTyrGluAlaTyrAsnSerSerSerSerThrThrCysValAsnTyrPasnGlnTyrTyr 320
Db 1423 GACTATGAGGCTTCAACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTTAC 1482
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
Db 1483 ACCAAGTGTCTCAGGGGGGAGACAAACCCCTTCAAGGGCGCCATCACTTGACCAACTT 1542
QY 341 GlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1543 GGCTATGCTGTGATGCCATCTTCCAGTTCATCAGCTGAGGGGTGGTGCACATCATG 1602
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1603 TACTTGTGATGATGCTCATTCCTTCTTCAATTTCATCTACTTCACTTCCTCATCATC 1662
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1663 GTGGGCTCCTTCTTCAATGATCAACCTGTGCTGTGTGATGTGCACGAGTTCTCAGAG 1722
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1723 ACCAAGCAGCGGAAGCAGCTGATGGGGAAGCAGGTGCGGTTCTGTCCAACGCC 1782
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1783 AGCAACCTGTAGCTTCTCTGAGCCCGCAGCTGCTATGAGAGCTGCTCAAGTACCTG 1842
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1843 GTGTACATCTTCTGTAAGCAGCCCGCAGCTGCTCAAGTCTTCTGGGCAAGAGTGTG 1902
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1903 CGGGTGGCTGTCAAGCAGCCAGACCCCTCGGGGGCCAGAGAACCCAGCCAGCAGC 1962
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500

Db 1963 AGCTGCTTCGCTCCACCGCCGCTATCCGTCCACCACCTGGTGACCACCACCAC 2022
QY 501 HISHISHISHISTYRHISLEUGLYASNGLYTHRLEUARGALAProARGALASerProGlu 520
Db 2023 CATCACCACTACCACTGGGCATGGGACGCTCAGGGCCCCCGGGCCAGCCGGAG 2082
QY 521 ILEGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 2083 ATCCAGGACAGGATGCCAATGGGTCCCGCAGGCTCATGTGCCACCACTCGACGCTT 2142
QY 541 AlaleuSerGlyAlaProProGlyValAGluSerValHISerPheTYRHISAlaasp 560
Db 2143 GCCCTCTCCGGGGCCCCCCTGGTGGCGCAGAGTCTGTGCACAGCTTCTACCATGCCGAC 2202
QY 561 CysHISleuGluProValArgCysGlnAlaProProProArgSerProserGluAlaSer 580
Db 2203 TGCACCTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTGAGGCATCC 2262
QY 581 GLYArgThrValGlySerGlyLysValTYRProThrValHISThrSerProProGlu 600
Db 2263 GGCAGGACTGTGGGCACGGGAAGGTATCCCACTGCACACAGCCCTCCACCGGAG 2322
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAserSerGlyProProThrLeuThr 620
Db 2323 ACGTGAAGAGAGAGGCACTAGTAGGTGGTGCCAGCTCTGGGGCCCCCACTCACC 2382
QY 621 SerLeuAsnIleProProGlyProTYRSerSerMetHISLysLeuLeuGluThrGlnSer 640
Db 2383 AGCCTCAACATCCCAACCCGGGCCCTACAGCTCCATGCACACAGCTGTGAGACACAGAGT 2442
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2443 ACAGGTGCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGCTGGA 2502
QY 661 AlaCysGlyProAspSerCysProTYRCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 2503 GCCTGTGTCCAGACAGCTGCCCTTACTGTGCCCCGGGCCAGGAGGTGGAGCTC 2562
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTYRGluPheThrGlnAspAla 700
Db 2563 GCCGACCGTGAATGCTGACTCAGACAGCAGGCAAGTTTATGAGTTCACACAGAGATGCC 2622
QY 701 GlnHISerAspLeuArgAspProHISerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2623 CAGCACAGGACCTCCGGGACCCCCACAGCCGGCGCAACGAGCCTGGGCCCAGATGCA 2682
QY 721 GluProSerSerValLeuAlaPheThrPArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2683 GAGCCCAAGCTGTGCTGGCTTCTGGAGGCTAATCTGTGACACCTTCCGAAAGATTGTG 2742
QY 741 AspSerLysTYRPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2743 GACAGCAAGTACTTTGGCCGGGGAATCATGATGCCATCTGGTCAACACACTCAGCATG 2802
QY 761 GLYIleGlyTYRHISGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2803 GGCATCGAATACACGAGCAGCCCGAGAGCTTACCACGCCCTAGAAATCAGCAACATC 2862
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTYRGlyProPhe 800
Db 2863 GTCTTCACCAAGCTCTTGGCCCTGAGATGCTGTGAAGCTGCTGTGATGGTCCCTTT 2922
QY 801 GLYTYRILELysAsnProTYRAsnIlePheAspGlyValIleValValIleSerValTrp 820
Db 2923 GGCTACATCAAGAAATCCCTACACATCTTCGATGTGTCAITGTGTCATCAGCGGTGG 2982
QY 821 GluIleValGlyGlnGlnGlyGlyLysLeuSerValLeuArgThrPheArgLeuMetArg 840
Db 2983 GAGATCGTGGGCGCAGAGGGGGGGCGGCTGTGGTGCTGGGACCTTCCGCTGATGCGT 3042
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 3043 GTGCTGAAGCTGTGTGGCTTCTGTGCCGGGCTGCAGCGGCAAGCTGTGTGCTCATGAAG 3102

QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 3103 ACCATGACAACAGTGGCCACTTCTGCATGTCTTATGTCTTCACTTCACTTCAAGC 3162
QY 881 IleLeuGlyMetHISleuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
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QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 3223 CCAGACCGGAAGAAATTGACTCTTGCTGTGGCCATGTCACACTGTCTTTCAGATCCTG 3282
QY 921 ThrGlnGluAspTrpAsnLysValLeuTYRAsnGlyMetAlaSerThrSerTrpAla 940
Db 3283 ACCCAGGAGACTGGAACAAGTCTCTACAAATGGTATGGCCTCCACGTCGTCCGGCG 3342
QY 941 AlaleuTYRPheIleAlaLeuMetThrPheGlyAsnTYRValLeuPheAsnLeuVal 960
Db 3343 GCCCTTATTTCATTGCCCCATGACCTTCGGCACTACGTGCTCTTCAATTGGCTGTC 3402
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
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QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyLysAspAlaAsnLysSerGlu 1000
Db 3463 CAGTTAAGCTGTATTCACTGCTGTGACTCCAGGGGGGAGATGCCAAAGTCCGAA 3522
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
Db 3523 TCAGAGCCGATTCTTCTCAACCCAGCCTGATGTATGGGAGACAGAGAAAGTGTCTTG 3582
QY 1021 AlaLeuValSerLeuGlyGlnHISProGluLeuArgLysSerLeuLeuProProLeuIle 1040
Db 3583 GCCTGTGTCCCTGGAGAGCACCCGAGCTGGCGGAAGACCTGTGCGCCTCTCATC 3642
QY 1041 IleHISThrAlaAlaThrPrometSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
Db 3643 ATCCACAGGGCCGCCACACCATGTGCTGCCCAAGACACAGCAGGCGCTGGCGAG 3702
QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 3703 GCGCTGGGCCCTGCGTCCGCCGCCACCAAGCAGCGGGTCCGCAAGACCTGGGGGCC 3762
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHISerProTrpSerAlaAla 1100
Db 3763 CACGAGATGAAGTCAACGCCCAAGCGCCGAGCTTCCGACAGCCCTGGAAGCGCTGCA 3822
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3823 AGCAGCTGACCAAGAGCGCTCCAGCCGGAACAGCTCGCGGACCAAGCCTGAAG 3882
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140
Db 3883 CGAGAGAGCCCAAGTGGAGCGGCGGTCCCTGTGTGGGAGAAAGCCAGAGAGCCAG 3942
QY 1141 AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHISArgHIS 1160
Db 3943 GATGAAGAGGAGAGCTCAGAAGAGGAGCGGCGCACCTGCGGCACTGACCATGCCAC 4002
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
Db 4003 AGGGGTCTCCGTGAGCGGAGGCCCAAGATTCTTTGAACCTGCCAGACACACTGCAAGTG 4062
QY 1181 ProGlyLeuHISArgThrAlaSerGlyArgGlySerAlaSerGluHISGlnAspCysAsn 1200
Db 4063 CCAGGGCTGCATGCACATGCAAGTGGCCGAGGGTCTCTTCTGAGCACAGACTGCAAT 4122
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
Db 4123 GGCAGTCGGCTTCAAGGGCGCTGGCCCGGCGCTGCGGCTGATGACCCCACTGAT 4182

QY	1221	GLYAspAspAlaAspAspGluGlyAsnLeuSerLysGlyIleArgValArgAlaTrpIle	1240
Db	4183	GGGATGACCGCATGACGAGGCGAACCTGACCAAGGGAAACGGGTCCGCGGTGGATC	4242
QY	1241	ArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTrpIlePhePro	1260
Db	4243	CGAGCCGCACTCCCTGCTGCTGCTCGAGCGAGACTCCTGTGACCTTACATCTTCCCT	4302
QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280
Db	4303	CCTCAGTCCAGGTTCCGCTCCTGTGTCAACGGATCATCACCAAGATGTTGCACCAC	4362
QY	1281	ValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle	1300
Db	4363	GTGGTCTTGTTCATCATCTTCTTAACGTGCATCACCATGCCATGGAGCGCCCAAAATT	4422
QY	1301	AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaVal	1320
Db	4423	GACCCCCACAGCGCTGAACGCATCTTCTGACCTTCCAATTACATCTTACCCGCACTC	4482
QY	1321	PheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGlnAla	1340
Db	4483	TTTCTGCTGAATGACAGTGAAGGTGTGGCACTGGCTGTGCTTCGGGAGCAGCG	4542
QY	1341	TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleSerValIleAsp	1360
Db	4543	TACCTGCGGAGCAGTTGGAACGTGTCGACGGGCTGTGTGCTCATCTCCGTCAATCAC	4602
QY	1361	IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu	1380
Db	4603	ATTCTGGTGTCCATGTCTCTGACAGCGGCAACCAAGATCCTGGGCATGCTGAGGGTGTG	4662
QY	1381	ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu	1400
Db	4663	CGGCTGCTGCGGACCTTGCCGCCCTCAGGGTGATCAGCCGGGCGAGGGGCTGAAGCTG	4722
QY	1401	ValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCys	1420
Db	4723	GTGTGAGAGACGCTGATGTCTCTCACTGAACCCATCGCAACATTTGTAGTCATCTGCTGT	4782
QY	1421	AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal	1440
Db	4783	GCCTTCTTCATCATTTTCGGCATCTTGGGGTGACGCTCTTCAAGGGAAGTTTTCGTG	4842
QY	1441	CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyr	1460
Db	4843	TGCCAGGGCGAGGATACAGGAACATCACCAATAATCGACTGTGCCGAGCCAGTTAC	4902
QY	1461	ArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe	1480
Db	4903	CGGTGGGTCCGGCACAGTACAACTTTGACAACTTTGGCCAGGCCCTGATGTCCCTGTTC	4962
QY	1481	ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGly	1500
Db	4963	GTTTGGCTTCCAAGGATGGTTGGGTGACATCATGTACGATGGGCTGTGTGTGGGC	5022
QY	1501	ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPhe	1520
Db	5023	GTGACACGACGACCCCATGATGAACACAAACCCCTGATGCTGTACTTCATCTCGTTC	5082
QY	1521	LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe	1540
Db	5083	CTGCTCATTTGTGGCTTCTTGTCTGAACATGTTTGTGGGTGTGGTGTGAGAACTTC	5142
QY	1541	HisLysCysArgGlnHisGlnGluGluGluValAlaArgArgArgGluGluLysArgLeu	1560
Db	5143	CACAAGTGTCCGACACCAAGAGAGAGAGAGGCGCGCGGAGAGAGAGCGCCTA	5202
QY	1561	ArgArgLeuGluLysLysArgArg-----LysAlaGlnCysLys	1573
Db	5203	CGAAGAAGTGAAGAAAAAGAGAGAGAGTAAGAGAGACAGATGCTGAAGCCCACTGCAAA	5262
QY	1574	ProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisIleCysThrSerHis	1593

Db	5263	CCCTACTACTCCGACTACTCCCGCTTCCGGCTCTCGTCCACCACCTTGTGCACCAGCCAC	5322
QY	1594	TyrLeuAspLeuPheIleThrglyValIleGlyLeuAsnValValThrMetAlaMetGlu	1613
Db	5323	TACCTGGACCTCTTCATCACAGGTGTCATCGGGCTGAACGTGTGCACATGGCCATGGAG	5382
QY	1614	HisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheThr	1633
Db	5383	CACtACCAGCAGCCCGACGATCTCGATGAGGCTCGAAGATCTGCAACTACATCTTCACT	5442
QY	1634	ValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePhe	1653
Db	5443	GTCATCTTTGTCTTGAGTCAGTTTCAAACTTGTGGCCTTGTGTTCCGTCGGTCTTTC	5502
QY	1654	GlnAspArgTyrPasnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThr	1673
Db	5503	CAGGACAGGTGGAACCACTGGACCTGGCCATTGTGCTGTGTCCATCATGGGCATCAGC	5562
QY	1674	LeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMet	1693
Db	5563	CTGGAGGAATCGAGGTCAACGCCCTCGCTGCCATCAACCCACCATCATCCGATCATG	5622
QY	1694	ArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAla	1713
Db	5623	AGGGTGTGGCGCATGTGCCGAGTGCTGAAGCTCTGAAGATGCTGTGGGCATGCGGGCG	5682
QY	1714	LeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMet	1733
Db	5683	CTGTCTGACACCGGTGATGCAGGCCCTGCCCCAGGTGGGAACCTGGGACTTCTTTCATG	5742
QY	1734	LeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAsp	1753
Db	5743	TGTGTGTTTTCATCTTGCAGCTCTGGGCGTGGAGCTCTTGGAGACCTGGAGTGTGAC	5802
QY	1754	GluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAla	1773
Db	5803	GAGACACACCCCTGTGAGGCGCTGGCGTCATGCCACCTTTCGAACTTTGGCATGGCC	5862
QY	1774	PheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThr	1793
Db	5863	TTCTTAACCTCTTCCGAGTCTCCACAGGTGACATTTGGAATGGCATTTGAAGACACC	5922
QY	1794	LeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIleSerProIleTyrPhe	1813
Db	5923	CTCCGGGACTGTGACCAAGGACTCCACCTGCTACACACGGTCATCTCGCCTATCTACTT	5982
QY	1814	ValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMet	1833
Db	5983	GTTGTCTTCTGTGTGACGGGCCAGTTCTGTCTAGTCAACGTGTGATCGCCGTCTGATG	6042
QY	1834	LysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeu	1853
Db	6043	AAGCACTGGAGAGAGACAACAAGAGGCCAAGAGAGAGGCCGAGCTAGAGGCTGAGCTG	6102
QY	1854	GluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeu	1873
Db	6103	GAGCTGAGATGAAGACCTTCAGCCCCCAGGCCCACTCGCCACTGGGACGCCCTTCTCTC	6162
QY	1874	TyrProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHisPro	1893
Db	6163	TGGCTTGGGGTTCGAGGGCCCCGACAGCCCCGACAGCCCCAAGCCTGGGGCTTGACACCA	6222
QY	1894	AlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnProHis	1913
Db	6223	GCGGCCCAAGGAGATCAGCTTCCACTTTTCCCTGAGACACCCCAAGATGAGCCCCAC	6282
QY	1914	ProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThr	1933
Db	6283	CCACGAGAGCTGCCAGACAGACTTACTGACTGTGCGGAAGTCTGGGGTCAAGCCGAACG	6342
QY	1934	HisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeu	1953

Db 6343 CACTCTGTGCCCAATGACAGCTACATGTGTGCGCATGGAGACACTGCCGAGGGGCCCTG 6402
QY 1954 GLYHisArgGlyTrpGlyLeuProlysaIaGlnSerGlySerValLeuSerValHisSer 1973
Db 6403 GGACACAGGGGCTGGGGGCTCCCAAGCTCAGTCAGGCTCCGCTTGTGTCCGTTACTCC 6462
QY 1974 GlnProAlaAspThrSerTyrIleLeuGlnLeuProlysaAspAlaProHisLeuLeuGln 1993
Db 6463 CAGCCAGCAGATACCAGCTACATCTTCAGACTTCCCAAGATGCACTCATCTGTCTCCAG 6522
QY 1994 ProHisSerAlaProThrTrpGlyThrIleProlySLeuProProProGlyArgSerPro 2013
Db 6523 CCCACAGCGCCCAACTGTGGGACCATCCCAAACTGCCCCACACAGACGCTCCCT 6582
QY 2014 LeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAspSerLeuAspValGln 2033
Db 6583 TTGGCTCAGAGGCCACTCAGCGCGCCAGCAGCAATTAAGACTGACTCTTGACGTTCCAG 6642
QY 2034 GlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAla 2053
Db 6643 GGTCGGGAGCGCGGAAGACCTGCTGGCAGAGTGAGTGGGCCCTCCCGCCCTGGCC 6702
QY 2054 ArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHis 2073
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QY 2074 SerLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrp 2093
Db 6763 AGCAAGATCTCCAAGCACATGACCCCGCCAGCCCTTGCCCAAGCCCAACTGG 6822
QY 2094 GlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIle 2113
Db 6823 GGCAAGGGCCCTCCAGAGACCAGAGAGCTTAGAGTTGACACGAGCTGAGCTGATT 6882
QY 2114 SerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLys 2133
Db 6883 TCAGAGAGACCTCTGCCCCCTGGCGGCAGAGAGAGCCCATCCCCACGGAGCTGAAG 6942
QY 2134 LysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlu 2153
Db 6943 AAGTGCTACAGGCTGGAGGCCCAGAGCTGCCAGCGCGGCTACGTCTGCTGATGAG 7002
QY 2154 GlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGly 2173
Db 7003 CAGAGGAGACTCTATCGCCGTCACTGCTTGACAGCGGCTCCCAACCCCACTGGGC 7062
QY 2174 ThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLys 2193
Db 7063 ACAGACCCCTTAACCTTGGGGGCCAGCTCTTGGGGGGCCGGGAGCGCGCCCAAGAAA 7122
QY 2194 LysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThrPro 2213
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QY 2214 ProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeu 2233
Db 7183 CCCAGCCCTGTATCTGCTCCGAGAGGGGCTCCGTCCAGGACTCCCAAGGATCCTTG 7242
QY 2234 AlaSerGlyProProAspSerMetAlaIaSerProSerProLysLysAspValLeuSer 2253
Db 7243 GCCTCTGGCCCCCTGACAGCATGGCTGCCTCGCCCTCCCAAGAAAGATGTGCTGAGT 7302
QY 2254 LeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7303 CTCTCCGGTTATCTCTGACCCAGCAGACCTGGAACCC 7341

RESULT 3
US-09-949-016-3859
; Sequence 3859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3859
; LENGTH: 7405
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3859

Alignment Scores:
Pred. No.: 0 Length: 7405
Score: 11241.00 Matches: 2162
Percent Similarity: 95.12% Conservative: 1
Best Local Similarity: 95.07% Mismatches: 1
Query Match: 94.43% Indels: 110
DB: 4 Gaps: 4

US-09-611-257A-37 (1-2266) x US-09-949-016-3859 (1-7405)

QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 373 ATGACGAGGAGGAGGATGAGCGGGCGCCGAGAGTCGGGACAGCCCGGAGCTTCATG 432
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 433 CGGCTCAACGACCTGTGGGGGCCGGGGGCCGGGGCCGGGGTCAAGCAAGAAAGGAC 492
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProVal 60
Db 493 CCGGGCAGCGCGGACTCCGAGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCCGGTGTT 552
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 553 TTCTTCTACTTGAGCCAGACAGCCGCCCGGAGCTGTGTCTCCGACGGTCTGTAAC 612
QY 81 Pro---TrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGly 99
Db 613 CCTACTGCTTTGAGCGGCATCAGCATGTGTGTCATCTTCTCACTGCGTGACCCCTGGGC 672
QY 100 MetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAla 119
Db 673 ATGTTCCGGCCATGCGAGACATCGCTGTGACTCCACGCGCTGCCGATCTGCAGGGCC 732
QY 120 PheAspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeu 139
Db 733 TTGTATGACTTCATCTTGGCTTCTTTCGCGTGAGATGTTGTAAGATGTTGGCTTG 792
QY 140 GlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIle 159
Db 793 GGCATCTTTGGAAAAAGTTTACCTGGAGACACTTGAACCGGCTTGACTTTTCATC 852
QY 160 ValIleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaVal 179
Db 853 GTCATGCAAGGATGCTGAGTAATCGCTGACCTGCAGACGTACAGTCTCACTGTG 912
QY 180 ArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIle 199
Db 913 AGGACAGTCCGTGTGCTGCAACCGCTCAGGGGCCATTAAACGGGTGCCAGCATGCCGATC 972
QY 200 LeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhe 219
Db 973 CTGTTCACGTTGTGCTGTGATACGCTGCCCATGCTGGGCAACGTCCTGCTGCTTC 1032
QY 220 PheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsn 239

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Db 1033 TTGCTCTTCTTCATCTTCGGCATCGTCGGCTCCAGCTGTGGGAGGGCTGCTTCGGAAC 1092
QY 240 ArgCysPheLeuProGluAsnPheserLeuProLeuSerValAspLeuGluArgTyrTyr 259
Db 1093 CGATGCTTCTACTGAGATTTCAGCCTCCCTCGAGCGTGAACCTGGACGCTATTAC 1152
QY 260 GlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMet 279
Db 1153 CAGACAGAGAACGAGATGAGAGCCCCCTTCATCTGCTCCAGCCAGCGAGAACGGCATG 1212
QY 280 ArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGly 299
Db 1213 CGGTCTTCAGAAAGCGTGCCACGCTGCGCGGGGACGGGGGCGGTGGCCCACTTGCGGT 1272
QY 300 LeuAspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyr 319
Db 1273 CTGGACTATGAGGCTTAACAACAGCTCCAGCAACACCACTGTGTCACTGGAAACAGTAC 1332
QY 320 TyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsn 339
Db 1333 TACACCAACTGCTCAGCGGGGAGACACAACCCCTTCAAGGGCGCCACTTGACAAC 1392
QY 340 IleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIle 359
Db 1393 ATTGGCTATGCTCGATCGCCATCTTCCAGGTCATCACGCTGAGGGCTGGGTCGACATC 1452
QY 360 MetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 379
Db 1453 ATGTACTTGTGATGATGATGCTCATCTCTTCAACAATTTCATCTACTCTCTCATC 1512
QY 380 IleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSer 399
Db 1513 ATCGTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGATGATGCCAGCAGTTCTCA 1572
QY 400 GluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsn 419
Db 1573 GAGACCAAGCAGCGGAAAGCCAGCTGATGCGGAGCAGCGTGTGCGTCTCTGCCAAC 1632
QY 420 AlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyr 439
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QY 440 LeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGly 459
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QY 460 ValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSer 479
Db 1753 GTGCGGGTTGGGCTGCTCAGCAGCCAGCACCCCTCGGGGCCAGAGAACCCAGCCAGC 1812
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Db 1813 AGCAGCTGCTCTCGCTCCACCGCGCCTATCCGTCACACCACTGTGCACACCAACACAC 1872
QY 500 HisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerPro 519
Db 1873 CACCATCACCACTACCACTGGGCAATGGGACGCTCAGGGCCCCCGGGCCAGCCCG 1932
QY 520 GluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThr 539
Db 1933 GAGATCCAGGACAGGGATGCCAATGGGTCCCGCGGCTCATGTGCCACCACTCGAGC 1992
QY 540 ProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAla 559
Db 1993 CTTGCCCTCTCCGGGGCCCCCTGTGTGGCGAGTCTGTGCACAGCTTCTTACCATGCC 2052
QY 560 AspCysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAla 579
Db 2053 GACTGCCACTTAGAGCCAGTCCGCTGCAGGCGCCCCCTCCAGGTCCCATCTGAGGCA 2112
QY 580 SerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProPro 599
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Db 2113 TCCGGCAGACTGTGGGAGCGGGAAGTGTATCCCAACCGTGCACACCAAGCCCTCCACCG 2172
QY 600 GluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeu 619
Db 2173 GAGACGCTGAAGAGAAGGCACTAGTAGAGGTGGCTGCCAGCTCTGGCCCCCAACCTTC 2232
QY 620 ThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGln 639
Db 2233 ACCAGCTCAACATCCACCCGGGCTTACAGCTCCATGCACAAGCTGTGGAGACACAG 2292
QY 640 SerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSer 659
Db 2293 AGTACAGTGCTGCCAAAGCTTGGCAAGATCTCCAGCCCTTGCTGAAAGCAGACAGT 2352
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Db 2593 GTGACAGCAAGTACTTTGGCCGGGGAATCATGATCGCCATCTGTCAACACACTCAGC 2652
QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
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Db 2713 ATCGTCTTACAGCCTCTTTGCCCTGAGATGCTGCTGAAGCTGCTGTGTATGCTGCC 2772
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819
Db 2773 TTTGCTACATCAAGAATCCCTACACATCTTCATGTGTCAATTGTGTCATCAGCGTG 2832
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Db 2833 TGGAGATCGTGCGCCAGCAGGGGGGCGCTGTGCTGTGCGGACCTCCGCGCTGATG 2892
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QY 1080 AlaHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAla 1099
Db 3544 GCCCAGCAGATGAAGTCAACGCCGCCAGCGCCGCAAGCTCTCCGACAGCCCTGGAGCGCT 3603
QY 1100 AlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeu 1119
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QY 1120 LysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnSer 1139
Db 3664 AAGCGAGAGCCCAAGTGAGAGCGCGGCTCCCTGTTGTGGGAAGAAGCCAGAGAGC 3723
QY 1140 GlnAspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHisArg 1159
Db 3724 CAGGATGAAGAGAGAGCTCAGAAGAGAGCGGGCCAGCCCTCGGGCAGTGACCATCGC 3783
QY 1160 HisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGln 1179
Db 3784 CACAGGGGGTCCCTGGAGCGGAGGCAAGAGTCTTGAACCTGCCAGACACACTGACAG 3843
QY 1180 ValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCys 1199
Db 3844 GTGCCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTGAGCACCAAGACTGC 3903
QY 1200 AsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProLeu 1219
Db 3904 AATGGCAAGTCGGCTTCAGGGCGGCTGGCCCGGCTGCGCCCTGATGACCCCCACTG 3963
QY 1220 AspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrp 1239
Db 3964 GATGGGAGTACGCCGATGACGAGGGCAACTGAGCAAGGGGAAACGGGTCCGCCGCTGG 4023
QY 1240 IleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhe 1259
Db 4024 ATCCGAGCCGACTCCCTGCTGCTGCTCGAGCGAGACTCTGTGTCAGCCTACATCTTC 4083
QY 1260 ProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAsp 1279
Db 4084 CCTCCTCAGTCCAGTTCGCGCTCTGTGTCAACCGATCATCAACCAAGATGTTGCAC 4143
QY 1280 HisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLys 1299
Db 4144 CACGTGCTCTTGTATCATCTTCTTAATGCATCACCATCGCATGAGCGCCCAAA 4203
QY 1300 IleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAla 1319
Db 4204 ATTGACCCCAACAGCGCTGAACGCATCTTCTGACCCCTCTCCAATTACATCTTACCGCA 4263

QY 1320 ValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGluGln 1339
Db 4264 GTCTTCTGGCTGAATATGACGTGAAGGTGTGGCACTGGGCTGTGCTTCGGGAGCAG 4323
QY 1340 AlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIle 1359
Db 4324 GCGTACCTCGGAGCAGTGAACGTGCTGAGCGGGCTGTGTGCTCATCTCCGTCATC 4383
QY 1360 AspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgVal 1379
Db 4384 GACATTCTGGTGTCCATGGTCTCTGACAGCGGCACCAAGATCTGGGCATGCTGAGG 4443
QY 1380 LeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLys 1399
Db 4444 CTGCGGCTGCTGCGGACCTGCGCCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAG 4503
QY 1400 LeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCys 1419
Db 4504 CTGGTGGTGAAGACGCTGATGTCTCTCACTGAACCCATCGGCACAACTGTATCATCTGC 4563
QY 1420 CysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePhe 1439
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QY 1440 ValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSer 1459
Db 4624 GTGTGCCAGGGCGAGGATACAGGAACATCACCAATAATCGACTGTGCCAGGCCAGT 4683
QY 1460 TyrArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeu 1479
Db 4684 TACCGGTGGGTCCGGCACAGTAACAATTGTGACAACTTGGCCAGGGCTGATGTCCCTG 4743
QY 1480 PheValIleuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaVal 1499
Db 4744 TTGCTTTTGGCTTCCAGGATGGTTGGGTGACATCATGTACGATGGGCTGGATGCTGTG 4803
QY 1500 GlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSer 1519
Db 4804 GGGTGCACACAGCAGCCCATATGAACCAACACCCTGATGCTGCTGTACTTCATCTCG 4863
QY 1520 PheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsn 1539
Db 4864 TTCCTGCTCATTTGGGCTTCTTGTCTGAACATGTTGTGGGTGTGGTGAAGAAC 4923
QY 1540 PheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluLysArg 1559
Db 4924 TTCCACAAGTGTCCGACAGCACCAAGAGAGAGAGCGCCGGCGGAGAGAGAGCGC 4983
QY 1560 LeuArgArgLeuGluLysLysArgArg-----LysAlaGlnCys 1572
Db 4984 CTACGAAGACTGAGAAAGAGAGAGAGTAAAGAGAGAGATGGCTGAAGCCCACTGC 5043
QY 1573 LysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSer 1592
Db 5044 AAACCTTACTACTCCGACTACTCCCGCTTCCGGCTCTCGTCCACACTTGTGCACAGC 5103
QY 1593 HisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMet 1612
Db 5104 CACTACCTGGAACCTTTCATCACAGGTGTCAATCGGGCTGAACGTGTGTCCATGCGCATG 5163
QY 1613 GluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePhe 1632
Db 5164 GAGCACTACACAGACGCCAGATTCGTGATGAGGCTCTGAAGATCTGCAACTACATCTTC 5223
QY 1633 ThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhe 1652
Db 5224 ACTGTCACTTTGTCTTGAGTCAAGTTTCAAACTTGTGGCTTGGTTCGCTCGGTTTC 5283
QY 1653 PheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIle 1672
Db 5284 TTCCAGACAGGTGGAACACGCTGACCTGGCCATGTGCTGTGCATCATATGGGCATC 5343
QY 1673 ThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIle 1692

Db 5344 ACGCTGAGGAATCGAGGTCAACGCTCGCTGCCATCAACCCACCATCATCCGCATC 5403
QY 1693 MetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAlaValGlyMetArg 1712
Db 5404 ATGAGGGTGCTGCGCATTTGCCGAGTGCTGAAGATGGCTGTGGCATGCGG 5463
QY 1713 AlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPhe 1732
Db 5464 GCGCTGCTGGACACGGTGATGCAGGCGCTGCCCAAGGTGGGGAACCTGGGACTTCTCTTC 5523
QY 1733 MetLeuLeuPhePheIlePheAlaAlaLeuGlyValGlyLeuPheGlyAspLeuGlyCys 1752
Db 5524 ATGTTGTTGTTTTCATCTTTGCAGCTCTGGGCGTGAGCTCTTTGGAGACCTGGAGTGT 5583
QY 1753 AspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMet 1772
Db 5584 GACGAGACACACCCCTGTGAGGGCGCTGGCGCTCATGCACCTTCGGAACCTTGGCATG 5643
QY 1773 AlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAsp 1792
Db 5644 GCCTTCCTAACCCCTCTCCGAGTCTCCACAGGTGACATTTGAATGGCATATGAAGGAC 5703
QY 1793 ThrLeuArgAspCysAspGlnGlySerThrCysTyrAsnThrValIleSerProIleTyr 1812
Db 5704 ACCCTCCGGGACTGTGACCAAGAGTCCACCTGTCTACAACACGGTCACTCCGCCTATCTAC 5763
QY 1813 PheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeu 1832
Db 5764 TTTGTGCTTCTGCTGACGGCCAGTTCTGTACTAGTCAACGTGTGATCGCCGTGCTG 5823
QY 1833 MetLysHisLeuGluGlySerAsnLysGlnAlaLysGluGlyValGluLeuGluAlaGlu 1852
Db 5824 ATGAAGCACCTGAGGAGAGCAACAAGAGGCGCAAGAGAGCGCGAGCTAGAGGCTGAG 5883
QY 1853 LeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlySerProPhe 1872
Db 5884 CTGGAGCTGGAGATGAAGACCTCAGCCCCCAGCCCCCACTCGCAGTGGGCGAGCCCCCTTC 5943
QY 1873 LeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyAlaLeuHis 1892
Db 5944 CTCTGGCCTGGGGTCAAGGGCCCCGACAGCCCCCAAGCCTGGGGCTCTGCAC 6003
QY 1893 ProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProThrMetGlnPro 1912
Db 6004 CCAGCGGCCACGCGGAGTCAAGCTCCACATTTCCTTGAGCACCCCAAGATGACAGCCC 6063
QY 1913 HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArg 1932
Db 6064 CACCCACGAGCTGCCAGGACACAGACTTACTGTGCGGAAGTCTGGGGTCAAGCCGA 6123
QY 1933 ThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyPro 1952
Db 6124 ACGCACTCTGTGCCAATGACAGCTACATGTGTGGCATGGAGCACTGCCAGGGGCC 6183
QY 1953 LeuGluHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySerValLeuSerValHis 1972
Db 6184 CTGGGACACAGGGGCTGGGGCTCCCCAAGCTCAGTCAAGGCTCCGTCTGTCCGTTCAAC 6243
QY 1973 SerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeu 1992
Db 6244 TCCAGCCAGCAGATACGACTACATCTGCAGCTTCCCAAGATGCACTCATCTGCTC 6303
QY 1993 GlnProHisSerAlaProThrTyrGlyThrIleProLysLeuProProGlyArgSer 2012
Db 6304 CAGCCCCACAGCGCCCAACTGGGGCACCATCCCAAACTGCCCCCAAGACGCTCC 6363
QY 2013 ProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspVal 2032
Db 6364 CTTTGGCTCAGAGGCCACTCAGGGCGCCAGGCAATTAAGACTGACTCTTGAGCGTT 6423
QY 2033 GlnGlyLeuGlySerArgGluAspLeuAlaGluValSerGlyProSerProProLeu 2052

Db 6424 CAGGTCCTGGGCAGCCGGAAGACTGTGGCAGAG----- 6459
QY 2053 AlaArgAlaTyrSerPheTyrGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSer 2072
Db 6459 ----- 6459
QY 2073 HisSerLysIleSerLysHisMetThrProProAlaProCysProGlyProGlnProAsn 2092
Db 6459 ----- 6459
QY 2093 TrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrp 2112
Db 6459 ----- 6459
QY 2113 IleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeu 2132
Db 6460 -----GAGGAGCCCCCATCCCCACGGGACCTG 6486
QY 2133 LysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAsp 2152
Db 6487 AAGAAGTGTCTACAGCTGGAGGGCCACAGCTGCCAGCGCGCCACAGTCTGTGCTGAT 6546
QY 2153 GlnGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeu 2172
Db 6547 GAGCAGAGGAGCACTTATCGCCGTCAAGTCCCTGGACACGGGCTCCCAACCCCACTG 6606
QY 2173 GlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLys 2192
Db 6607 GGCACAGACCCCTTAACCTTGGGGCCAGCCTTGGGGGCGCTGGAGCGGCGCCAAG 6666
QY 2193 LysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGlyProArgThr 2212
Db 6667 AAAAAGCTCAGCGCCGCTAGTATCACCATAGACCCCCCGAGAGCCAAAGTCTCGGACC 6726
QY 2213 ProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSerLysAspPro 2232
Db 6727 CCGCCAGCCCTGTATCTGCTCCGAGAGAGGCTCCGTCAAGCACTCCAAGGATCCC 6786
QY 2233 LeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLysAspValLeu 2252
Db 6787 TTGGCCTCTGGCCCCCTGACAGCAATGCTGCTCGCCCTCCCCAAGAAGAATGTGCTG 6846
QY 2253 SerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6847 AGTCTCTCGGTTTATCTCTGACCCAGACAGACCTGACCCC 6888

RESULT 4

US-09-398-522-51
; Sequence 51, Application US/09398522
; Patent No. 6783933
; GENERAL INFORMATION:
; APPLICANT: Issa, Jean-Pierre
; TITLE OF INVENTION: CACNA1G POLYNUCLEOTIDE POLYPEPTIDE AND
; FILE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: JH01590
; CURRENT APPLICATION NUMBER: US/09/398,522
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 3993
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CAGNA1G - a gene encoding a T-type calcium channel
; NAME/KEY: CDS
; LOCATION: (373)...(3993)
US-09-398-522-51
Alignment Scores: 0 Length: 3993
Pred. No.: 6315.50 Matches: 1207
Score:

Percent Similarity: 98.13% Conservative: 0
Best Local Similarity: 98.13% Mismatches: 0
Query Match: 53.05% Indels: 23
DB: 4 Gaps: 1

US-09-611-257A-37 (1-2266) x US-09-398-522-51 (1-3993)

QY	1	MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20
DB	373	ATGACAGAGAGAGATGAGCGGGCCGAGAGTCGGGACAGCCCCGAGCTTCATG	432
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyPProGlySerAlaGluLysAsp	40
DB	433	CGGCTCAACGACTGTCCGGGGCCGGGGCCGGCCGGGGTCAAGAAAGAGAC	492
QY	41	ProGlySerAlaAspSerGlyAlaGlyLeuProTyrProAlaLeuAlaProValVal	60
DB	493	CCGGGACGGCGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTGGCCCCGGTGGTT	552
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
DB	553	TTCTTCTACTTGAGCCAGACAGACGCCGCCGAGAGCTGTGTCTCCGACCGGTCTTAAC	612
QY	81	ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	613	CCCTGTTTGAGCGCATCAGCATGTGTGTCATCCTTCTCACTGCGTGACCTGGGCATG	672
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	673	TTCCGGCCATGCGAGGACATCGCCTGTGACTCCACGCGCTGCCGATCCTGCAGGCTTT	732
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	733	GATGACTTCATCTTTGCCCTTCTTTGCCGTGAGATGTGTGTAAGATGTGGCCTTGGGC	792
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal	160
DB	793	ATCTTTGGGAAAAAGTGTACTCGTGAGACACTTGGAACCGGCTTGACTTTTTCATCGTC	852
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	853	ATCGCAGGGATGCTGAGTACTCGCTGGACTGCAGAACGTCACTTCTCAGCTGTCAAG	912
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	913	ACAGTCCGTGTGTGCGACCGCTCAGGGCATTAAACCGGGTGCCACGATGCGCATCTT	972
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	973	GTCACGTTGCTGTGATACGCTGCCCATGTGGCAACGTCTGTCTGTCTTCTTTC	1032
QY	221	ValPhePheIlePheGlyIleValaGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
DB	1033	GTCTTCTTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGGCAAGGCTGCTTCGGAACCGA	1092
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
DB	1093	TGCTTCTACCTGAGAAATTTCAGCCTCCCTTGAGCGTGACCTGGAAGCGCTATTACAG	1152
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
DB	1153	ACAGAGAAGAGATGAGAGCCCTTCACTGTCTCCAGCCACGCGAGAAACGCGCATGCGG	1212
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
DB	1213	TCCTGCAGAAAGCTGCCACGCTGCGGGGAGCGGGGCGGTGCCACCTTGCGGTCTG	1272
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320
DB	1273	GACTATGAGGCTTACAAACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTAC	1332
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340

DB	1333	ACCAACTGCTCAGCGGGGAGCACAAACCCCTTCAAGGGCGCCATCAACTTGGACAACATT	1392
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
DB	1393	GGCTATGCTGATCGCATCTTCCAGGTCAATCAACGCTGAGGGCTGGGTGCACATCATG	1452
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
DB	1453	TACTTTGTATGATGATGTCATTCCTTCTACAAATTTCATCTACTTCACTCCTCATCATC	1512
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
DB	1513	GTGGGCTCCTTCTTCATGATCAACCTGTGCTGGTGTGATTGCCAGCAGTCTCAGAG	1572
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
DB	1573	ACCAAGCAGCGGGAAGCCAGCTGATGCGGAGCAGCGTGTGCGGTCTGTCCAACGCC	1632
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440
DB	1633	AGCACCTGGCTAGCTTCTTGAGCCCGGACAGCTGCTATGAGAGAGCTGCTCAAGTACCTG	1692
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
DB	1693	GTGTACATCCTTGTAAAGCAGCCCGCAGGCTGTGCTCAGGTCTCTCGGGCAGCAGGTGTG	1752
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
DB	1753	CGGGTTGGGCTGCTCAGACGCCACAGACCCCTCGGGGGCCAGAGACCAGCCAGCAGC	1812
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
DB	1813	AGCTGCTCTCGCTCCACACCGCCGCTATCCGTCAACCACTGTGCACCAACCACCCAC	1872
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
DB	1873	CATCACCACTACTACCTGGGCAATGGAGCTCAGGGCCCCCGGGCCAGCCCGGAG	1932
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
DB	1933	ATCCAGACAGGATGCCAATGGTCCCGCGGCTCATGCTGCCACCACTCGACGCCT	1992
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
DB	1993	GCCCTCCCGGGGCCCCCTGGTGCGCAGAGTCTGTGCACAGCTTTCATCATGCCGAC	2052
QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
DB	2053	TGCCACTTAGAGCAGTCCGCTGCCAGCGGCCCTCCAGGTCCCCATCTGAGGCATCC	2112
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
DB	2113	GGCAGGACTGTGGCAGCGGGGAAGGTATATCCACCGTGCAACACGACCTCCACCGGAG	2172
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
DB	2173	ACGCTGAAGAGAAGGCACTAGTAGAGGTGGCTGCAGCTGTGGGCCCCCAACCTCAC	2232
QY	621	SerLeuAsnIleProProGlyProTyrSerSerSerMetHisLysLeuLeuGluThrGlnSer	640
DB	2233	AGCCTCAACATCCCAACCGGGCCCTACAGCTCCATGCACAAGCTGCTGAGACACAGAGT	2292
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
DB	2293	ACAGGTGCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAAGCAGACAGTGA	2352
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680
DB	2353	GCCTGTGTCCAGACAGCTGCCCTACTGTGCCCGGGCCGGGCGAGGGAGGTGAGCTC	2412
QY	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
DB	2413	GCCGACCGTGAATGCTGTACTCAGACAGCAGGCAAGTATTATGAGTTCAACAGGATGCC	2472

QY 701 GlnHisSerAspLeuArgAspProHisSerArgGlnArgSerLeuGlyProAspAla 720
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Db 2473 CAGCACAGCGACCTCGGGAGACCCACACAGCCGGCGCAACGAGCCTGGGCCAGATGCA 2532
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
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Db 2533 GAGCCAGCTCTGTGCTGGCCTTCTGGAGGCTAATCTGTGACACCTTCGGAAGATTGTG 2592
QY 741 AspSerLysTrpPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
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Db 2593 GACAGCAAGTACTTGGCCGGGGAATCATGATCGCATCTGTGTCAACACTCAGCATG 2652
QY 761 GlyIleGluTrpHisGlnGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
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Db 2653 GGCATCGAATACACGAGCAGCCCGAGGAGCTTACCAGCCCTAGAAATCAGCAACATC 2712
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrglyProPhe 800
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Db 2713 GTCTTACCAGCCTCTTGGCCCTGGAGATGCTGGAAGCTGTGTGATGTGCTCCCTTT 2772
QY 801 GlyTrpIleLysAsnProTyrrAsnIlePheAspGlyValIleValIleSerValTrp 820
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Db 2773 GGCTACATCAAGAAATCCCTACAACATCTTCGATGTGTCTCATTTGTGTATCAGCGTGTG 2832
QY 821 GluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMetArg 840
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Db 2833 GAGATCGTGGCGCAGCAGGGGGGGGGCGCTGTGTGTCTGCGACCTTCGCGCTGATGCGT 2892
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
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Db 2893 GTGCTGAAGCTGTGCGCTTCTCTGCGCGCTGCGCAGCGCAGCGCTGTGTCTCATGAAG 2952
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
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Db 2953 ACCATGGACACAGCTGGCCACCTTCTGCATGCTGCTTATGCTCTTCATCTTCATCAGC 3012
QY 881 IleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
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Db 3013 ATCTTGGGCATGCATCTCTTCGGCTGCAAGTTGCTGTAGCGGGAGGAGACACCTGT 3072
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
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Db 3073 CCAGACCGGAAGAAATTTGAATCTCTGCTCTGGGCCATCGTCACTGTCTTTCAGATCCTG 3132
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrrAsnGlyMetAlaSerThrSerSerTrpAla 940
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Db 3133 ACCCAGGAGGACTGGAACAAGTCTCTACAATGTATGGCTCCACGTCGTCTGGGCG 3192
QY 941 AlaLeuTyrrPheIleAlaLeuMetThrPheGlyAsnTyrrValLeuPheAsnLeuVal 960
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Db 3193 GCCCTTATTTCATGTGCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTGTGCTGTG 3252
QY 961 AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly 980
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Db 3253 GCCATTCTGTGTGAGGGCTTCAGGGCGAG----- 3282
QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyLysAspAlaAsnLysSerGlu 1000
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Db 3283 -----GGAGATGCCAACAAAGTCCGAA 3303
QY 1001 SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu 1020
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Db 3304 TCAGAGCCCGATTCTTCTTCACCCAGCCTGGATGTGATGGGACAGAGAAGAGTGTCTTG 3363
QY 1021 AlaLeuValSerLeuGlyGlnHisProGluLeuArgLysSerLeuLeuProLeuIle 1040
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Db 3364 GCCTTGGTGTCCCTGGAGAGCACCCGAGCTGCGAAGAGCCTGTGCGCCTCTCATC 3423
QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
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Db 3424 ATCCACAGCGCGCCACACACCATGTGCTGCCAAGAGCACACGAGCGGGCTGGGCGAG 3483

QY 1061 AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
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Db 3484 GCGTGGGCCCTCGCTCGCGCCGACACAGCAGCAGCGGCTCGGACAGACCTGGGGGGCC 3543
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
|||||
Db 3544 CACGAGATGAAGTCAACGCCACGCCCGCCAGCTCTCCGCACAGCCCCCTGGAGCGCTGCA 3603
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
|||||
Db 3604 AGCAGCTGGACCAAGCGCGCTCCAGCCGGAACAGCCTCGCGCTGACCCAGCCTGAAG 3663
QY 1121 ArgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln 1140
|||||
Db 3664 CGGAGAAGCCCAAGTGAGAGCGGCGGTCCCTGTGTGGGAGAAAGCCAGAGAGCCAG 3723
QY 1141 AspGluGluSerSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHis 1160
|||||
Db 3724 GATGAAGAGAGAGCTCAGAAAGAGCGGGCCAGCCCTGGGGCAGTGACCATCGCCAC 3783
QY 1161 ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal 1180
|||||
Db 3784 AGGGGTCTCTGGAGCGGGAGGCCAAGATTCTTTGACTTGCCACACACTGCAGGTG 3843
QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn 1200
|||||
Db 3844 CCAGGGCTGCATCGCACTGCCAGTGGCGAGGGTCTGCTTGAGCACACAGAGACTGCAAT 3903
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
|||||
Db 3904 GGCAAGTCGGCTTCAAGGCGCCTGGCGCGGCCCTGCGGCTGATGACCCCCACTGGAT 3963
QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeu 1230
|||||
Db 3964 GGGGATGACGCCGATGACGAGGGCAACTG 3993

RESULT 5
US-08-984-709A-49
; Sequence 49, Application US/08984709A
; Patent No. 6320032
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark E.
; APPLICANT: Stauderman, Kenneth A.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
; TITLE OF INVENTION: METHODS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, Suite 700
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/984,709A
; FILING DATE: 02-DEC-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 450-8400
; TELEFAX: (619) 587-5360
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7898 base pairs

/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ FEATURE:
/ NAME/KEY: Coding Sequence
/ LOCATION: 249...7307
/ OTHER INFORMATION:
US-08-984-709A-49

Alignment Scores:
Pred. No.: 0 Length: 7898
Score: 6214.50 Matches: 1367
Percent Similarity: 65.17% Conservative: 212
Best Local Similarity: 56.42% Mismatches: 516
Query Match: 52.21% Indels: 328
DB: 3 Gaps: 59

US-09-611-257A-37 (1-2266) x US-08-984-709A-49 (1-7898)

QY 7 GLYAlaGLYAlaGLuGLuSerGlyGlnProArGSerPheMetArGLeuAsnAspLeuSer 26
Db 317 GGC GTTGGTGGGGCGCTCCCGGAGAGCCCCGG----- 349
QY 27 GLYAlaGLYGLYArGProGLYPro-GlySer----- 36
Db 350 GCGCGCCGGAGCGGAGCGGAGCGGGGGTCCGAGCTCGGCGTGTCAACCTCCGAGAGCCC 409
QY 37 ----AlaGLuYsAspProGLYSerAlaAspSerGLuAlaGLuGLYLeuProTYrProAl 55
Db 410 GCGGCGCGAGCGCGCGCGAGCTGGGTGCCGAGAGAGCAGCGCGTCCCGTACCGCGC 469
QY 55 aLeuAlaProValValPhePheTYrLeuSerGLnAspSerArGProArGSerTPCysLe 75
Db 470 CTTGGCGGCCACGCTCTTCTTCTGCTCGGTCAAGACCAACGCGCGCGCAGCTGTGCCT 529
QY 75 uArGThrValCysAsnProTrpPheGLuArgLeSerMetLeuValLeuLeuAsnCy 95
Db 530 CCGGCTGGTGTGCAACCCATGTGTGACACAGTGACATGCTGTAATCATGCTCAACTG 589
QY 95 sValThrLeuGLYMetPheArGProCYsGLuAspIleAlaCYsAspSerGLnArGYSAr 115
Db 590 CGTGACCCCTGGCATGTTCCGGCCCTGTGAGGACGTTGAGTGCCTCCGAGCGCTGCAA 649
QY 115 gIleLeuGLnAlaPheAspAspPheIlePheAlaPhePheAlaValGLuMetValValY 135
Db 650 CATCCTGGAGGCTTTGACGCCCTTCAATTTGCTTTTTCGGGTGAGATGTCATCAA 709
QY 135 sMetValAlaLeuGLYIlePheGLYLYsLYsCYsTYrLeuGLYAsPTThrTPAsnArGLe 155
Db 710 GATGTGGCTTGGGGCTGTTCCGGCAGAAAGTGTACCTGGGTGACACAGTGAACAGGCT 769
QY 155 uAspPhePheIleValIleAlaGLYMetLeuGLuTYrSerLeuAspLeuGLnAsnValSe 175
Db 770 GGATTTCTTCATCGTGTGCGGGCATGATGAGTACTGCTTGGAGACGACACACAGTGAG 829
QY 175 rPheSerAlaValArGThrValArGVAlleuArGProLeuArGAlaIleAsnArGVAlPr 195
Db 830 CCTCTCGGCTATCAGGACCGTGGGGTCTGGCGCCCTCCGCCATCAACCGCGTGCC 889
QY 195 oSerMetArGIIleuValThrLeuLeuLeuAspThrLeuProMetLeuGLYAsnValLe 215
Db 890 TAGCATGCGGATCTGTGCTCACTGTGCTGTGATACGCTGCCATGCTCGGGAACGTCTCT 949
QY 215 uLeuLeuCYsPhePheValPhePheIlePheGLYIleValGLYValGLnLeuTPAlaGL 235
Db 950 TCTGCTGTGCTTCTTCTGCTTCTTCAATTTCCGCATCGTTGGCGCTCCAGCTCTGGGCTGG 1009
QY 235 YLeuLeuArGVAsnArGYSpheLeuProGLuAsnPheSerLeuProLeuSerValAsp-- 254

Db 1010 CCTCTGCGGGAACCGCTGCTTCTCTGACAGTGCCTTTGTCTCAGGAACAACACTGACCTT 1069
QY 255 -LeuGLuArGTYrTYrGLnThrGLuAsnGLuAspGLuSerProPheIleCYsSerGLnPr 274
Db 1070 CCTGGCGCCGTACTACCAAGAGGAGGAGGCGCGGAGAGAACCCGTTCACTGTCTCTCAGC 1129
QY 274 oArGVAsnGLYMetArGSerCYsArGVAlPro-----ThrLeuArGVLYAs 291
Db 1130 CCGAGACAACGGCATGCAAGTGTCTGCACATCCCGCGCCGCGAGCTGCGC----- 1184
QY 291 pGLYGLYGLYProProCYsGLYLeuAspTYrGLuAlaTYrAsn----- 306
Db 1185 -----ATGCCCTGCACCCCTGGGCTGGAGGCTTACACGCAAGCCGAGCGCGA 1231
QY 307 -----SerSerSerAsnThrThrCYsValAsnTPAsnGLnTYrTYrThrAsnCYsSe 324
Db 1232 GGGGGTGGCGCTGCACGCAACGCTGCATCACTGGAACCACTGACTCAACGCTGCGC 1291
QY 324 rAlaGLYGLuHISAsnProPheLYsGLYAlaIleAsnPheAspAsnIleGLYTYrAlaTr 344
Db 1292 CTCGGGTGACTCCAAACCCCAACAACGGTGCCATCACTTGACAAACATCGGCTACGCCCTG 1351
QY 344 pIleAlaIlePheGLnValIleThrLeuGLuGLYTrpValAspIleMetTYrPheValMe 364
Db 1352 GATTGCCATCTTCAGAGTGATCAAGCTGAAGGCTGGGTGAGACATCATGTACTACGTCAAT 1411
QY 364 tAspAlaHISerPheTYrAsnPheIleTYrPheIleLeuLeuIleIleValGLYSerPh 384
Db 1412 GGACGCCCACTCATTTCAACTTCACTTATTTCACTCTGCTCATCATGTGGGCTCCTT 1471
QY 384 ePheMetIleAsnLeuCYsLeuValValIleAlaThrGLnPheSerGLuThrLYsGLnAr 404
Db 1472 CTTCAATGATCAACCTGTGGCTGTGTGATGTCACGACGAGTCTCGAGACGAAGCAGCG 1531
QY 404 gGLuSerGLnLeuMetArGVGLuGLnArGVAlArGpHeLeuSerAsnAlaSerThrLeuAl 424
Db 1532 GGAAGTCAAGTATGATCGGGAGCAGCGGACGCCACCTGTCCAACGACGACAGCTGGC 1591
QY 424 aSerPheSerGLuProGLYSerCYsTYrGLuGLuLeuLeuLYsTYrLeuValTYrIleLe 444
Db 1592 CAGCTTCTCCGAGCTGGAGCTGTCTACGAAGAGCTGTGAAGTACGTGGGCCCATATATT 1651
QY 444 uArGVsAlaAlaArGVArGVleuAlaGLnValSerArGVAlaGLYValArGVAlGlyLe 464
Db 1652 CCGCAAGCTCAAGCGGCGGCACTTGCGCTTACGCCCGCTGGCAGAGCGCTGGCGCAA 1711
QY 464 uLeuSerSerProAlaProLeuGLYGLnGLuThrGLnProSerSerSerCYsSerAr 484
Db 1712 GAAGTGGACCCCAAGTGTGTGCAAGGCCAG-----GTRCCCGGCAACGCCAGCGCGC 1765
QY 484 gSerHISArGVArG--LeuSerValHISISleuVal--HISHISHISHISHISHI 502
Db 1766 GCGAGGAGGACACAGAGCTCGGTGCACCACTGTCTACCAACCACTACCAACCA 1825
QY 502 SHISHTYrHISleuGLYAsnGLYThrLeuArGVAlaProArGVAlaSerProGLuIleGL 522
Db 1826 CCACCACTACCATTTCAAGCATGGCAGCCCCCGCAGGCCCCCGAGCCAGCGCGCTG 1885
QY 522 nAspArGVsAlaAsnGLYSerArGVArGVleuMetLeuProProProSerThrProAlaLe 542
Db 1886 CGAC-----ACCAAGGCTGTGCCAGCTGGCGGCCCCCTCGCCACCTTTC 1930
QY 542 uSerGLYAlaProProGLYGLYAlaGLuSerValHISerPheTYrHISAlaAspCYsHI 562
Db 1931 CCCAGCGCGGAGACCCCGGACGAGAGTGTGTGACAGCATCTACCATGCGCACTGCCA 1990
QY 562 sLeuGLu-----ProValArGVsGLnAlaProProProArGVSerProSerGLuAlaSe 580
Db 1991 CATAGAGGGGCGGACAGAGAGGGCCGGGTGGACATGCCGACCACTGCCGCTGCCAG 2050
QY 580 rGLYArG---ThrValGLYSerGLYLYsVal---TYrProThrVal----- 593

Db 2051 CCTCAGGCTGGCCACAGGGCTGGCACCATGAATACCCCAGCATCCTGCCCTCAGGGGT 2110
QY 594 -----HisThSerPro-----ProPr 599
Db 2111 GGGCAGCGGCAAGGCACAGCAGCCCGGACCCCAAGGGAAGTGGCCGGTGAGACCGCC 2170
QY 599 oGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerglyProProthrl 619
Db 2171 AGGCACC-----GGGGGCACGGCCGTTGAGCTT 2200
QY 619 uThrSerLeuAsnIleProProGlyProTyrSerSerMethIstLysLeuLeuGluThrGl 639
Db 2201 GAACAGC-----CCTGATCCCTACGAGAAGATCCCGCATGTGGTCCGGGAGCA 2248
QY 639 nSerThrGlyAlaCysGlnSer-----SerCysLysIleSerSe 652
Db 2249 TGGACTGGGGCCAGGCCCTGGCCCATCTGTCCGGCCTCAGTGTGCCCTGCCCTGCCAG 2308
QY 652 rProCysLeuLysAlaAspSerglyAlaCysGlyProAspSergCysProTyrCysAlaAr 672
Db 2309 CCCC-----CCAGCGGGCACACTGACCTGTGAGCTGAAGAGCTGCCCTACTGCACCCG 2362
QY 672 gAla---GlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSergl 691
Db 2363 TGCCCTGGAGGACCCGGAGGGTGAGCTCAGCGGCTCGAAAGTGAGACTCAGATGGCCG 2422
QY 691 uAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspPro----- 708
Db 2423 TGGCGTCTATGAATTCAAGCAGACGCTCCGGCAGCGTGACCGCTGGGACCCCACGCAGCC 2482
QY 709 -----HisSerArgGlnArgSe 715
Db 2483 ACCCCGTGCGACGCACACAGGCCAGGCCAGGCCAGCCCGGGGGCACAGCA 2542
QY 715 rLeuGlyProAspAlaGluProSerSerValLeuAlaPheTyrArgLeuIleCysAspTh 735
Db 2543 GAGGGCAGCCCCGGCGGACGAGGCTGGATGGCGCCCTCTGGGTTACCTTCAGCGGCAA 2602
QY 735 rPheArgLysIleValaAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuVa 755
Db 2603 GCTGCGCCGATCGTGAGACAGAACTTACGCGCTGATCATGATGCCATCTTGT 2662
QY 755 lAsnThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaIe 775
Db 2663 CAACACGCTGAGCATGGCGGTGAGTACCATGAGCAGCCCGAGAGCTGACTAATGCTCT 2722
QY 775 uGluIleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuIe 795
Db 2723 GGAGATCAGCAACATCGTGTTCACACGACATGTTGCCCTGGAGATGCTGTAAGCTGCT 2782
QY 795 uValTyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleVa 815
Db 2783 GGCTGCGGGCCCTCTGGGCTTACATCCGGAACCCGTACAACATCTTCGACGGCATCATCGT 2842
QY 815 lValIleSerValTyrGluIleValGlyGlnGlnGlyGlyLysLeuSerValLeuArgTh 835
Db 2843 GGTTCATCAGCGTCTGGAGATCGTGGGCGAGGCGGAGCTGTGTGTGTGCTGCGCAC 2902
QY 835 rPheArgLeuMetArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnIe 855
Db 2903 CTTCCGGCTGCTGCTGTGTGAAGCTGTGCGCTTCTGCGAGCCCTGCGCGCCAGCT 2962
QY 855 uValValleuMetLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPh 875
Db 2963 CGTGTGCTGTGTAAGACCATGACACAGTGCTACTTCTGCACGCTGCTCATGCTCTT 3022
QY 875 eIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluAr 895
Db 3023 CATTTTCATCTTCAGCATCTTGCGGCATGCACCTTTTCGGCTGCAAGTTCAAGCTGAAGAC 3082
QY 895 gAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTyrPalalIeVa 914
Db 3083 AGACACCGGAGACACCGTGCTGACAGGAAGAACTTCGACTCCCTGCTGTGGGCCATCGT 3142

QY 914 lThrValPheGlnIleLeuThrGlnGluAspTyrAsnLysValLeuTyrAsnGlyMetAl 934
Db 3143 CACCGTGTTCAGATCTTGACCCAGAGGAACTGGAACTGTGTCTGTACAAACGGCATGCG 3202
QY 934 aSerThrSerSerTyrPalalaleuTyrPheIleAlaLeuMetThrPheGlyAsnTyrVa 954
Db 3203 CTCACCTCTCTGGCGCCGCTTACTTGTGGCCCTCATGACCTTCGCAACTATGT 3262
QY 954 lLeuPheAsnLeuLeuValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerly 974
Db 3263 GCTCTCAACCTGTGTGGCCATCTGTGAGAGGCTTCCAGCGGAG----- 3311
QY 974 sArgGluAspAlaSerGlyGlnLeuSerCysIleGlnLeuProValaAspSerglnGlyGl 994
Db 3312 -----GG 3313
QY 994 yAspAlaAsnLysSergLysGluProAspPhePheSerProSerLeuAspGlyAsp-- 1013
Db 3314 CGATGCCAACAGATCCGACACGAGCAGACCAAGACGTCCGTCCACTTCGAGAGGACTT 3373
QY 1014 -----GlyAspArgLysLysCysLeuAlaLeuValSerie 1025
Db 3374 CCACAAGCTCAGAGAACTCCAGACACAGAGCTGAAGATGTGTTCCTGCCCTGAGCCG 3433
QY 1025 uGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAl 1045
Db 3434 CAACGGGACACCTGGAGGAGCAGAGCAGCTGTCCCTCCCTCATCATGTGCACAGCTGC 3493
QY 1045 aThrPrometSerLeuProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAl 1065
Db 3494 CACGCCCATGCTTACCCCAAGAGCTCACCATTCCTGTGATGCAGCCCCAGCCTCCGAGA 3553
QY 1065 aSerArgArgThrSerSerSergLysSerAlaGluProGlyAlaAlaHisGluMetLysSe 1085
Db 3554 CTCTCGGCGTGAGACAGCAGACTCCGGGAGCCGCCA-----CTGGAGACCAAGAACCC 3607
QY 1085 rProProSerAlaArgSerSerProHisSerProTyrSerAlaAlaSerSerTyrPheSe 1105
Db 3608 TCCGGCCAGCCTCGGAAGTTCTCCCTGTGCCCCCTGGGGCCCCCAGTGGCGCTGAGAGCAG 3667
QY 1105 rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProSe 1125
Db 3668 CCGGCGCTCCAGCTGAGACAGCCTGGGCGGTGCCCCAGCCTCAAGCGCGGCCAGTGT 3727
QY 1125 rGlyGluArgArgSerLeuLeuSerGlyGluGlnGlnLysSerGlnAspGluGluGluSe 1145
Db 3728 TGGGGAACGTGATCCCTGCTGTGTGGCGAAGGCAAGGCGACGACGACGAGAA----- 3782
QY 1145 rSerGluGluGluArgAlaSerProAla-----GlySerAspHisArgHisArgGlySe 1163
Db 3783 -GCTGAGGACGGCAGGGCGCGCGCGGCCCTGTGCCACCCCACTGCGGGCGGCGAGTTC 3841
QY 1163 rLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu----- 1178
Db 3842 CTTGGAACCAAGGCCCTCGGCGCGGCCCTCCGCTTACCAAGTGCAGCGGATCGCGA 3901
QY 1179 -----GlnValProGlyLeuHis-----ArgThrAlaSerGlyArgGlySe 1192
Db 3902 CGGGCAAGTGTGGCCCTGCCAGCAGCTTCTTCCTGCGCATGCACAGCCAGCTGAGGA 3961
QY 1192 rAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaIe 1212
Db 3962 TGCAAGCCGAGCTTGACGACGACTCGGAGGACAGCTGTGCTCGGCTGCATAAAGTGT 4021
QY 1212 uArgProAspAspProProLeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerly 1232
Db 4022 GGAGCCCTTACAAGCCC----- 4037
QY 1232 sGlyGluArgValArgAlaTyrIleArgAlaArgLeuProAlaCysTyrLeuGluArgAs 1252
Db 4038 -----CAGTGTGCGCGAGC-----CGCGA 4057

QY	1252	pSerTrpSerAlaTyrTllePheProProGlnSerArgPheArgLeuLeuCySHisArgIl	1272
Db	4058	GGCCTGGGCCCTTAACCTTCTCCCAAGAACCGGTCCGCTCTCCGCAAGAGGT	4117
QY	1272	eIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCySileTh	1292
Db	4118	CATCACACACAAGATGTTGATACAGTGTCTCTTCATCTTCTCAACTGCGTCAC	4177
QY	1292	rIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrIe	1312
Db	4178	CATCGCCCTGAGAGGCTTGACATTGACCCCGCAGACCGAGCGGTCTTCTCAGCGT	4237
QY	1312	uSerAsnTyrTllePheThrAlaValPheLeuAlaGluMetThrValLysValAlaIe	1332
Db	4238	CTCCAAATTACATCTTACCGCCCATCTTCGTGGCGGAGATGATGTGAAGTGGTGGCCT	4297
QY	1332	uGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsnValLeuaspGlyIe	1352
Db	4298	GGGGCTGCTGTCGGCGAGACACGCCCTACCTGCAGACAGCTGGAACCTGCTGATGGGCT	4357
QY	1352	uLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLy	1372
Db	4358	GCTGGTGCTGTGTCCCTGGTGACATTGTGTGGCCATGGCCTCGGCTGGTGGCCAA	4417
QY	1372	sIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIl	1392
Db	4418	GATCCTGGGTGTCTGCGCGTGCTGCGTGTGCGGACCTTGCGGCTTAAGGTTCAT	4477
QY	1392	eSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIl	1412
Db	4478	CAGCCGGGCCCCGGGCTCAAGCTGTGTGAGACGCTGATATCGTCGCTCAGGCCAT	4537
QY	1412	eGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyValGl	1432
Db	4538	TGGGAACATCGTCCCTCATCTGCTGCGCCTTCTTCATCATTTTGGCATCTTGGGTGCA	4597
QY	1432	nLeuPheLysGlyLysPhePheValCysGlnGlyLysAspThrArgAsnIleThrAsnLy	1452
Db	4598	GCTCTTCAAAAGGAAGTTCTACTGCGAGGGCCCCGACACCAAGAACATCTCCACCA	4657
QY	1452	sSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnIe	1472
Db	4658	GGCACAGTGC GGCGCCCACTACCGCTGGTGCGACCAAGTACCACTTCGACAACCT	4717
QY	1472	uGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMe	1492
Db	4718	GGGCAGGCGCTGATGTGCTGTTCGTGTCATCCAGAGATGATGGTGAACATTCAT	4777
QY	1492	tTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTr	1512
Db	4778	GTAACAGCGGCTGGATGCCGTGGGTGTCGACCAGCAGCCTGTGCAAGAACCAACCCCTG	4837
QY	1512	pMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPh	1532
Db	4838	GATGCTGCTGATCTTCATCTCTTCTCTGCTCATGCTCAGCTTCTTCTGCTCAACATGTT	4897
QY	1532	eValGlyValValValGluAsnPheHisLysCysArgGlnHisGlnGluGluGluAl	1552
Db	4898	CGTGGCGCTGTGTGCGAACTTCCACAAGTGCCGGCAGACCAAGAGGCGGAGGAGGC	4957
QY	1552	aArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArg-----	1568
Db	4958	GCGGCGCGAGAGAGAGAGGGGCTGCGGCGCTAGAGAGGAGCGCAGAGCACTTTCCTC	5017
QY	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuVa	1586
Db	5018	CAGCCCAAGAGGCCAGCGCGGCTACTATGCGCACTACTCGCCACGCGCGCTCCAT	5077
QY	1586	lHisHisLeuCySThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAs	1606
Db	5078	TCACTCGCTGTGCAACCACTATCTCGACCTTTCATCACCTTCATCATCTGTGTCAA	5137
QY	1606	nValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLy	1626

Db	5138	CGTCATCACCATGTCATGAGACATAAACCACCAAGTCGTCGACGAGGCCCTCAA	5197
QY	1626	slleCyAsnTyrIlePheThrValIlePheValIleuGluSerValPheLysLeuValAl	1646
Db	5198	GTACTGCAACTACGCTCTTCACCACCTCGTGTGTCTTCGAGGCTGCACTGAAGCTGTAGC	5257
QY	1646	apheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValle	1666
Db	5258	ATTGGGTTCCGTCGGTCTTCAAGGACAGGTGAACCAGCTGGACCTGGCCATCGTCT	5317
QY	1666	uLeuSerIleMetGlyIleThrLeuGluGlnIleGluValAsnAlaSerLeuProIleAs	1686
Db	5318	GCTGTCACTCATGGGCATCAGCGCTGAGAGAGATAGAGATGAGCGCGCGCTGCCATCAA	5377
QY	1686	nProThrIleIleArgIleMetArgValIleuArgIleAlaArgValIleuLysLeuLeuLy	1706
Db	5378	CCCCACCATCATCCGCATCATGCGCGTCTTCGATTGCCCGCTGCTGAAGCTGCTGAA	5437
QY	1706	sMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGl	1726
Db	5438	GATGGCTACGGGCATGCGCGCCCTGTGACACTGTGTGTCMAAGCTCTCCCCAGGTGGG	5497
QY	1726	YAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLe	1746
Db	5498	GAACTGGGCTCTTTTCATGCTCTGTTTATCTATGCTGCGTGGAGTGAGCT	5557
QY	1746	uPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaTh	1766
Db	5558	GTTCCGGAGGCTGGAGTGCAGTGAAGACAACCCCTGCAGGGCTGAGCGGACAGCCAC	5617
QY	1766	rPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTr	1786
Db	5618	CTTCAGCACTTCGGCATGCGCTTCCTCACGCTGTTCCGCGTGTCCACGGGGACAAC	5677
QY	1786	pAsnGlyIleMetLysAspThrLeuArgAspCys-----AspGlnGluSerThrCy	1803
Db	5678	GAACTGGATCATGAAGACACAGCTGCGGAGTGTCCCGTGAGGACAAGCACTGCCTGAG	5737
QY	1803	stYrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheVa	1823
Db	5738	CTACCTGCGCGCTGTGCGCCGTCTACTTCGTGACCTTCGTGCTGTGGCCAGTTGCT	5797
QY	1823	lleuValAsnValValIleAlaValIleuMetLysHisLeuGluGluSerAsnLysGluAl	1843
Db	5798	GCTGTGAACGTGTGTGTGCGCCGTCTCATGAAGACAACCTGGAGAGAGACAAGAGAGC	5857
QY	1843	alysGluGluAlaGluLeuGluAlaGluLeuGluGluMetLysThrLeuSerProGl	1863
Db	5858	ACGGGAGGATCGCGAGCTGGAACGCCGAGATCGAGCTGGAGATG-----	5900
QY	1863	nProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerPr	1883
Db	5901	-----GCGCAGGGGCCCCGGGAGTGC	5920
QY	1883	o-----AspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAl	1900
Db	5921	ACGCGGATGACGCGGACAGGCT-----	5945
QY	1900	asErHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuProGly--	1919
Db	5946	-----CCCTTGCCCCAGAGAGTCCGGGCGC	5971
QY	1920	-----ProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerle	1936
Db	5972	CAGGATGCCCCAAACCTGGTT--GCACGCAAGTGTCCGTGTCCAGGATGCTCTCGCT	6028
QY	1936	uProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyPro-----	1952
Db	6029	GCCCAACGACAGTACATGTTTCAGGCCCCGTGTGCTGCTGCGGCCCCCACCCCCGCC	6088
QY	1953	-----LeuGluHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySe	1967

Db 6089 GCTGCAGAGGTGAGATGAGACCTATGGGGCCGGACACCC--TTGGGCTC 6139
QY 1967 rValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAs 1987
Db 6140 CGTTGCCTCTGTGCACTCTCCGCCCGCAGAGTCTGTGCCTCCCTCCAGATCCCA----- 6194
QY 1987 pAlaProHisLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysLeuPr 2007
Db 6195 -----CTGGCTGTGTGTCCTCCCAAGCAGAGCGGCGGACCCCTCCACGCCCTGTC 6244
QY 2007 oProProGly-----ArgSerProLeuAlaGlnArgProLeuArgGlnAlaAla1 2025
Db 6245 CCCTCGGGCAGACGCCGCTCCCGCAGTCAAGCCGCTGCTGTGACAGACAGAGGCTGT 6304
QY 2025 eArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlnAspLeu-----Al 2043
Db 6305 GCACACCGATTCTTGAGAGGAG--ATTGACAGCCCTAGGGACACCTGGATCCTGC 6361
QY 2043 aglValSerGlyProSerPro-----ProLeuAlaArgAlaTyrSerPheTyrGly-- 2060
Db 6362 AGAGCCTGTGAGAAAACCCCGGTAGGCGGTGACCCAGGGGGCTCCCTGCAGTCCCC 6421
QY 2061 ----GlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysH 2079
Db 6422 ACCACGCTCCCGCAGCGCCCGCAGCGTCCGCACTCGTAAGCATACC--TTCGACAGCA 6478
QY 2079 sMetThrProProAlaPro--CysProGlyProGluProAsnTyrGlyLysGlyProPr 2098
Db 6479 CTGCGTCTCCAGCGCGCGCGCGCCAGCGGAGAG----- 6515
QY 2098 oGluThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTyrIleSerGlyAspLeuLe 2118
Db 6516 -GAGGCCGAGGCTTCGACCCAGCCGAGAGAGGTCAACCATATCACAGCTCCGCTG 6574
QY 2118 uPro-----ProGlyGlnGlnGluProPro-----SerPr 2129
Db 6575 CCCCCTGGCAGCCACAGCCGAGCCCATGCGCCCGAAGCCTCTCCGGTGGCCGCGCGCA 6634
QY 2129 oArgAspLeuLysLysCysTyrSerValGlnAlaGlnSerCysGlnArgArgProThrSe 2149
Db 6635 GCGGACCTGCGCAGGCTTACAGCGTGAAGCTCAGGGCTTCTCGACAAAGCCG--GG 6691
QY 2149 rTyrLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerG 2169
Db 6692 CCGGCGACAGCAGCAGTGGCGGCGCTCGCGCAGCTGGCAGCGGGAGCCTGGGAGGC 6751
QY 2169 nProHisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProGlySe 2189
Db 6752 GAAGGCTGGGGCCCTGAG-----GCCGAGCC-----GCTCTGGGTGC 6790
QY 2189 rArgProLysLysLysLeuSerProProSerIleThrIleAspProPro--GlnSerG 2208
Db 6791 GCGCAGAAAGAAAGATGAGCCCCCTGCACTCGGTGAACCCCTGCGGAGGACGA 6850
QY 2208 nGlyProArgThrProProSerPro-----GlyTleCysLeuArgArgAlaPr 2225
Db 6851 GGGCTCTGCGCGGCTCTCCGCGCAGAGGGCGGACACACACTGAGCGCAGGACCCC 6910
QY 2225 oSerSerAspSerLys----- 2230
Db 6911 GTCTGTGAGGCGCACGCTCAAGGAATCCCTGAGCCACACAGAGGCTCAGGCGCGG 6970
QY 2231 ----AspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2249
Db 6971 GGGGGAACCTTGACGCGCAAGGGGAGCGCTGGGGCAGGCC-----TCCTGCGGGC 7021
QY 2249 sAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeu----- 2264
Db 7022 TGAGCACCCTGACCGTCCCAAGCTTTGCTTTGAGCGCTGGACCTCGGGGTCCCCAGTGG 7081
QY 2265 -AspPro 2266
Db 7082 AGACCTT 7088

RESULT 6
US-09-404-650-1
; Sequence 1, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-404-650-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 3 Gaps: 55

US-09-611-257A-37 (1-2266) x US-09-404-650-1 (1-6816)
QY 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
Db 264 CAGCCCGAGCCCGGAGCCCGCCATCCTCCCGCAGCGCTGAGAGAGCTCTGATGGA 323
QY 51 -----LeuProTyrProAlaLeuAlaProvalValPhePheTyrLeuSerGln 66
Db 324 GCTGATCCTCATGTCCACACACCGACCTGGCGCTATTGCTTCTTGCCCTGCGACAG 383
QY 67 AspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgIle 86
Db 384 ACCACAGAGCCCGGAACTGGTGATCAAGATGTGTGCAACCCGTGTTGAATGTGTC 443
QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 444 AGCATGCTGTGATCTCTGTAAGTGGTGACACTTGCGATGTACAGCCGTGCGACGAC 503
QY 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
Db 504 ATGACTGCCTGTCCGACCGCTGCAAGATCCTGCAGGCTCTTGATGACTTTCATCTTATC 563
QY 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys 146
Db 564 TTCTTTGCCATGAGATGTGTCTCAAGATGTGGCCCTGGGGATTTTGGCAGAAGATGC 623
QY 147 TyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
Db 624 TACCTCGGAGACATGGAACCGCTGATTTCTTCATGTCATGGCAGGATGTGTCAG 683
QY 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 684 TACTCCCTGACCTTCAAGACATCAACTGTACGCCATCCGACCGGTGCGCTCTGAGG 743
QY 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
Db 744 CCCCTCAAGGCATCAACCGCGTGCAGATGATGCGATCCTGTGAACCTGCTCCTGAC 803
QY 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226
Db 804 ACACTGCCCATGTGGGGAATGTCTGTCTGTCTCTTGTGCTTCTTCATCTTTGGC 863

QY 227 ILeValGIValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
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Db 864 ATCATAGGTGTGCAGCTCTGGGCGGGCTGCTGCGTAACCGCTGCTTCTTGAGAGAGAAC 923
QY 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
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Db 924 TTCACCATACAAAGGAGATGTGGCTTGCCCCCATACTACCAAGCCGAGAGAGATGATGAG 983
QY 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
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Db 984 ATGCCCTTCAATCTGCTCCCTGTGGGCGACAATGGATATGGGCTGCGCATGATCCCC 1043
QY 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
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Db 1044 CCGCTCAAGAGACAG-----GGCCGTGAGTGTGCTGCTGTCCAAGACGAGCTCTAC 1094
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
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Db 1095 GACTTTGGGGGGGGGGCGCCAGGACCTCAATGCCAGCGGCTGTGTCAACTGGAAACCGT 1154
QY 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheIleGlyAlaIleAsnPheAsp 338
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Db 1155 TACTACAATGTGTGCGCACGGGCGAGCGCCAAACCCACAAAGGGTGCATCACTTTTGAC 1214
QY 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAsp 358
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Db 1215 AACATCGGTATGTCTTGATTTGCATCTTCCAGGTGATCACTTGGAAGGCTGGGTGAG 1274
QY 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeu 378
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Db 1275 ATCATGTACTACGTGATGATGATGCTCACTCTTACAACCTCATCTTCACTGCTT 1334
QY 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
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Db 1335 ATCATAGTGGGCTCTTCTTCAATGATCAACCTGTGCCTCGTTGTATAGCGACCGAGTTC 1394
QY 399 SerGluThrIleGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
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Db 1395 TCGAGACCAAGCAACGGAGACACCGGCTGATGCTGAGACGCGGACGCGTACTGTTC 1454
QY 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys 438
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Db 1455 --TCCAGCAGCGTGGCCAGCTACGCGGAGCCTGGCACTGCTACGAGAGATCTTCAG 1511
QY 439 TyrLeuValTyrIleLeuArgIleAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 458
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Db 1512 TATGTCTGCCACATCTTCCGCAAGGCCAAGCGC-----CGCGCCCTG 1553
QY 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478
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Db 1554 GGCTCTTACCAGGCCCTGCAGAGCCGGGCCCAAGCCCTGGC----- 1595
QY 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisIleValHisHis 498
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Db 1595 ----- 1595
QY 499 HisHisHisHisHisIleTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer 518
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Db 1595 ----- 1595
QY 519 ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer 538
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Db 1596 -----CCGAG 1601
QY 539 ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis 558
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Db 1602 GCGCCGGGCG-----CCCGCAAACCTGGCG-----CAC 1631
QY 559 AlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGlu 578
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Db 1632 GCCAAG-----GAGCCCCGGCACTACGAGCTGTGCCCCGCAACATAGCCCCCTGGAT 1682

QY 579 AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro 598
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Db 1683 GCGAGCCCCACACCCCTG-----GTGCAAGCCCATC 1712
QY 599 ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr 618
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Db 1713 CCGGCCACGCTG----- 1724
QY 619 LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr 638
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Db 1724 ----- 1724
QY 639 GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp 658
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Db 1724 ----- 1724
QY 659 SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
Db 1725 -----GCTTCGATCCCGCAGCTGCGCTTGCTGCCAGCATGAGAGCGCGCGGCC 1778
QY 673 AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla 692
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Db 1779 TCGGCGCTGGGACAGACCGAC--TCGGCCAGAGAGGGCTCGGCTCCGGAAGCTCCGCT 1835
QY 693 ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg 712
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Db 1836 GGTGGCAG-----GACGAGCGGATGGGAGCGGGCCCGGAGCAGCGAGCAGCGAGCC 1889
QY 713 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu----- 726
Db 1890 TCCTCAGAAGTGGGAGAGAGAGAGAGAGAGAGAGAGCGGATGGGCGGTCTGGCTG 1949
QY 727 -----AlaPheTyrArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr 744
Db 1950 TCGCGGAGTGTGTGGCGGAGACCGGAGCCAAAGCTGCGCGGCATCGTGACAGCAAGTAC 2009
QY 745 PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr 764
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Db 2010 TTCAACGGGGCATCATGATGAGCATCTGCTGCAACACCGTCAGCATGGGCATCGAGCAC 2069
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Db 2070 CACGAGCAGCCGAGAGAGAGTGAACCAACATCTTGAGATCTGCAATGTGTCTCACACAGC 2129
QY 785 LeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys 804
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Db 2130 ATGTTGCCCTTGAGATGATCTGAAGCTGGCTGCAATTGGGCTCTTGCATACCTGCGT 2189
QY 805 AsnProTyrAsnIlePheAspGlyValIleValValIleSerValTrpGluIleValGly 824
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Db 2190 AACCCCTAACACATCTTCGACAGCATCATTTGTCTATCATCAGCATCTGGGAGATCGTGGG 2249
QY 825 GlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844
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Db 2250 CAGGCGGAGGTGGCTGTGTGTGCTGCGGACCTTCCGGCTGCTGCGGTGTAACACTG 2309
QY 845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864
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Db 2370 GTGGCCACCTTCTGCATGTGCTCATGCTTTCATCTTCAAGCATCTTGGGATG 2429
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Db 2430 CATATTTTGGCTGCAAGTTTACGCTCCGCAAGGACACTGGAGACACGGTCCGACAGG 2489
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Db 2490 AAGAATTGCACTCCCTGTGTGGGCATGTCTACTGTGTTCAGATCTTCAACCCAGAGAG 2549
QY 924 AspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyr 943

||||| 2550 GACTGGAACGTCTCTCTACATGCGATGGCTCCACTTCTCCCTGGGCTCCCTTAC 2609
QY 944 PheIleAlaIeuMetThrPheGlyAsnTyrValIeuPheAsnIeuValAlaIleIeu 963
Db 2610 TTTGTGCCCCCTGATGACCTTCGGCACTATGCTCTTCAACCTGTGTGGCATCTCTG 2669
QY 964 ValGluGlyPheGlnAlaGluGluIleSerIleArgGluAspAlaSerGlyGlnIeuSer 983
Db 2670 GTGGAGGGCTTCCAGCGCGAG----- 2690
QY 984 CysIleGlnIeuProValAspSerGlnGlyGlyAspAlaAsnIysSerGluSerGluPro 1003
Db 2691 -----GGTGA CGCAATCGCTCTACTCGGACGAG 2720
QY 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013
Db 2721 GACCAAGAGCTCATCCAACATAGAGATTGATAAGCTCCAGAGAGGCTTGACAGCAGC 2780
QY 1014 GlyAspArgIleIysCysIleuAlaIeuValSerIeuGlyGluHisProGluIeuArgIys 1033
Db 2781 GGAGATCCCAAGCTCTGCCCAATCCCATGACCCCAATGGGCAC----- 2825
QY 1034 SerIeuIeuProIeuIleIleHisThrAlaAlaThrProMetSerIeuProIysSer 1053
Db 2826 -----CTGACCCC-----AGTCTCCCACTGGGT 2849
QY 1054 ThrSerThrGlyIeuGlyGluAlaIeuGlyProAlaSerArgArgThr----- 1069
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QY 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 2910 CCCATGCTGTGGCTGGCTGCCCTCCGAAAGAGCAGTGTATGTCTAGGGAGGATGAGC 2969
QY 1081 HisGluMetIysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
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QY 1121 ArgArgSerProSerGlyGluArgArgSerIeuIeuSerGlyGlu--GlyGlnGluSer 1139
Db 3072 CACAAAGCCGCGCTCGCGGAGCATGAGTCCCTGCTCTGCGGAGCGGCGCGCGCGCC 3131
QY 1140 GlnAspGluGluIleSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGGTCTGCGAGGTGCGCGGAGCAGAGGGCGCGCGCGCGCACCCCTGCACACCCCA 3191
QY 1158 His-----ArgHisArgGly 1162
Db 3192 CACGCCCAACCATTCATCAGGGCCCCCATCTGGCGCAACGCCCAACCAACGCCCGG 3251
QY 1163 SerIeuGluArgGluAlaIysSerSerPheAspIeuProAspThrIeuGlnValProGly 1182
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Db 3608 CGTCGTCTGCGCTTCATCTTCTCACTGCATCACCATCGCCCTGGAGCGGCTCAGAT 3667
QY 1300 eAspProHisSerAlaGluArgIlePheIeuThrIeuSerAsnTyrIlePheThrAlaVa 1320
Db 3668 CGAGCGCGGACACCGAACGCACTTCTTCACCGGTCCCACTACATCTTCACGGCCAT 3727
QY 1320 lPheIeuAlaIeuMetThrValIysValAlaIeuGlyTrpCysPheGlyGluGlnAl 1340
Db 3728 CTTGCTGGCGAGATGACATTGAAGTAAGTCTCGCTGGGCTGTACTTCGGCGAGCAGC 3787
QY 1340 aTyrIeuArgSerSerTrpAsnValIeuAspGlyIeuIeuValIeuIleSerValIleAs 1360
Db 3788 GTACCTACGACAGAGCTGGAACGTGCTGATGGCTTCTGTCTTCGTCATCATCGA 3847
QY 1360 lIleIeuValSerMetValSerAspSerGlyThrIysIleIeuGlyMetIeuArgValle 1380
Db 3848 CATCGTGTGTCTCTGGCTCAGCGCGGGGAGCCCAAGATCTTGGGGTCTCCGAGTCTT 3907
QY 1380 uArgIeuIeuArgThrIeuArgProIeuArgValIleSerArgAlaGlnGlyIeuIysIle 1400
Db 3908 GCGGCTCCTCGCAACCTACGCCCCCTGCGTGCATCAGCGGGCGCGGCTGAAGCT 3967
QY 1400 uValValGluThrIeuMetSerSerIeuIysProIleGlyAsnIleValValIleCysCy 1420
Db 3968 GGTGTGAGAGACTCATCTCTCCCTCAAGCCATCGGCAACATCGTGCATCTGCTG 4027
QY 1420 sAlaPhePheIleIlePheGlyIleIeuGlyValGlnIeuPheIysGlyIysPhePheVa 1440
Db 4028 TGCCTTCTTCATCATCTTGGCATCCCTGGGAGTGACAGCTCTCAAGGCAAGTTCTACA 4087
QY 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnIysSerAspCysAlaGluAlaSerTy 1460
Db 4088 CTGTCTGGCGGTGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCCGCACTA 4147
QY 1460 rArgTrpValArgHisIlystYrAsnPheAspAsnIeuGlyGlnAlaIeuMetSerIeuPh 1480
Db 4148 CCGCTGGTCAATCAACAATACAACTTCGACCAACTGGGCCAGGCTGTATGTCCCTTT 4207
QY 1480 eValIeuAlaSerIysAspGlyTrpValAspIleMetTyrAspGlyIeuAspAlaValG1 1500
Db 4208 TGTCTGCGCATCAAGAGATGTTGGGTGAACATCATGTACAAATGCACTGATGCTGTGC 4267
QY 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetIeuIeuTyrPheIleSerPh 1520
Db 4268 TGTGACCAAGCAGCCTGTGACCAACCAACCCCTGGATGCTGCTACTCATCTCCTT 4327
QY 1520 eleuIeuIleValAlaPhePheValIeuAsnMetPheValGlyValValGluAsnPh 1540
Db 4328 CTTGCTCATCGTCAAGCTTCTTGTGCTCAACATGTTGTGGGTGTCTGCTGAGAACTT 4387
QY 1540 eHisIysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluIlylsArgIle 1560
Db 4388 CCACAAGTGCGGACACCAAGAGGCTGAAGAAGCAGCGCGGCTGAGAGAAGCGGCT 4447
QY 1560 uArgArgIeuGluIlylsArgArgIysAlaGlnCysIysProTyrTrpSerAspTyrIse 1580
Db 4448 GCGGCGCTGAGAGAAGCGCGGAAGGCCAGCGGCTGCCCTAATGACCATCTATTG 4507
QY 1580 rArgPheArgIeuIeuValHisIleIeuCysThrSerHisTyrIeuAspIeuPheIleTh 1600
Db 4508 TCACACCCGCGCTGTCTCATCTCACTCCATGTGCACACGCACTACTGGAACATCTTCATAC 4567
QY 1600 rGlyValIleGlyIeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI1 1620
Db 4568 CTTCAATCATCTGCTCAACGTTGTCACCATGTCTCCCTGGAGCACTACATCAGCCACGTC 4627
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Db 6578 CCCCTCGTGGCGCCGAC-----CGCAGCAAGACCCCCCGCGC 6619
QY 2264 uaspro 2266
Db 6620 GGCACCG 6626

RESULT 7

US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 4 Gaps: 55

US-09-611-257A-37 (1-2266) x US-09-935-541-1 (1-6816)

QY 31 ArgProGlyProGlySeraIaGlulysAspProGlySeraIaAspSerGluAlaGlulGly 50
Db 264 CAGCCCCGAGCCCCGAGCCCATCTCCCGCCAGCGCTGAGAGCGCTCTGATGGA 323
QY 51 -----LeuProTyrProAlaLeuAlaProValPhePheTyrLeuSerGln 66
Db 324 GCTGATCCTCATGTCCACACCCAGACCTGGCGCTATTGCCCTTCTGCGCAGAC 383
QY 67 AspSerArgProArgSerTyrPheValArgThrValCysAsnProTyrPheGluArgIle 86
Db 384 ACCACCAAGCCCCGGAACCTGCTGATCAAGATGTGTGCAACCCGTTTGAATGTGTC 443
QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 444 AGCATGCTGTGATCCTGCTGAACCTGCGTACACTTGCGATGTACCAAGCGTGCAGAC 503
QY 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
Db 504 ATGGAAGTGGCTGTCCGACCGCTGCAAGATCCTGCAAGTCTTGATGACTTCATCTTATC 563
QY 127 PhePheAlaValGluMetValValIysMetValAlaLeuGlyIlePheGlyLysLysCys 146
Db 564 TTCTTTGCCATGAGATGTGTCTCAAGATGTGGCCCTGGGGATTTTGGCAAGAAGTGC 623
QY 147 TyrLeuGlyAspThrTyrPheAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
Db 624 TACCTGGGGACACATGGAACCGCTGATTTCTTCATCGTCATGGCAGGATGTGCGAG 683
QY 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 684 TACTCCCTGGACCTTCAGAACATCAACCTGTCAAGCATCCGACCGTGGCGTCTGAGG 743

QY 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAsp 206
Db 744 CCCCTCAAGCCATCAACCGCGTGCAGATGCGGATCTGTGAACCTGTCTCTGGAC 803
QY 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226
Db 804 ACATGCCCATGCTGGGAATGTCTGCTGCTGTCTTCTTGTCTTCTTCATCTTTGGC 863
QY 227 IleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
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QY 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
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QY 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
Db 984 ATGCCCTTCATCTGCTCCCTGTGGCGCAATGGATATGGGCTGCCATGATCCCC 1043
QY 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
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QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTyrPheAsnGln 318
Db 1095 GACTTTGGGGGGCGCCAGACCTTCATGCCAGCGGCTGTGTCACTGGAACCGT 1154
QY 319 TyrTyrThrAsnCysSeraIaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
Db 1155 TACTACAATGTGTGCCGACGCGGACGCCCAACCCCAAGGGTCCATCACTTGTAC 1214
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QY 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
Db 1275 ATCATGTACTACGTGATGATGTCTACCTCTTCAACACTTCATCTTCACTTCTGCTT 1334
QY 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
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QY 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478
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QY 659 SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
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QY 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
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Db 3072 CACAAGCCCGCTGCGGAGCATGAGTCCCTGTCTTGCGGAGCGGCGGCGGCGGCC 3131
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QY 1158 His-----ArgHisArgGly 1162
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Db 3428 TCGCGGGGAGGATGAGGAGGAATCGACTACACCTGTGCTTCCGCTCCGCAAGATGAT 3487
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Db 3548 TCCCGAAGACAGGTCCGGGCTCCTGTGTACAGCAATTATTGCCCAAACTCTTCAGACTA 3607
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Db 3788 GTACCTACGACAGCTGGAACGTGCTGATGGCTTCTTGTCTTCGTCCATCATCGA 3847
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QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuIysIle 1400
Db 3908 GCGGCTCCTGCGCACCTTAAGCCCCCTGCTGTATCAGCCGGCGCGCCCTGGAAGCT 3967
QY 1400 uValValGluThrLeuMetSerSerLeuIysProIleGlyAsnIleValValIleCysCy 1420
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Db 4388 CCAACAAGTCCCGGACGACCAAGAGGCTGAAGAGGCACGCGGCTGAGAGAGAAGCGCT 4447
QY 1560 uArgArgLeuGluIulysIysArgArgIysAlaGlnCysIysProTyrTyrSerAspTyrSe 1580
Db 4448 GCGGCGCTTGAAGAAGCGCGGAAAGGCCCAAGCGGCTGCCCTACTATGCCACCTATTG 4507

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QY 1620 eLeuAspGluAlaLeuIysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe 1640
Db 4628 CTTGAGACAGCCCTCAAGTACTGCACATATATGTTACCACTGTCTTGTGTGAGAGC 4687
QY 1640 rValPheIysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnIle 1660
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QY 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680
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QY 1876 yValGluGlyProAspSerProAsp----- 1884
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QY 1885 -----SerProIysProGlyAlaLeu----- 1891
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QY 1892 -----HisProAlaAlaHisAla----- 1897
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QY 1898 -----ArgSerAlase 1901
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QY 1901 r-----HisPheSerLeuGluHisProThrMetGlnPro----- 1912
Db 5642 CATCCTGCTGGGTGACGACCTGAGTTCGAGGACCCACAGCCTGCCCCACCTGGCCGCAA 5701
QY 1913 ----HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly----- 1929
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US-09-404-650-3
; Sequence 3, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/404,650
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-404-650-3
Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5484.00 Matches: 1237
Percent Similarity: 59.93% Conservative: 211
Best Local Similarity: 51.20% Mismatches: 507
Query Match: 46.07% Indels: 462
DB: 3 Gaps: 56
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Db 324 GGTGATCCTCATGTCCACACACAGACCTGGCGCCTATTGCCCTTCTTGCTGCGACAG 383
QY 67 AspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgile 86
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QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
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QY 147 TyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166

Db 624 TACCTCGGACACATGAAGAACCGCTGGATTCTTCATCGTCATGACGAGATGTCGAG 683
QY 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 684 TACTCCCTGACCTTCAGAACATCAACCTGTCAAGCATCCGACCGGTGCGCTCGAGG 743
QY 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
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QY 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226
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QY 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGlnAsn 246
Db 864 ATCATAGGTGTGACGCTCTGGGCGGCGCTGTGCTAACCGCTGTCTTCCTGAGAGAAC 923
QY 247 PheSerLeuProLeuSerValAspLeuGlnArgTyrTyrGlnThrGlnAsnGlnAspGln 266
Db 924 TTCACCATACAGGGGATGTGGCCTTGCCCCCATACTACCAAGCCGAGAGATGATGAG 983
QY 267 SerProPheIleCysSerGlnProArgGlnAsnGlyMetArgSerCysArgSerValPro 286
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QY 287 ThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu----- 300
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QY 301 AspTyrGlnValTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
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Db 2721 GACCAGAGCTCATCCACATAGAGATTGTGATAAGCTCCAGAAAGCCTGGACAGACAGC 2780
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RESULT 9
US-09-935-541-3
; Sequence 3, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGilvern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-09-935-541-3
Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5484.00 Matches: 1237
Percent Similarity: 59.93% Conservative: 211
Best Local Similarity: 51.20% Mismatches: 507
Query Match: 46.07% Indels: 462
DB: 4 Gaps: 56
US-09-611-257A-37 (1-2266) x US-09-935-541-3 (1-6855)
QY 31 ArgProGlyProGlySerAlaGluYsAspProGlySerAlaaspserGluAlaGluGly 50
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 :::|||||:::|||||:::||||| |||
Db 384 ACCACACGCCCCCGGAAGTGTGTCATCAAGATGTGTGCAACCGTGTGAATGTGC 443
QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
 ||||| ||||| ||||| |||
Db 444 AGCATGTGTGTATCTCTGCTGAACCTGCGACACTTGCGATGTACACGCGGTGCGAGAC 503
QY 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126

Db 504 ATGGACTGCCTGTCCGACCGCTGCAAGATCCTGAGAGTCTTGATGATCATCTTTATC 563
 :::||||| |||:::||||| |||
QY 127 PhePheAlaValGluMetValValIlysmetValAlaLeuGlyIlePheGlyLysLysCys 146
 |||||:::|||||:::||||| |||
Db 564 TTCTTTGCCATGAGATGGTGTCTCAAGATGTGGCCCTGGGATTTTGGCAAGAAGTGC 623
QY 147 TyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
 |||||:::|||||:::||||| |||
Db 624 TACCTCGGGGACACATAGGAACCGCTGATTCTTCATCTCATATGGCAGGATGTCTGAG 683
QY 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
 |||:::|||||:::||||| |||
Db 684 TACTCCTTGACCTTCAAGACATCAACCTGTACGCCATCCGACCGTGCCTGAGG 743
QY 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
 |||||:::|||||:::||||| |||
Db 744 CCGCTCAAGCCATCAACCGCGGTGCCAGTATGCGGATCTGTGAACCTGCTCTTGAC 803
QY 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuLeuCysPhePheValPhePheIlePheGly 226
 |||||:::|||||:::||||| |||
Db 804 AACTGTCCCATGTCTGGGGAATGTCTGTCTGTCTTGTCTTCTCATCTTTGGC 863
QY 227 IleValGlyValGlnLeuThrAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
 |||:::|||||:::||||| |||
Db 864 ATCATAGGTGTGACGCTCTGGCGGGCGCTGCTGCTAACCCTGCTTCTTGAGAGAGAAC 923
QY 247 PheSerLeuProLeuSerValAspLeuGluArgTyrGlnThrGluAsnGluAspGlu 266
 |||:::|||||:::||||| |||
Db 924 TTCACCATACAAGGGAGATGGCCTTGCCCCCATTACTACAGCCGAGAGAGATGATGAG 983
QY 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
 |||||:::|||||:::||||| |||
Db 984 ATGCCCTTCATCTGCTCCCTGTGCGGCGACAAATGGGATATGGCTGCCATGAGATCCCC 1043
QY 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
 |||:::||||| |||
Db 1044 CCGCTCAAGAGACAG-----GGCGTGAGTGTGCTGCTCCAAAGACGAGCTCTAC 1094
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
 |||:::|||||:::||||| |||
Db 1095 GACTTTGGGGCGGGCGCGCCAGCACTCAATGCCAGCGCCTGTGTCTCACTGGAACCGT 1154
QY 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
 ||| ||| ||| |||
Db 1155 TACTACATGTGTGCGCGCAGCGGACGCCCAACCCCAAGGTTGCCATCACTTTGAC 1214
QY 339 AsnIleGlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAsp 358
 ||||| ||| ||| |||
Db 1215 AACATCGGTTATGCTTGATGTTCATCTTCCAGGTGATCACTGGAAGGTGGGTGAG 1274
QY 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
 |||||:::|||||:::||||| |||
Db 1275 ATCATGTACTAGTATGATGATGCTCACTCCTTCACTTCACTTCACTTCACTTCTGCTT 1334
QY 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
 ||||| ||| ||| |||
Db 1335 ATCATAGTGGGCTCCTTCTTATGATCAACCTGTGCTGTGTATAGCAACCAAGTTTC 1394
QY 399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
 |||||:::|||||:::||||| |||
Db 1395 TCGAGACCAAGCAACGGAGACCGGCTGATGTGAGAGCAGCGGCAAGCTTACTGTCC 1454
QY 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLys 438
 :::|||||:::|||||:::||||| |||
Db 1455 --TCCAGCACGGTGGCCAGCTACGCGAGCCTGGGACTGTACGAGAGATCTTCAG 1511
QY 439 TyrLeuValTyrIleLeuArgLysAlaIleArgArgLeuAlaGlnValSerArgAlaAla 458
 |||:::|||||:::||||| |||
Db 1512 TATGTCTGCCACATCTCTGCGCAGGCAAGCGC-----CGCGCCCTG 1553
QY 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478
 |||:::||||| |||

Db 1554 GGCCCTTACCAGCCCTGCAGAGCCGCCCGCCAGCCCTGGCC----- 1595
QY 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHis 498
Db 1595 ----- 1595
QY 499 HisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSer 518
Db 1595 ----- 1595
QY 519 ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer 538
Db 1596 -----CCGGAG 1601
QY 539 ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis 558
Db 1602 GCCCCCGGCC-----CCCGCCAAACCTGGGCC-----CAC 1631
QY 559 AlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGlu 578
Db 1632 GCCAAG-----GAGCCCCGGCACTACCACTGTGCCCCGCAACATAGCCCCCTGGAT 1682
QY 579 AlaserglyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro 598
Db 1683 GCGACGCCCCACACCTG-----GTGCAGCCCCATC 1712
QY 599 ProGluThrLeuYseGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr 618
Db 1713 CCGGCCACGCTG----- 1724
QY 619 LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr 638
Db 1724 ----- 1724
QY 639 GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp 658
Db 1724 ----- 1724
QY 659 SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
Db 1725 -----GCTTCCGATCCCGCCAGCTGCCCTTGCTGCCAGCATGAGAGCGCCGCGGCC 1778
QY 673 AlaGlyAlaGlyLysValGluLeuAlaAspArgGluMetProAspSerAspSerGlyAla 692
Db 1779 TCGGGCCTGGGCAGCACCGAC--TCGGGCCAGAGGGCTCGGGCTCGGGAGACTCCGCT 1835
QY 693 ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg 712
Db 1836 GGTGGCGGAG-----GACCAAGCCGGATGGGGAGCGGCCCGGAGCAGCAGCAGGCC 1889
QY 713 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu----- 726
Db 1890 TCCTCAGAACCTGGGAAGGAGGAGGAGGAGCAGCAGCGGATGGGCGGCTCTGGCTG 1949
QY 727 -----AlaPheTyrArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr 744
Db 1950 TCGCGGGATGTGTGGCGGAGACGCGAGCCAAAGCTGCGCGCATCTGCACAGCAAGTAC 2009
QY 745 PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr 764
Db 2010 TTCAACCGGGGCATCATGTGCCATCTCTGTCAACCGTCAGCATGGGCATCGAGCAC 2069
QY 765 HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784
Db 2070 CACGAGCAGCCGGAGAGTGAACCAACATCTCTGAGATCTGCAATGTGTCTTCACACAGC 2129
QY 785 LeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys 804
Db 2130 ATGTTTGGCCCTGAGATGATCTGAAGCTGGCTGCATTTGGGCTCTTCGACTACCTGCGT 2189
QY 805 AsnProTyrAsnIlePheAspGlyValIleValValIleSerValTyrGluIleValGly 824
Db 2190 AACCCCTACAAACATCTTCGACAGCATCATTTGTCATCATCAGCATCTGGGAGATCGTGGG 2249

QY 825 GlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844
Db 2250 CAGCGGACGGTGGGCTGTGGTGCTGCGGACCTTCCGGCTGCTGCGGCTGTGAACCTG 2309
QY 845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864
Db 2310 GTGCGCTTCATGCTGCGCTGCGGCGCAGCTCGTGTGCTCATGAAGACCATGACAAC 2369
QY 865 ValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMet 884
Db 2370 GTGGCCACCTTCTGCATGTGCTCATGCTCTTCATCTTCATCTTCAGCATCTTGGGATG 2429
QY 885 HisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAspThrLeuProAspArg 903
Db 2430 CATATTTTGGCTGCAAGTTCAAGCTCCGCAAGACGACACTGGAGACACGGTGCCGACAG 2489
QY 904 LysAsnPheAspSerLeuLeuTyrPalaIleValThrValPheGlnIleLeuThrGlnGlu 923
Db 2490 AAGAACTTCGACTCCCTGTGTGGGCATGCTCACTGTGTTCCAGATCTCACCCAGAG 2549
QY 924 AspTyrAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTyrPalaIleLeuTyr 943
Db 2550 GACTGAAAGTGTCTCTACAATGGCATGGCCTCCACTTCTCCCTGGCCTCCTCTAC 2609
QY 944 PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeu 963
Db 2610 TTTGTGCCCCCTCATGACCTTCGGCACTATGTGCTTCAACCTGTGTGGCCATCTCTG 2669
QY 964 ValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer 983
Db 2670 GTGAGGGCTTCCAGGCGGAG----- 2690
QY 984 CysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPro 1003
Db 2691 -----GGTAGCCCAATGCTCTTACTCGGAGCAG 2720
QY 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013
Db 2721 GACCAGAGCTCATCCAAACATAGAAGATTGATAGCTCCAGGAAGCCTGGACAGCAGC 2780
QY 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033
Db 2781 GGAGATCCCAAGCTTGCCCAATCCCATGACCCCAATGGGCAC----- 2825
QY 1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrPrometSerLeuProLysSer 1053
Db 2826 -----CTGACCCC-----AGTCTCCCACTGGGT 2849
QY 1054 ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr----- 1069
Db 2850 GGGACCTAGTGTCTGTGGGCTGGGAGCTGCCCCCGACTCTCACTGCAAGCCGAC 2909
QY 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080
Db 2910 CCCATGCTGTGGCCCTGGGCTCCGAAAGACAGATGTATGTCTTAGGAGATGAGC 2969
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTyrSerAlaAla 1100
Db 2970 TATGACCAAGCGCTCCCTGTCCAGCTCCGAGACTCTACTACGGGCCATGGGCGGAGC 3029
QY 1101 SerSerTyrThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3030 GCGGCTGGGCCAGCCGTGCTCCAGCTGAAC-----AGCCTCAAG 3071
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu---GlyGlnGluSer 1139
Db 3072 CACAAGCCGCGGTGGCGGAGCATGAGTCTCTGCTGCGGAGCGGGCGGCGGCC 3131
QY 1140 GlnAspGluGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGCTGTGCGAGTTGCGCGGAGGAGGCGCGCGGCGCGGACCCCTGCACACCCCA 3191

QY	1158	His-----	-----ArgHisArgGly	1162
Db	3192	CACGCCACCACCATTCATCAGGGCCCCCATCTGGCGCACCGCCACCACCATCGCGG	3251	
QY	1163	SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly	1182	
Db	3252	ACGTCGTCCCTCGACACACAGGAACTCGGTGACCTGGCCGAGCTGTGCCCCGGGTGGC	3311	
QY	1183	LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn	1200	
Db	3312	GCCCACCCCCGGCGCCTGGAGGGCGCAGGCCCGGCCCGGCATGAGAACTGCAAT	3371	
QY	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu-As	1220	
Db	3372	GGCAGGAT-GCCCAAGCATCGC---CAAGAAGCTTTCACCAAGATGGCGCAGCGCGGGA	3427	
QY	1220	PGLysAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpI	1240	
Db	3428	TCCGGGGGAGATGAGAGGAAATCGACTACACCTGTGCTTCGCGTCCGCAAGATGAT	3487	
QY	1240	eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr	1260	
Db	3488	CGACGTCTATAAGCCCGAAGTGTGCGAGGTCCGCGAAGACTGGTCTGTCTACTCTTCTC	3547	
QY	1260	oProGlnSerArgPheArgLeuLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi	1280	
Db	3548	TCCCGAACAACAGTTCCGGGTCTGTGTACAGACCAATTATGCCACAACCTCTTGCACTA	3607	
QY	1280	sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysI	1300	
Db	3608	CGTCGTCTCTGCGCTTCACTTCTTCAACTGCATCACCATCGCCCTGAGCGGCTCAGAT	3667	
QY	1300	eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa	1320	
Db	3668	CGAGGCCCGCAGCACCGAAGCATCTTCTCACCGTGTCCAATACTACATCTTACGGCCAT	3727	
QY	1320	IlePheLeuAlaGluMetThrValLysValAlaLeuGlyTrpCysPheGlyGluGlnAl	1340	
Db	3728	CTTCGTGGGCGAGATGACATTGAAGTAGTCTCGCTGGGCTGTACTTCGCGCAGCAGGC	3787	
QY	1340	aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs	1360	
Db	3788	GTAACCTACGACAGCTGGAACGTGCTGATGGCTTCTTGTCTTCGTCCATCATCGA	3847	
QY	1360	PileLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValIe	1380	
Db	3848	CATCGTGTGTCCCTGGCTCAGCCGGGAGCAAGATCTTGGGGTCTCCGAGTCTT	3907	
QY	1380	uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysIe	1400	
Db	3908	GCGGCTCCTGCGCACCTTACGCCCTGCGTGTCAACCGGGCGCGGCTGAAGCT	3967	
QY	1400	uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy	1420	
Db	3968	GGTGTGGAGACATCATCTCTCCCTCAAGCCCATCGGCAACATCGTGTCTCATCTGCTG	4027	
QY	1420	sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa	1440	
Db	4028	TGCTTCTTCAATCATCTTGGCATCTCTGGAGTGCAGCTCTTCAAGGGCAAGTCTTACA	4087	
QY	1440	lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy	1460	
Db	4088	CTGTCTGGCGTGACACCGCAACATCACCAACCGCTCGGACTGCATGCGCCCACTA	4147	
QY	1460	rArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh	1480	
Db	4148	CCGCTGGGTCCATCACAAATACAATTGACAACCTGGGCGAAGCTGTGATGTCCCTCTT	4207	
QY	1480	eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValGl	1500	
Db	4208	TGTCTTGGCATCCAAGATGCTTGGGTGAACATCATGTATCAATGGAAGTGCCTGTTGC	4267	
QY	1500	yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh	1520	

Db	4268	TGTGACCAACGACCTGTGTGACCAACCAACCCCTGGATGTGCTGACTTCACTTCCTT	4327
Qy	1520	eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPh	1540
Db	4328	CCTGCTCATCTGCTCAGCTTCTTTGTGCTCAACATGTTTGGGTGTCTGTGTGAAGAACTT	4387
Qy	1540	eHisIlyeCyAsArgGlnHisGlnGluGluGluAlaArgArgGluGluIlyAsArgIle	1560
Db	4388	CCACAAGTGC CGGACAGCACCAGAGGCTGAAGAAGCACGGCGCGGTGAAGAGAAGCGCT	4447
Qy	1560	uArgArgLeuGluIlySlySArgArgIlyAlaGlnCysIlySProTyrTyrSerAspTyrSe	1580
Db	4448	GCGGCGCTTGAGAGAAGACGCCCGGAGGCCCAAGCGCGCTGCCCTACTATGACCACTATTG	4507
Qy	1580	rArgPheArgLeuLeuValHisIleuCysThrSerHisTyrIleuAspLeuPheIleTh	1600
Db	4508	TCACACCCGCGTCTCATCCACTCCATGTGCAACGACCACTACCTGAGCATCTTCATCAC	4567
Qy	1600	rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI	1620
Db	4568	CTTCATCATCTGCTCTCAACGTGTACCATGTCTCCCTGGAGCACTACAAACCCACGTC	4627
Qy	1620	eLeuAspGluAlaLeuIlySileCysAsnTyrIlePheThrValIlePheValLeuGluSe	1640
Db	4628	CCTGGAGACAGCCCTCAAGTACTGCACACTATATGTTCAACCACTGTCTTGTGTGAGAGC	4687
Qy	1640	rValPheIlyLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe	1660
Db	4688	TGTGCTGAAGCTGTGTCATTTGGTCTGAGCGCTTCTTCAAGGACCGATGGAACCAAGCT	4747
Qy	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs	1680
Db	4748	GGACCTGGCCATTGTGCTACTGTCACTGAGCATCGGCATCACCTGGAGAGATCGAGATCAA	4807
Qy	1680	nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr	1700
Db	4808	TGCGGCCCTGCCCATCATCCACCACATCATCCGATCATGAGGGTTCTGCCATTGCCCG	4867
Qy	1700	gValLeuIlyLeuLeuIlySmetAlaValGlyMetArgAlaLeuLeuAspThrValMetG	1720
Db	4868	AGTGCTGAAGCTGTGAAGATGGCCACAGAAATGCGGGCCTGCTGACACGCGTGTGCA	4927
Qy	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl	1740
Db	4928	AGCTTGGCCCCAGGTGGGCAACCTGGGCGCTTCCTTCATGTCTCTTCATCTATGC	4987
Qy	1740	aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG	1760
Db	4988	TGCTCTCGGGGTGAAGCTCTTTGGGAAGCTGTGTCGAACGACGAAACCCGTGCGAGGG	5047
Qy	1760	ylLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa	1780
Db	5048	CATGAGCCGCGATGCCACCTTGAGAACTTGCGCATGGCCTTCTCACACTCTTCAGAGT	5107
Qy	1780	IserThrGlyAspAsnTrpAsnGlyIleMetIlyAspThrLeuArgAspCys--AspG	1799
Db	5108	CTCCACGGGTGACAACTGGAACGGGATCATGAAGAACACGCTGCGGAGCTGCACCCACGA	5167
Qy	1799	nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa	1817
Db	5168	CGAGCGCAGCTGCTGAGCAGCCTGCAGTTTGTGTGCGCGCTGTACTTCGTGAGCTTCGT	5227
Qy	1817	IleuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetIlyHisLeuG	1837
Db	5228	GCTCACCGCGCAGTTCGTGCTCATCAACGTGTGTGTGCTGTGCTCATGAACACCTTGA	5287
Qy	1837	uGluSerAsnIlySgluAlaIlySgluAlaGluLeuGluAlaGluLeuGluIlyeGluMe	1857
Db	5288	CGACAGCAACAGAGAGCGCAGAGAGACGCCGAGATGGATGCCGAGCTGAGCTGGAGAT	5347
Qy	1857	t---IysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG	1876

Db 500 TTCAGTGTGTGAGCATGCTGGTTATCTCTGCTGAACGTGTGTGACCCCTGGGCATGTACCAG 559
QY 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAsp 122
Db 560 CCATGTGATGACATGGAGTGCCTGTGCGAACCGGTGCAAGATCCTGCAGAGTCTTCGATGAC 619
QY 123 PheIlePheAlaPhePheAlaValGluMetValValIysMetValAlaLeuGlyIlePhe 142
Db 620 TTCATCTTCATCTTCTTTGCCATGGAGATGGTGCTTAAGATGGTGCCCTGGGCATTTT 679
QY 143 GlyIysIysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAla 162
Db 680 GGCAAGAGTGTACTACCTCGAGACACATGGAAACCGCTGATTTCTTCATTGTCAATGGCA 739
QY 163 GlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrVal 182
Db 740 GGGATGTTGAGTACTCTCTGACCTACAGAACATCAACCTGTCAAGCCATCCGCACCTGTG 799
QY 183 ArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThr 202
Db 800 CGTGTCTGTAGGCTCTCAAGGCCATCAACCGTGTACCCAGCATGCGGATCCTGTGTAAC 859
QY 203 LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhe 222
Db 860 CTGCTGCTCGACACGCTGCCCATGCTGGGGAACGTGCTCTGCTTCTTCCTCTTC 919
QY 223 PheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPhe 242
Db 920 TTCATCTTCGGCATCATTTGGCGGTGACGCTCTGGGCAAGCCTGTCTACGGAACCGCTGCTTC 979
QY 243 LeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGlu 262
Db 980 CTGGAAGAGAACTTCACCATACAGGGGATGTGGCCCTGCCCTTATTACCAACAGAG 1039
QY 263 AsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCys 282
Db 1040 GAGATGACGAGATGCCCTTATCTGCTCCTGACTGGGGAATGGCATCATGGGCTGC 1099
QY 283 ArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 1100 CACGAGATCCCCCACTGAAGGACAG-----GGCCGGGAATGCTGCCTGTCCAA 1150
QY 301 -----AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysVal 314
Db 1151 GATGATGTGTATGACTTCGGGGCGGGGCGCCAGGACCTCAACGCCAGCGGTCTGTGCGTC 1210
QY 315 AsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGlnHisAsnProPheIysGlyAla 334
Db 1211 AACTGGAACCGCTACTACAAACGTCGTGCGCACGGGCAACGCCAACCTCACAAGGGCGCC 1270
QY 335 IleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlu 354
Db 1271 ATCAACTTTGACAACATTTGGCTATGCGGAGTTGTGATTTTCCAGGTGATCACTGTGAA 1330
QY 355 GlyTrpValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyr 374
Db 1331 GGTGGGTGGAGATCATGTACTATGTGATGAGCAGCATCTTTCTCAACACTCATCTAC 1390
QY 375 PheIleLeuLeuIleIleValGlySerPhePheMetIleAsnLeuCysLeuValIle 394
Db 1391 TTCATTTCTGTCATCATAGTGGGCTCTTCTTCATGATCACTGTGCTCGTGTGCATA 1450
QY 395 AlaThrGlnPheSerGluThrIlyeGlnArgGluSerGlnLeuMetArgGluGlnArgVal 414
Db 1451 GCAACCCAGTTCTCTGAGACCAAGCAACGGGAGCACCGGCTGATGCTGGAGCAACGCCAG 1510
QY 415 ArgPheLeuSerAsnAlaSerThrIleuAlaSerPheSerGlnProGlySerCysTyrGlu 434
Db 1511 CGCTACCTGTCC--TCCAGCACGGGTGCGCAGTTACGCTGAGCCCGGTGATTGCTATGAG 1567
QY 435 GluLeuLeuIysTyrLeuValTyrIleLeuArgIysAlaIlaArgArgLeuAlaGlnVal 454
Db 1568 GAGATCTTCCAATATGTCTGTACACATCTTTCGAAAGCCAAAGCCGCTGACCTAGGCCCTC 1627

QY 455 SerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGln 474
Db 1628 TACCAGGCCCTGCAGAACCGG----- 1648
QY 475 GluThrGlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisIleu 494
Db 1648 ----- 1648
QY 495 ValHisHisHisHisHisHisHisHisIleTyrHisIleuGlyAsnGlyThrLeuArgAla 514
Db 1648 ----- 1648
QY 515 ProArgAlaSerProGluIleGlnAspArgAlaAsnGlySerArgArgLeuMetLeu 534
Db 1649 -----CGCCAGGCCATGGG----- 1663
QY 535 ProProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHis 554
Db 1664 -----CCGGGACACACAGCC-----CCTGCCAAGCCTGGGCC----- 1696
QY 555 SerPheTyrHisAlaAspCysHisIleuGluProValAlaArgCysGlnAlaProProArg 574
Db 1697 -----CATGCCAAG-----GAGCCAGCCACTGCAAGCTGTGCCACAGACAC 1738
QY 575 SerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHis 594
Db 1739 AGCCCTCTGAC----- 1762
QY 595 ThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSer 614
Db 1763 ACACGTGTGCAGACC----- 1777
QY 615 GlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLys 634
Db 1777 ----- 1777
QY 635 LeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysIysIleSerSerProCys 654
Db 1778 -----ATCTCTGCCATT 1789
QY 655 LeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
Db 1790 CTGGCTCTGAC-----CCACAGACTGCCCTCACTGCAGCAGCAGAGCA 1834
QY 673 -----AlaGlyAlaGlyGlyValGluLeuAlaAspArgGluMetProAspSer 688
Db 1835 GGCAAGCGGCCCTCTGGCTGGCGCAGCACTGAC--TCAGGCCAGGAAGCTCAGGTTCT 1891
QY 689 AspSerGluAlaValTyrGluPheThrGlnAspAla--GlnHisSerAsp-LeuArgAs 707
Db 1892 GGTGGCTCTGCAGAGCGCGAAGCCAATGGGATGGACTCCAGAGACAGTGGGATGGGTC 1951
QY 707 PProHisSer-----ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSe 724
Db 1952 TCCTCGAACCTGGGGAAGAGAGGAACAGAGACGGGG-----CAGCCGACTG 2002
QY 724 rValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTy 744
Db 2003 TGTGGG-GATGTGTGGCGGAGACACGAAAAAAGCTGCGGGCATGTGACACGAAAGTA 2061
QY 744 rPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerSerMetGlyIleGluTy 764
Db 2062 CTTCAACAGAGTATCATGATGGCTATCTGTGTAAACACAGTCAGCATGGGCATCGAGCA 2121
QY 764 rHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSe 784
Db 2122 CCACGAACAGCCCGAGAGGTGACCAACATCCTGAGAGATCTGCAATGTGCTTCAACCAG 2181
QY 784 rLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLely 804
Db 2182 TATGTTTGGCCCTGAGATGATCCTGAAACTGGCGCCTTTGGGCTCTTGACTACCTGCG 2241

QY	804	sAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValG	824
Db	2242	GAACCCCTTACAACATCTTTGACAGCATCATCGTATCATCAGCATCTGGAAATCGTGGG	2301
QY	824	yGInGInGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValIleuLysLe	844
Db	2302	GCAGGCGGACCGGTGGCTGTCTGTGTGCTGCCACCTTCCGGTGTGCTGGGTGAAGCT	2361
QY	844	vValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAs	864
Db	2362	GGTGCCTTCATGCCGCGCTGGCGCGCAGCTCGTGTGCTCATGAAGACCATGGACA	2421
QY	864	nValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMe	884
Db	2422	CGTGGCCACCTTCTGCATGTCTACTCATGTCTGTTCATCTTCATCTTCAGCATCTTGGAT	2481
QY	884	tHisLeuPheGlyCysIysPheAlaSerGluArgAsp---GlyAspThrLeuProAspAr	903
Db	2482	GCATATCTTTGGCTGCAAAATTCAGCCTCCGCACGGACACGGAGACACCGTTCCGTACAG	2541
QY	903	gLyAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGInG	923
Db	2542	GAAGAACCTTCGATCTTACTGTGGCCATCGTACAGTGTTCAGATCCTCACTCAGGA	2601
QY	923	uAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTy	943
Db	2602	GGACTGGAAACGTTGTCTCTGTACAATGGCATGACCTCCACACACCCCTGGGCTCCCTCA	2661
QY	943	rPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIle	963
Db	2662	TTTTGTGGCTCATGACCTTTGGCAACTACGTTCTTCAATCTCCTGTGGCTATCTCT	2721
QY	963	vValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSe	983
Db	2722	GGTAGAGGGTTTCCAGGCTGAG-----	2743
QY	983	rCysIleGlnLeuProValAspSerGInGlyGlyAspAlaAsnLysSerGluSerGluPr	1003
Db	2744	-----GGTGATGCTAATCGTTCTGCTGTGATGA	2772
QY	1003	oAspPhePheSerProSer-----LeuAspGlyAs	1013
Db	2773	GGACCAGAGCTCATCCAAATTGGAGGAGTTTGACAAGCTCCACAGAGGCGCTGACAACAAG	2832
QY	1013	pGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLy	1033
Db	2833	TAGAGATCTCAAGCTCTGCCCAATACCATGACACCAATGGACAC-----	2878
QY	1033	sSerLeuLeuProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSe	1053
Db	2879	-----CTGGACCT-----AGCTCCCT-----	2896
QY	1053	rThrSerThrGlyLeuGlyAlaIleuGlyProAla-----	1065
Db	2897	-----CTGGGTGGCATCTGGGTCTGTGTAACATGGGTACTGCCCCCG	2943
QY	1066	-----SerArgArgThrSerSerSe	1072
Db	2944	CCTCTCACTGCAGCCAGACCCCGTACTGTGGTGGCTTACACTCTGGAAAAAGCAGTGTCTAT	3003
QY	1072	rGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSe	1092
Db	3004	GTCCTTGGGCAGG-----ATGAGCTATGATCAGCGATCCTTGTCCAGCTCCCGAGCTC	3057
QY	1092	rProHisSerProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSe	1112
Db	3058	CTACTACGGGGCCCTGGGGCCGAGTGGGACCTGGGCTAGCCGCGCTCCAGCTGAAC--	3115
QY	1112	rLeuGlyArgAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLe	1132
Db	3116	-----AGCCTGAACAACAAGCCGCCCTCAGCTGAGCATGAGTCTTACT	3155
QY	1132	uSerGlyGluGlyGlnGluSerGlnAspGluGlu--GluSerSerGluGluGlu-----	1149

Db	3160	GTCTGGGGAGGGGTGGAGGTAGCTGCTCAGAGGCTTGTAAGGCGCCCGGGAGAGAGCGCC	3219
Qy	1150	----ArgAlaSerProAlaGlySerAspHis-----	1158
Db	3220	AACTCGACCGCACCCCTGTCATGCTCCACAGCGCACCGGACCATGATGACCCCACT	3279
Qy	1159	-----ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAs	1173
Db	3280	GGACACACCGTCAACCGACACCGGACTGTCCTTGATACAGGACTCTGTGA	3339
Qy	1173	PLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer-----GlyArgG	1191
Db	3340	CCTGGAGAGCTGTGCTCCCGTGGTGGGTGCCCACTACGGGCGCTTGAGGGGGGGCGG	3399
Qy	1191	ySerAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAl	1211
Db	3400	TCAGGCCCTGGGCGACGAGGACTGCAATGGCAGAATGCCACACATAGCCCAAGATGCTT	3459
Qy	1211	AlaLeuArgProAspAspProProLeuAspGlyAspAspAlaAspAspGlyLysLeuSe	1231
Db	3460	CACCAAGATGATGACCGCGCGACCGCGGGAGAGAC--GAGAGAGATCGACTATAC	3516
Qy	1231	rLysGlyGluArgValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrlLeuGluAr	1251
Db	3517	CCTGTGTTCCGGGTCCGCAAGATGATGTGTATCAAGCCGGACTGTGCGAAGTCCG	3576
Qy	1251	gAspSerTrpSerAlaTyrlIlePheProGlnSerArgPheArgLeuLeuCysHisAr	1271
Db	3577	CGAGACTGTGGTCTACCTCTTCCCGCGAGAACAAAGTTCGGATCCTGTGTACAGAC	3636
Qy	1271	gIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeuAsnCysI	1291
Db	3637	CATCATGTGCTCACAAGCTTTTGTACTACGTGTCTTGCCCTTATCTTCTCACTGTAT	3696
Qy	1291	eThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuTh	1311
Db	3697	CACCATGTCTGTGGAGAGACCCAGATTGAAGCTGTAGCACTGAGCGCATCTTCTCAC	3756
Qy	1311	rLeuSerAsnTyrlIlePheThrAlaValPheLeuAlaGluMetThrValLysValAla	1331
Db	3757	GGTGTCTAATACTATCTTCAACAGCCATCTTCTGGGCGAGATGACACTGAAAGTGTTC	3816
Qy	1331	AlaLeuGlyTrpCysPheGlyGluGlnAlaTyrlLeuArgSerSerTrpAsnValLeuAspG	1351
Db	3817	TCTGGGCTGTACTTGTGTGAGCAGCGCTACTCGCTAGCAGCTGGAATGTACTGATGG	3876
Qy	1351	yLeuLeuValLeuIleSerValIleAspIleLeuValSerMetValSerAspSerGlyTh	1371
Db	3877	TTTCCTGTGCTTGTGTTCATCATCATGATATCGTAGTCCGTGCGCTCTGCTGGGGAGC	3936
Qy	1371	rLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgVa	1391
Db	3937	CAAGATTCTGGGGTCTCCGGGTCTGCGGCTCTGCGTACTTACGTCCTTTGAGGGT	3996
Qy	1391	IleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysPr	1411
Db	3997	TATCAGCCGCGCCCTGGGCTGAAGCTGTGTAGAGACGCTCATCTCCTCCCTCAAGCC	4056
Qy	1411	oIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGlyIleLeuGlyVa	1431
Db	4057	CATTGGGAACATCGTCTCATCTGCTGTGCTTCTTTCATCATCTTGGCATCCTGGGGGT	4116
Qy	1431	IleGlnLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnIleThrAs	1451
Db	4117	GCAGCTTTTCAAGGCAAGTTCTACCATTTGTTGGAGTGAGACACCGAAACATCACCAA	4176
Qy	1451	nLysSerAspCysAlaGluAlaSerTyrlArgTrpValArgHisLysTyrlAsnPheAspAs	1471
Db	4177	CCGATCTGACTGCGTGGCGGCAACTACCGCTGGTGATCACAAATACAACTTTGACAA	4236
Qy	1471	nLeuGlyGlnAlaLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspI	1491

Db 4237 CCTGGCCAGGCATTGATGTCCTCTTTGCTTGCGCTCCAGAGCAGCGCTGGTGAACAT 4296
QY 1491 eMetTyrAspGlyLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnPr 1511
Db 4297 CATGATATAATGGATTAGATGCTGTGTGTGGACGACGACGACGATGACGAACCAACACCC 4356
QY 1511 oTrpMetLeuLeuTyrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMe 1531
Db 4357 CTGGATGCTACTGTACTTCTCATTTTCGTTCTGCTCATCGTCAGCTTCTTGTGTCTCAACAT 4416
QY 1531 tPheValGlyValValValGlnAsnDheHisLysCysArgGlnHisGlnGluGluGlu 1551
Db 4417 GTTTGTGGCGGTGGTCGTGGAGAACTTCCACAAGTGCCGGCAGCACACGAGGCTGAGGA 4476
QY 1551 uAlaArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArgLysAlaGlu 1571
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QY 1571 nCysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysTh 1591
Db 4537 GAGGCTGCCCTACTATGCTACTACTGTCCACAAGGCTGCTCATCCACTCCATGTGCAC 4596
QY 1591 rSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAl 1611
Db 4597 CAGCCACTACTCGACATCTTCATTACTTCATCATCTGCTCAATGTGTCTCACCATGTC 4656
QY 1611 aMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle 1631
Db 4657 CCTGGAGCACTACCAACCAAGCTTACCTCCCTAGAGACAGCCCTTAAGTACTGCACTACAT 4716
QY 1631 ePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgAr 1651
Db 4717 GTTCACCACCTGCTTGTGTGTGAGGCTGTGTGAAGCTGTGTGCATTGTGGCTGAGGCG 4776
QY 1651 gPhePheGlnAspArgTTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlu 1671
Db 4777 TTTCTTCAAGGACCGATGGAAACAGCTGGAACCTGGCCATTGTGCTGTCCGTCAATGGG 4836
QY 1671 yIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleAr 1691
Db 4837 CATCACACTGAGAGATCGAATCAATGCCGCCCTTCCCATCAACCCACCATCATCCG 4896
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Db 4897 TATCATGCGTGTCTGCGTATCGCCCGGTGTGAAGCTATTGAAGATGCCACAGGAAT 4956
QY 1711 tArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLe 1731
Db 4957 GCGGGCCCTGTGGACACAGTGTGACAGGCTCTGCCCCAGGTGGGCAACCTGGGCTGCT 5016
QY 1731 uPheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGlu 1751
Db 5017 CTTTCATGCTGCTCTTCTTCATCTATGCTGCTGTGGAGTGAGCTCTTGGAAAGCTGGT 5076
QY 1751 uCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlu 1771
Db 5077 CTGCAATGACGAGAACCCGTTGAGGGGATGAGCCGCGCACGCCACCTTTGAAAACTTGGG 5136
QY 1771 yMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLys 1791
Db 5137 CATGGCCTTCTTCACGCTCTTCAGGTCCTCCACAGGCGATTACTGGAATGAATATGAA 5196
QY 1791 sAspThrLeuArgAspCys---AspGlnGluSerThrCysTyrAsnThrVal-----Il 1808
Db 5197 GGACACCCCTGCGAGACTGTACCCATGATGAGCGCACGTCGCTTAAGCAGCCTGCAAGTTGT 5256
QY 1808 eSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValVa 1828
Db 5257 GTCAACCGCTTACTTTGTGAGCTTCGTCTCAAGCTCAGTTCTGCTCATCAACGTGGT 5316
QY 1828 lIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGlu 1848
Db 5317 GGTGGCCGTGTGATGAACAATCTGTGATGACAGCAACAAAGGAGGCCACGAGGATGCAGA 5376

QY 1848 uLeuGluAlaGluLeuGluLeuGluMet---LysThrLeuSerProGlnProHisSerPr 1867
Db 5377 GATGATGCTGAGATCGAGCTGAGATGAGCCATGAGCCTCGGCCCTGCCCT----- 5428
QY 1867 oLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLy 1887
Db 5429 -----GGCCCCCTG 5436
QY 1887 sProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHi 1907
Db 5437 CCCTGGT----- 5443
QY 1907 sProThrMetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrVal----- 1925
Db 5444 -CCCTGCCCCCTGCCCCCTGCCCCCTGTGCTGGCCCCGAGGCTGCCCACTAGTTCACC 5502
QY 1926 -----ArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSerTy 1941
Db 5503 TGGGGCTCCGGGGCGAGGATCGGAGGGGCGAGTGCTGGAGGC---GACACCGAGAGTCA 5559
QY 1941 tMetCysArgHisGlySerThrAlaGluGlyProLeuGluHisArgGlyTrpGlyLeuPr 1961
Db 5560 CCTGTGCCG----- 5569
QY 1961 oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIle 1981
Db 5569 ----- 5569
QY 1981 eLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlu 2001
Db 5570 -----CACTGCTATTCTCCAGCCCGAGAGACCCCTGTGG-- 5602
QY 2001 yThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArgProLeuArgAr 2021
Db 5603 -----CTGGACAG 5610
QY 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLe 2041
Db 5611 CGTCTCTTAATCATCAAGAGACTCCTTGAG-----GGGAGCTGACCAT 5655
QY 2041 uLeuAlaGluValSer-GlyProSer-ProProLeuAlaArgAlaTyrSerPheTrpGly 2060
Db 5656 CATTGACAACTGTGTGGTCCGCTTCCACCACCTACCGCTCAGCGGCTGGCAA 5715
QY 2061 GlnSerSerThrGlnAlaGlnGlnHisSerArgSer-----HisSerLysIleSer 2077
Db 5716 GTGTCAACATGACAAAGCAAGACAGGTCTTCATCCATCCTGCTGGGGGATGACCTGAGT 5775
QY 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097
Db 5776 -----CTTGAGAGACCCACGCGCTGCCA-----CAGGGCCCC 5808
QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db 5809 AAGGAGAGCAAG-----GTTGAACCTA 5829
QY 2118 LeuProProGlyGlyGlnGluProProSerProAlaArgAspLeuLysCysTyr--- 2136
Db 5830 GAGCCTCCG-----GAGCCCATGCAAGCTGGAAGACCTGGATGATGCTTTGG 5877
QY 2137 -----SerVal----- 2138
Db 5878 CCCTTGGCCAAAGCGAGCGAGTGTCCACAGGCCCCAGAGCCTGTGTGCGAGATGGGGGC 5937
QY 2139 ---GluAlaGlnSerCys-GlnArgArgProThrSerTrpLeuAspGluGlnArgArgHi 2157
Db 5938 CATTCATTCACACCTGTGCAG-----TCCTGGCTCAAAACAGAGACAGCCA 5985
QY 2157 sSerIleAlaValSerCysLeuAspSerGlySerGlnPro----- 2170
Db 5986 AGCACCCAGAGCCCTTTCTCCCGGATGGCTCAGCCCTCTCCTGTAGATGCTGCTGA 6045

QY 2171 -----HisLeuGlyThrAspProSerAsnLeuGlyGlnProLeuGlyGlyProG1 2188
Db 6046 GTTCTTCACCCCTGCTGTGTCTGCCAGCCAGAGGGGCGAGAACCCGGCATGAGTCAGG 6105
QY 2188 ySerArgProLysLeuLysLeuSerProProSerIleThrIleAspProProGluSerG1 2208
Db 6106 AACCTGCCCCAAGATTGCACTTCAG-----GGGTCCCTG 6138
QY 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6139 GGCAATCGCTGAGGTCAACGAGTGTCAACTGCACCTCTTGCGCCAGGCTACTGTGAGTGA 6198
QY 2228 pSerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLy 2248
Db 6199 CACGTCC-----TTGATGCCAGTCCCTAGCAGCTCAGCGGCGACCTACAGACCACT 6252
QY 2248 sLysAspValLeuSerLeuSer 2255
Db 6253 GGAAGACAGCTGACTGTGAGT 6274

RESULT 11
US-09-935-541-12
; Sequence 12, Application US/09935541
; Patent No. 6589787
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGivern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-935-541-12

Alignment Scores:
pred. No.: 0
Score: 5418.50
Percent Similarity: 60.47%
Best Local Similarity: 51.57%
Query Match: 45.52%
DB: 4
Length: 6503
Matches: 1212
Conservative: 209
Mismatches: 446
Indels: 484
Gaps: 53

US-09-611-257A-37 (1-2266) x US-09-935-541-12 (1-6503)

QY 27 GlyAlaGlyGlyArgProGlyProGlySerAlaGlyLysAspProGlySerAlaAspSer 46
Db 320 GGAATCACTGAGCAGCCGGGGCCCCGGAGTCCCCCTCCATCCCTCCAGGCTTGAGAGAG 379
QY 47 GluAlaGlyGly-----LeuProTyrProAlaLeuAlaProValValPhePhe 62
Db 380 CCATTGGAAGGAACCAACCTGACGTCCACATCCAGACCTGGCTCTGTTGCTTCTTC 439
QY 63 TyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyr 82
Db 440 TGCTTGCGCCAGACCAACGAGCCCAAGAACTGGTGCATCAAGATGTTGTAACCCGTGG 499
QY 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102
Db 500 TTGAGTGTGTGAGCATGTGTTATTCTGCTGAAGTGTGTGACCCCTGGCATGTACAG 559
QY 103 ProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAsp 122
Db 560 CCATGTGATGACATGAGAGTGCCTGTGGAACCGTTGCAAGATCCTGCAGAGTCTTCGATGAC 619
QY 123 PheIlePheAlaPhePheAlaValAlaGluMetValValIlyMetValAlaLeuGlyIlePhe 142

Db 620 TTCATCTTCATCTTCTTGGCCATGAGATGTGCTTAAGATGTGTGCCCTGGCATTTT 679
QY 143 GlyLysLysCysTyrLeuGlyAspThrTyrPAsnArgLeuAspPheIleValIleAla 162
Db 680 GGCAAGAAGTGTAACTCGAGACACATGGAACCGCCTGATTTCTTCATTGTTCATGCA 739
QY 163 GlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrVal 182
Db 740 GGGATGTTGAGTAAGTCTGTGACCTACAGAACATCAACCTGTCAAGCATCCGACATGTG 799
QY 183 ArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThr 202
Db 800 CGTGCTGAGGCTCTTCAAGCCATCAACCGTGTACCCAGCATGGGATCCTGTGTAAAC 859
QY 203 LeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhe 222
Db 860 CTGCTGCTGACACGCTGCCCATGTGGGGAACGTGCTCTCTCTGTTCTTCTGCTTTC 919
QY 223 PheIlePheGlyIleValGlyValGlnLeuTyrPAlaGlyLeuLeuArgAsnArgCysPhe 242
Db 920 TTCATCTTGGCATATGTCGCGTGAAGTCTGGGAGGCTGTCTACGGAACCGCTGCTTC 979
QY 243 LeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGlu 262
Db 980 CTGGAAGAGAACTTCAACCATACAAGGGAGTGTGCCCTGCCCTTATTACCAACCAAGAG 1039
QY 263 AsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCys 282
Db 1040 GAGGATGACGAGATGCCCCCTTATCTGCTCCCTGACTGGGACATGGCATCATGGGCTGC 1099
QY 283 ArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 1100 CACGAGATCCCCCACTGAAGAGACAG-----GGCCGGAAATGCTGCTGTCCAA 1150
QY 301 -----AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysVal 314
Db 1151 GATGATGTGATGATCTTGGGGGGGGGCCAGACCTCAACGCCAGCGTCTGTGCGTC 1210
QY 315 AsnTyrAsnGlnTyrTyrThrAsnCysSerAlaGlyGlyIleHisAsnProPheLysGlyAla 334
Db 1211 AACTGGAACCGTAATAACAAGTCTGCCGACGGGCAACGCCAACCTCACAAGGGCGCC 1270
QY 335 IleAsnPheAspAsnIleGlyTyrAlaTyrPheAlaIlePheGlnValIleThrLeuGlu 354
Db 1271 ATCAACTTTGACAAATTTGGCTATGCGGGAGTTGTGATTTTCCAGGTGATCACTTGAA 1330
QY 355 GlyTyrValAspIleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyr 374
Db 1331 GGCTGGGTGAGATCATGTACTATGTATGAGACGACATTTCTTCAACTTCATCATCTAC 1390
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Db 1451 GCAACCCAGTTCTGTGAGACCAAGCAAGGAGACACCGGCTGATGCTGAGCAACGCCAG 1510
QY 415 ArgPheLeuSerAsnAlaSerThrLeuAlaSerPheSerGlnProGlySerCysTyrGlu 434
Db 1511 CGCTAAGTGTCC---TCCAGCAGCGGTGCCAGTTACGCTGAGCCGGTGAATTGCTATGAG 1567
QY 435 GluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnVal 454
Db 1568 GAGATCTTCCAATATGTCTGTACATCTTTCGCAAGCCAGCCGCTAGGCCCTC 1627
QY 455 SerArgAlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGln 474
Db 1628 TACCAGGCCCTGCAACCGG----- 1648
QY 475 GluThrGlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeu 494

Db 1648 ----- 1648
QY 495 ValHisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAla 514
Db 1648 ----- 1648
QY 515 ProArgAlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeu 534
Db 1649 ----- 1663
QY 535 ProProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHis 554
Db 1664 ----- 1696
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QY 615 GlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLys 634
Db 1777 ----- 1777
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Db 1778 ----- 1789
QY 655 LeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
Db 1790 CTGGCCTGTGAC----- 1834
QY 673 ----- 1835
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QY 707 pProHisSer-----ArgArgGlnArgSerLeuGlyProAspAlaGluProSerSe 724
Db 1952 TCCTCGGACCTGGGGAAGAGAGGAACAAGAGAGCGGG-----CAGCCGCACTG 2002
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Db 2122 CCACGAACAGCCCGAAGAGCTGACCAACATCTTGAGATCTGCAATGTGTTCTTCACCA 2181
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QY 983 rCysIleGlnLeuProValAspSerGlnGlyLysAspAlaAsnLysSerGluSerGluPr 1003
Db 2744 ----- 2772
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Db 2897 -----CTGGTGGCATCTGGTCTGTGTGTAACATGGTACTGCCCCCG 2943
QY 1066 ----- 1072
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QY 1173 pLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSer-----GlyArgG1 1191
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Db 5569 ----- 5569
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Db 5776 -----CTTGAGGACCCCGCGCTGCCCA-----CAGGGCCCC 5808
QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db 5809 AAGAGAGCAAG-----GGTGAACATA 5829
QY 2118 LeuProProGlyGlyGlnGluProProSerProArgAspLeuLysCysTyrr-- 2136
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QY 2137 -----SerVal----- 2138
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Db 5938 CATTCATTCACAACCTGTCCAG-----TCCTGGCTCAAAACAGACGAGCAGCCA 5985
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RESULT 12
US-09-949-016-15601
; Sequence 15601, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15601
; LENGTH: 70308
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15601

Alignment Scores:
Pred. No.: 2.33e-127 Length: 70308
Score: 2237.00 Matches: 730
Percent Similarity: 21.93% Conservative: 25
Best Local Similarity: 21.20% Mismatches: 64
Query Match: 18.79% Indels: 2626
DB: 4 Gaps: 19

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QY 36 SerAla-----GluLysAspProGly----- 42
Db 9662 ACCACACCTGCTTAGCCTCAGATGAGCCAGAGCTAAACGAGAGAGAGTGTAGGGCG 9721
QY 43 SerAlaAspSerGluAlaGluGlyLeuProTyrrProAlaLeuAlaProValPhePhe 62
Db 9722 GGGTCGGGGGGCGCGCTCAGCTCCAGCCTTGCCAGCTGTTCC----- 9766
QY 63 TyrrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrp 82
Db 9767 -----TTGACTGCCAGTACTGG 9784
QY 83 PheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArg 102
Db 9785 TTTGAGCGCATCAGCATGTGGTCACTCTTCAACTGCGTGACCCCTGGCATGTCCGG 9844
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QY 196 ----- 196
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Db 12904 CGGCGTCAGCTGTGGGCAAGGCTGTTCGGAAACCGATGCTTCTTACCTGAGAAATTTACG 12963
QY 248 rLeu----- 249
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Db 13504 GCGCTATTACAGACAGAGAAGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGA 13563
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Db 13564 GAACGGCATGCGGTCTCTGAGAGAAGCGTGCCACGCTGCGGGGACGGGGCGGTGGCCC 13623
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QY 316 pAsnGlnTyrTyrThrAsnCysSerAlagIyGluHisAsnProPheIleGlyAlaIleAs 336
Db 13684 GAACCACTACTACACCAACTGCTCAGCGGGGAGCAAACTTCAAGGGCGCCATCAA 13743
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Db 13744 CTTTGACAACATTGGCTATGCTGATCGCATCTTCAGGTGGGCGAGCCTGGCCCCCG 13803
QY 349 ----- 349
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QY 349 ----- 349
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QY 361 yrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle- 380
Db 13984 ACTTGTGATGATGTCTCATTTCTTCAAAATTCATCTTCACTCATCTCATCAT- C 14042
QY 380 ----- 380
Db 14043 GTGAGTACTCTCAGATCCCCGTGGGATGGGCGATCTGGGACACCTGTGGGGCAG 14102
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QY 380 ----- 380

Db 14223 GTC AAGCGG GACTTA A CTGCTAT TGGGACT TGGGCA AGTCAT TCTCCAT GAGGCTCC 14282
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Db 14283 AGCACTGCTCTGGGCTCTGTTCTTCTTCA TGGGTA AAATGA ATGTTCTCAACCTGAGATG 14342
QY 380 ----- 380
Db 14343 ATACCACTCTCCAGAGGGCATTGGAAATGGGAAAGGTGATTCGTGTTGATTTT 14402
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Db 14403 TTTAATAGCTTATGAGACATACTCACA TATCAT TCAATTCA TCCCTTGAATGAATC 14462
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Db 14703 AGCAGCATATTTAATAGTTTATCACTACCATTCATAGTTAATACTTCATCGCACCC 14762
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QY 857 1 857
Db 19761 G 19761
RESULT 13
US-08-984-709A-51
Sequence 51, Application US/08984709A
Patent No. 6320032
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 4250 Executive Square, Suite 700
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1669 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-984-709A-51
Alignment Scores:
Pred. No.: 3.36e-113 Length: 1669
Score: 1971.50 Matches: 423
Percent Similarity: 57.77% Conservative: 38
Best Local Similarity: 53.01% Mismatches: 83
Query Match: 16.56% Indels: 255
Gaps: 8
US-09-611-257A-37 (1-2266) x US-08-984-709A-51 (1-1669)
QY 109 CysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAlaPhePhe 128
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QY 129 AlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCysTyrLeu 148

Db 62 GCGGTGAGATGTCATCAAGATGGTGGCCTTGGGGCTGTCGGGAGAGAAGTGTACCTG 121
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Db 122 GGTGACACGTGGAACAGGCTGGATTCTTCATCGTCGTGGCGGGCATGATGAGTACTCG 181
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RESULT 14
US-09-268-163-3
; Sequence 3, Application US/09268163B
; Patent No. 6353091
; GENERAL INFORMATION:
; APPLICANT: Lipscombe, Diane
; APPLICANT: Schorge, Stephanie
; TITLE OF INVENTION: HUMAN N-TYPE CALCIUM CHANNEL ISOFORM AND USES THEREOF
; FILE REFERENCE: B1055/7000
; CURRENT APPLICATION NUMBER: US/09/268,163B
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 60/077,901
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 7376
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..7174
; US-09-268-163-3

Alignment Scores:
Pred. No.: 8.8e-101 Length: 7376
Score: 1786.50 Matches: 635
Percent Similarity: 38.95% Conservative: 371
Best Local Similarity: 24.58% Mismatches: 838
Query Match: 15.01% Indels: 741
DB: 3 Gaps: 77

US-09-611-257A-37 (1-2266) x US-09-268-163-3 (1-7376)

QY 27 GlYAlaGlyGlyArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSer 46
| | | | | : : : : :
Db 218 GGGGGCCGGGGGGGGGGGGGGTCCCGGGGGCTGCAGCCCGCCAGCGGTCCTC 277

QY 47 GluAlaGluGlyLeuProGlyProAlaLeuAlaProValPhe----- 61
| | | | | : : : : :
Db 278 TACAAGCAATGCATCGCGCAGCGCGCGGACCATGCGCTGTACAACCCCATCCCGTC 337

QY 62 -----PheTyrLeuSerGlnAspSerArgPro 70
| | | | | : : : : :
Db 338 AAGCAGAACTGCTTCAACCTCAACCGCTCGCTTCTTCAAGCGAGACAACGTCGTC 397

QY 71 ArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIleSerMetLeuVal 90
| | | | | : : : : :
Db 398 CGCAATATACGGAAGCGCATCACCGAGTGGCTCCATTGAGTATATGATCTGGCCACC 457

QY 91 IleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAsp 110
| | | | | : : : : :
Db 458 ATCATCGCCAATGCATCGTGTGGCCCTG-----GAGCAGCACTTCCCTGAT 505

QY 111 SerGlnArgCysArgIleLeuGlnAlaPheAspAsp-----PheIlePheAlaPhe 127
| | | | | : : : : :
Db 506 GGGGACAAACGCCCCATGCTCCGAGCGGCTGGACGACAGGAGCCCTATTTCATCGGATC 565

QY 128 PheAlaValGluMetValValIysMetValAlaLeuGly---IlePheGlyLysLysCys 146
| | | | | : : : : :
Db 566 TTTTGTCTTCAGGCGAGGATCAAAATCATCGCTGTGGGCTTTGCTTCCACAAGGCTCT 625

QY 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
| | | | | : : : : :
Db 626 TACCTGCGGAACGGCTGGAACTGATGACTTCTGTGTCCTCTCACAGGATCCTTGCC 685

QY 167 TyrSer-----LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArg 183
| | | | | : : : : :
Db 686 ACGCTGAAGTACTGCTTCAGCTTCCGA-----ACACTGAGGGCTGTGCGT 730

QY 184 ValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeu 203
| | | | | : : : : :
Db 731 GTGTGAGGCGCCCTGAAGCTGTGTCTGGATTCCAAAGTTTGACAGGTGTGCTCAAGTCC 790

QY 204 LeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePhe 223
| | | | | : : : : :
Db 791 ATCATGAAGGCCATGCTTCCACTCTCCAGATTGGGCTGCTTCTTCTTGGCCATCTTC 850

QY 224 IlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeu 243
| | | | | : : : : :
Db 851 ATGTTGCCATCATTTGGCCTGAGTTCTACATGGGCAAGTTCCACAAGGCTGTTTC--- 907

QY 244 ProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsn 263
| | | | | : : : : :
Db 908 -----CCCAACACACAGATGCGGAG----- 928

QY 264 GluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArg 283
| | | | | : : : : :
Db 928 ----- 928

QY 284 SerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeuAspTyrGlu 303
| | | | | : : : : :
Db 929 -----CCCGTG-----GGTGACTTCCCTGTGGCAAGAGGCCCA 964

QY 304 AlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCys 323
| | | | | : : : : :
Db 965 GCCCGGCTGTGCGAGGGCGACACTGAGTGC-----CGGAGTACTGCCA----- 1009

QY 324 SerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAla 343
| | | | | : : : : :
Db 1010 -----GCACCAACTTTGGCATCACCAACTTTGACAATATCTGTTGCC 1054

QY 344 TrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMetTyrPheVal 363
| | | | | : : : : :
Db 1055 ATCTTGACGGTGTCCAGTGCATCACCATGAGGGCTGAGTGCATCTTATAATACA 1114

QY 364 MetAsp---AlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGly 382
| | | | | : : : : :
Db 1115 AAGCATGCGCGCGCAACACTGGAAGTGGCTTACTTCATCTCTCATCATCATCGCG 1174

QY 383 SerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrLys 402
| | | | | : : : : :
Db 1175 TCCTTCTTCATGCTCAACCTGTGCTGGCGTGTCTCGGGGAGTTTGCCAAGAGCGCA 1234

QY 403 GlnArgGluSer-----GlnLeuMetArgGlnGlnArgValArgPhe 416
| | | | | : : : : :
Db 1235 GAGAGGGTGAGAACCGCGCGCTTCTTGAAGCTGCCCGGACAGACAGATCGAG--- 1291

QY 417 LeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeu 436
| | | | | : : : : :
Db 1292 -----CGAGAGCTC 1300

QY 437 LeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArg 456
| | | | | : : : : :
Db 1301 AAGCGGTACCTGAGTGGATCTTCAAGCGGAGAGAGTCAATGCTGGCCGAGAGACAG 1360

QY 457 AlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlnGluThr 476
| | | | | : : : : :
Db 1361 AATGCA-----GAGAGAGAG 1375

QY 477 GlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHis 496
| | | | | : : : : :
Db 1376 TCCCTTTGGACGTGTGAAGAGAGCGGCCACCAAGAGAGCAAGAAATGACCTGATCCAG 1435

QY 497 HisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArg 516
| | | | | : : : : :
Db 1435 ----- 1435

QY	517	AlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProPro	536
Db	1436	---GCAGAGGAGGAGAGACCGGTTTGACAGAT-----	1465
QY	537	ProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPhe	556
Db	1465	-----	1465
QY	557	TyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSerPro	576
Db	1465	-----	1465
QY	577	SerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSer	596
Db	1465	-----	1465
QY	597	ProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyPro	616
Db	1465	-----	1465
QY	617	ProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeu	636
Db	1465	-----	1465
QY	637	GluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLys	656
Db	1466	-----CTGTGTCTGTGGATCCCCCTTCGCCGCC	1495
QY	657	AlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGly	676
Db	1496	GCCAGCCTCAAGAGCGGGAAGACAGAGAGCTCGTCATCTTCGGAGG-----	1543
QY	677	GluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPhe	696
Db	1544	-----AAGAGAAGATGTTCCGGTTT	1564
QY	697	ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeu	716
Db	1564	-----	1564
QY	717	GlyProAspAlaGluProSerSerValLeuAlaPheThrArgLeuIleCysAspThrPhe	736
Db	1565	-----TTATATC	1570
QY	737	ArgLysIleValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn	756
Db	1571	CGGCGCATGCTGAAGGCTCAGAGCTTCTACTGGGTGGTCTGCGTGTGGCCCTGAAC	1630
QY	757	ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu	776
Db	1631	ACACTGTGTGTGGCCATGCTGCATTACAACCAGCCGCCGCTTACCACGACCTGTAT	1690
QY	777	IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuVal	796
Db	1691	TTTGACAGATTGTTTCTCTGGGTCTCTTCTCACAGAGATGTCCTGAAGATGTATGGC	1750
QY	797	TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal	816
Db	1751	CTGGGGCCAGAGCTACTTCGGTCTCTCTCACTGCTTGGGGTCACTCGTG	1810
QY	817	IleSerValTyrGluIleValGlyGln-----GlnGlyGlyGlyLeuSer	831
Db	1811	GGGAGCGCTCTTGAAGTGTCTGGGCGGCATCAAGCCGGGAAGCTCCTTTGGGATCAGT	1870
QY	832	ValLeuArgThrPheArgLeuMetArgValIleLysIleValArgPheLeuProAlaLeu	851
Db	1871	GTGCTGCGGGCCCTCCGCTGCTGAGGATCTTCAAAGTCACGAAGTACTGAGACTCCCTG	1930
QY	852	GlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeu	871
Db	1931	CGGAACCTGGTGTGTCTCTGCTGAACCTCATGAAGTCCATCATCAGCCTGCTTCTTG	1990
QY	872	LeuMetLeuPheIlePheIlePheSerIleLeuGlyMetHisLeuPheGlyCysLysPhe	891

Db	1991	CTCTTCCTGTTGATTTGTGTCTTCGCCCTGTGGGATGCAGCTGTTGGGGACAGTTTC	2050
QY	892	AlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrp	911
Db	2051	AACTTCCAGGATGAGACTCCACAC-----ACCAACTTCGACACCTTCCCTGCC	2098
QY	912	AlaIleValThrValPheGlnIleLeuThrGlnLysAspTrpAsnLysValLeuTyrAsn	931
Db	2099	GCCATCCTCACTGTCTTCCAGATCCTGACGGGAGAGACTGGAAATGCATGTATTCAC	2158
QY	932	GlyMet-----AlaSerThrSerSerTrpAlaIleuTyrPheIleAla	946
Db	2159	GGGATCGAATCGCAAGCGCGCTGCAGCAAAAGCATGTTCTCGTCTTTTACTTCAATTGTC	2218
QY	947	LeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGly	966
Db	2219	CTGACACTGTTCCGAAACTACACTCTGTGATGTCTTCTGGCCATCGCTGTGACAAC	2278
QY	967	Phe---GlnIleGluIleSerLys-----ArgGluAspAlaSerGlyGln	981
Db	2279	CTGGCCACCGCCCAAGACTGACCAAGCATGAAGAGATGGAAGAGCAATCAG	2338
QY	982	-----LeuSerCysIleGln	986
Db	2339	AAGCTTGCTCTGCAAAAGGCCAAAGAGTGCGCTGAAGTCAGCCCCCATGTCTGCCGGAAC	2398
QY	987	LeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluProAspPhePhe	1006
Db	2399	ATCTCCATGCGCGCCAGGCAGCAGAACTCGGCCAAGCGCGCTCGGTGGGAGCAGCGG	2458
QY	1007	SerProSerLeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGly	1026
Db	2459	GCCAGCCAGCTACGCGCTGCAGAACTCGCGGCACGCTCGAGGCGCTGTACAGCAGATG	2518
QY	1027	Glu-----HisProGluLeuArgLys	1033
Db	2519	GACCCCGAGAGCGGCTGCGCTTGCACACTACGCCACCTGCGGCCGACATGAAGACG	2578
QY	1034	SerLeuLeuProProLeuIleIleHisThr-AlaAlaThrPrometSerLeuPro----	1051
Db	2579	CACCTGACCGCGCGCTGTGTGTGAGCTGGCGCGGACGCGCGGGGCGCGTGGA	2638
QY	1052	-----LysSerThrSe	1055
Db	2639	GGCAAAAGCCGACCTGAGGCTGCGGAGGCCCCCGAGGGCGGTGCACCTCCGCGCAGGCAC	2698
QY	1055	rThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSer-----	1071
Db	2699	CACCGGACCGCGCAAGGACAAAGACCCCCCGCGGGGGGACCAAGACCGACAGAGCC	2758
QY	1072	-----SerGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProPr	1087
Db	2759	CCGAAGCGGAGAGCGGGGAGCCCGGTGCGCGGAGAGAGCGCGCGCGCCGACCGCAGC	2818
QY	1087	oSerAlaArg-----SerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe	1105
Db	2819	CACAGCAAGAGGCGCGCGGGGCCCCCGGAGCGCGGAGCGAGCGCGCCGACGAGCC	2878
QY	1105	rArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLysArgArgSerProse	1125
Db	2879	CCCGAGGGCGGCGCGGCAACCAACGCGCGGCTCCC-----CGAGGAGGCGGCGGAG	2932
QY	1125	GlyGlu-----	1127
Db	2933	CGGAGCCCCGACGCCACCGCGCGCACCGGCAACAGATCCGAGCAAGAGTGCGCCGCC	2992
QY	1127	-----	1127
Db	2993	GCCAAGGCGAGCGCGCGCGGCAACCGCGCGGCCCCCGAGCGGGGCCCCGGAGGCG	3052
QY	1128	-----ArgArgSerLeuLeuSe	1133

Db	3053	GAGAGCGGGAGAGACCGCGCGCGCACCGCGCCGACAAAGCGCAGCCTGCTCAC	3112
Qy	1133	r-GlyGluGlyGln-GluserGlnAspGluGluGluSerSerGluGluGluArgAlaSer	1152
Db	3113	GAGGCTGTGAGAGAGAGACCAACGAGAGAGAGGCCACGAGAGAGGCTGAGATAGTG	3172
Qy	1153	ProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPhe	1172
Db	3173	GAAAGCCGACAAAGAAAGAGAGCTCCGGAAACCAAGCCCGGAGCCACACTGTGACCTG	3232
Qy	1173	AspLeuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySer	1192
Db	3233	GAGACCAAGTGGAGCTGTGACTGTGGGTCCTCATGACACACTGCCACGACCTGTCTCCAG	3292
Qy	1193	AlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeu	1212
Db	3293	AAGGTGAGGAACAGACAGCAGAGATGCAGACAATCAGCGGAACGTCACTCGCATGGGCAGT	3352
Qy	1213	ArgProAspAspPro-----ProLeuAsp	1220
Db	3353	CAGCCCCAGACCCGAAACACTATTGTACATATCCAGTGAATGCTGACGGGCCCTTGTGGG	3412
Qy	1221	GlyAspAspAlaAspAspGluGlyAsnLeu-----SerLysGlyGluArg	1235
Db	3413	GAAAGCCACGGTCGTTCCCAAGTGGTAAAGTGAACCTGGAAGCCAAAGCAGAGGGGGAAGAAG	3472
Qy	1236	-----ValArgAlaTyrIleArgAlaArgLeuProAlaCysTyr	1248
Db	3473	GAGGTGGAAGCGGATGACGTGAAGAGAGCGCGCCCGCCTATCGTCCCATACAGC---	3529
Qy	1249	LeuGluArgAspSerTyrSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeu	1268
Db	3530	-----TTCATGTTCGTGTTAAGCCCAACCAACCTGCTCCGCGCTTC	3571
Qy	1269	CysHisArgIleIleThrHisLysMetPheAspHisValValLeuValIleIlePheLeu	1288
Db	3572	TGCCACTACATCGTGACCATGAGGTACTTTCGAGGTGGTCAATTCGCTGTCATCGCCTTG	3631
Qy	1289	AsnCysIleThrIleAlaMetGluArgProLysIleAspProHisSerAlaGluArgIle	1308
Db	3632	AGCAGCATCGCCCTGCTGCTGAGGAGCCCA--GTGCGCACAGACTCGCCCAAGAACAC	3688
Qy	1309	PheLeuThrLeuSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLys	1328
Db	3689	GCTCTGAATAATACCTGGATTACATTTTCACTGCTGCTTTACCTTGAAGATGCTGATAAAG	3748
Qy	1329	ValValAlaLeuGlyTyrCysPheGlyGluGlnAlaTyrLeuArgSerSerTyrAsnVal	1348
Db	3749	ATGATCGACTTGGAGCTGCTCTTCAACCTGAGGCTTATTTCCGGGACTTGTGGAACATT	3808
Qy	1349	LeuAspGlyLeuLeuValLeuIleSerValIleAspIle--LeuValSerMetValSer	1367
Db	3809	CTGGACTTCATTGTGTGTCAGTGGCGCCCTGTGGCGTTCCTTCTCGAGCTTTCGTGGGA	3868
Qy	1368	AspSerGlyThrLysIleLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg	1387
Db	3869	GGATCCAAAGGGAAGACATCAATACCATCAAGTCTGTGAGAGTCTTCGTCTCTCGCGG	3928
Qy	1388	ProLeuArgValIleSerArgAlaGlnGlyLeuLysLeuValValGluThrLeuMetSer	1407
Db	3929	CCCCCTCAAGACCATCAAAACGGCTGCCCAAGCTCAAGGCTGTGTGACTGTGTGTGAAC	3988
Qy	1408	SerLeuLysProIleGlyAsnIleValValIleCysCysAlaPhePheIleIlePheGly	1427
Db	3989	TCCCTGAAGAATGTCTCTCAACATCTTGATTGTCTACATGCTCTTCATGTTCATATTGCC	4048
Qy	1428	IleLeuGlyValGlnLeuPheLysGlyLysPhePheValCysGlnGlyGlu-----	1444
Db	4049	GTCATTTGGGTGCAAGCTCTTCAAAAGGAAGTTTCTTACTGCACAGATGAATCCAAGAG	4108
Qy	1445	-----AspThrArgAsn-----IleThrAsnLysSerAspCysAlaGluAlaSer	1459
Db	4109	CTGAGAGGAGACTGCAGGGGCTGACTATTGTGATTATGAGAGAGGAAGTGAAGCTCAG	4168

Oy	1460	TyrArg---	TrpValArgHisIleSTyrAsnPheAsnLeuGlyAlaLeuMetSer	1478
Db	4169	CCCAGCAGTGGAGAATAAATACACTTCCTCACTACGACAATGTGCTTGCGCTCTGCTGACG	4228	
Oy	1479	LeuPheValLeuAlaSerIysAspGlyTyrValAspIleMetTyrAspGlyLeuAspAla	1498	
Db	4229	CTGTTCAcAGTGTCCACCgGAGAAgGCTGGCCCATGTGTCTGAACAcACTCCGTGATGCC	4288	
Oy	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTyrMetLeuLeuTyrPheIle	1518	
Db	4289	ACCTATGAGAGACAGGGTCCAAgCCCTGGGTACCCCATGGAAGCTGTCCACTCTTCAAGTG	4348	
Oy	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu	1538	
Db	4349	GTTACTTTGTGTCTTCCCTTCTCTTCTGTCATCAcATTCTTGTGGCTTTGATCATCATC	4408	
Oy	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLys	1558	
Db	4409	ACCTTC-----CAGAGCAGGGGACAAGTGATGTGAA-----	4444	
Oy	1559	ArgLeuArgArgLeuGluLysLysArgArgLysAla-----GlnCysLys	1573	
Db	4445	-----TGCAGCCTGGAGAGAACGAGAGGGCTTGCAATTGACTTCGCCATCAGCGCCAAA	4498	
Oy	1574	ProTyr-----TyrSerAspTyrSerArg-----PheArgLeuLeuValHisHisLeu	1589	
Db	4499	CCCCTGACACGGTACATGCCCCCAAACCGGCAGTCGTTCCAGTATTAAGCSTGGACATT	4558	
Oy	1590	CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr	1609	
Db	4559	GTTGTTCCCCCGCCCTTTGAATACTTCATCATGGCCATGATAGCCCTCAACACTGTGTG	4618	
Oy	1610	MetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsn	1629	
Db	4619	CTGATGATGAAGTCTATGATGACACCCCTATGAGTAGCAGACTGATGCTGAATGCTGAAC	4678	
Oy	1630	TyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPhe	1649	
Db	4679	ATCGTGTTCACATCCATGTTCTTCATGGAATGCGGTGTAAGATCATCGCCTTGGGGTG	4738	
Oy	1650	ArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuLeuSerIle	1669	
Db	4739	CTGAActATTTCAGAGATGCTGGAATGCTTTGACTTGTCTCACTGTGTGGGAAGTATT	4798	
Oy	1670	MetGlyIleThrLeuGluGluIle---GluValAsnAlaSerLeuProIleAsnProThr	1688	
Db	4799	ACTGATATTTTAGTAACAGAGATTGGGAAACGAAC-----AATTTCATC	4843	
Oy	1689	IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLysMetAla	1708	
Db	4844	AACCTCAGCTTCCTCCGCCCTTTGAGCTGCGCGCTGATCAAGCTGCTCGCCACAGGC	4903	
Oy	1709	ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu	1728	
Db	4904	TACACCATCCGCATCTGCTGTGACCTTTGTCCAGTCTTCAAGGCCCTGCCCTACGTG	4963	
Oy	1729	GlyLeuLeuPheMetLeuLeuPhePheIlePheAlaIalaLeuGlyValGluLeuPheGly	1748	
Db	4964	TGTCTGCTCATGTCATGCTGTCTTTCATCTACGCCCATCATCGGCATGACAGTGTTTGGG	5023	
Oy	1749	AspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg	1768	
Db	5024	AATATTGCCCTGGATGATGAC-----ACCAGCATCAACCGCACAAcAACTTCCGG	5074	
Oy	1769	AsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTyrAsnGly	1788	
Db	5075	ACGTTTTTGCAAGCCCTGATGCTGTCTTCAAGAGCGCCACGGGGAGGCGCTGGCACAGAG	5134	
Oy	1789	IleMetLysAspThrLeuArgAsp-----CysAspGlnGlu-----SerThrCysTyr	1804	
Db	5135	ATCATGCTGTCTGCTGAGCAACcAGGCTGTGATGACAGCGCCAAATGccACCGAAGTGT	5194	

QY	1805	AsnThrValIleSerProIleTyrPheValSerPheValLeuThraIaGlnPheValLeu	1824
Db	5195	GGAAGTGACTTTGGCTTAATTCTAATTCGTCCCTCAATCTCTGTGCCTTTCTGATG	5254
QY	1825	ValAsnValValIleAlaValLeuMet-----	1833
Db	5255	TTGAACCTCTTTGTGGCTGTGATCATGACAATTTTGAATACTCACGCCGACTTTCC	5314
QY	1834	-----LysHisLeuGluGlu-SerAsnLysGluAlaLysGluAlaGluLe	1849
Db	5315	ATCCTAGTCTCTACCACTTGGATGAGTTCAATCCGGGTCTGGCGCTGATAACGACCCGCT	5374
QY	1849	UGLuAlaGluLeuGluLeuGluMetLysThrLeu-SerProGlnProHisSerProLeug	1869
Db	5375	GCGTGTGGGGCCATCAGTTTAAATGACATGTGTTGAGATGCTGAATAACACATGTCCCCGCT	5434
QY	1869	LysSerProPheLeuTyrProGlyValGluGlyProAspSerProAspSerProLysProG	1889
Db	5435	CTGGG-----GCTGGGGAAGAATGCCCTGCTCGAGTTGCTTACAAGCCGCTG	5482
QY	1889	IylAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisProt	1909
Db	5483	GTTTCG--CATGAACATGCCCATCTCCAACGAGACATGACTGTTCACTTACAGTCACG	5539
QY	1909	hmetGlnProHisProThr-----GluLeuProGlyPro-----	1920
Db	5540	CTGATGGCCCTCATCCGCAAGGCACTGAGATCAAGCTGGCCCACTGGACAAGCAG	5599
QY	1921	-----AspleuLeuThrValArgLysSergly----	1929
Db	5600	CATCAGTGAGCCGGAATTGAGGAAGAGATTTCGTTGTGTGGCCAATCTGCCCCAG	5659
QY	1929	-----	1929
Db	5660	AAGACTTTGACTTGTGTTACCACCCCATTAAGCCTGATGAGATGACAGTGGGGAAGTT	5719
QY	1930	-----ValSerArgThrHisSerLeuProAsna	1939
Db	5720	TATGCAGCTCTGATGATATTGACTTCTACAAGCAGAACAAAACACAGAGACCATG	5779
QY	1939	spsertYrmetCysarg-----HisGlyserThrAlaGluGlyPro-----Leug	1954
Db	5780	CAGCAGGCTCCTGAGGCCCTCTCCAGATGGGTCTGTGCTCTGTTCCACCCTCTGAAG	5839
QY	1954	LYHis-----ArgGlyTyrGlyLeuPro-LysAla	1963
Db	5840	GCCACCCTGAGACAGACACAGCCGCTGTGCTCCGAGAGCCCGGTTTTCTTCACACAG	5899
QY	1964	GlnserGlyserValLeuSer-----ValHisserGlnProLa-	1976
Db	5900	AAGAGTTCCACCTCCCTCAGCAATGGCGGGGCCATACAAAACCAAGAGAGTGGCATCAA	5959
QY	1977	--AspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnPro--	1994
Db	5960	GAGTCTGTCTCTGGGGCACTCAAGAGACCAGAGATGCAACCCATGAGGCCAGGCCACC	6019
QY	1995	-----HisserAlaProThrTyrGlyThrIleProLysLeuProProGly	2010
Db	6020	CTGAGCGTGGCCACTCCACAGAGATC-----CCTGTGGGG	6055
QY	2011	ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArg-----	2026
Db	6056	CGGTCAAGAGACATGGCTGTGACGTTCAAGATGCAGAGCATAAACCCGAGAGGGCCCTGAT	6115
QY	2027	-----ThrAspserLeuAspValGlnGlyLeuGlySerArgGluAspleuLeuAla	2043
Db	6116	GGGGAGCCCAAGCCTGGGCTGGAAGACCAAGGTCGAGCGGCTCCATGCCCCGCTTGG	6175
QY	2044	GluValSerglyPro-----SerProProLeuAlaArgAlaTyrSerPheTyrGly	2060
Db	6176	GCCGAGACTCAGCCCCTCACAGATGCCAGCCCATGAAGCGCTCCATC-----	6223
QY	2061	GlnserSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet	2080

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Db      6224  -----TCCACGCTGGCCACGCG-----CCCCGTGGAG-TCATCTTTGACGACCACCC 6273
QY      2081  ThrProProAlaProCysProGly-----ProGluProAsnTrpGlyLysGlyPro 2097
Db      6274  GGACCGCCCAACCCCTTAGCCAGCGGTGCTGCACCAACCACCA-----CCA 6318
QY      2098  ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db      6319  CCG-----CTG 6324
QY      2118  LeuProProGlyGlyGlnGlu--GluProProSerProArgAspLeuLysCysTyr 2136
Db      6325  CCACCGCCGACGAGACGAGAGCAGAGGTCTCTGAGAAGGGGCCAGCTGTCTGC-- 6381
QY      2137  SerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArg 2156
Db      6382  -----CGATATGATGGCGCACCAAGCAG----- 6405
QY      2157  HisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspPro 2176
Db      6406  -----TGCTGTGGGGCGGGGCTGCCCGCGGAGAGGGGCTA-CAG 6446
QY      2177  SerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSer 2196
Db      6447  GCTGCCCGCGGAAACGAGAGCGCGGACGAGCGGGGCTCCAGAGACGGAGCGAGC 6506
QY      2197  ProProSerIleThrIleAspProProGluSerGln----- 2208
Db      6507  CCT-----CATCTCTCTCTCGAGAGACGCGCTTACTCTCGAGC 6551
QY      2209  -----GlyProArgThrProProSerProGlyIleCysLeuArgArg 2223
Db      6552  GCTTTGGGGCGGTGAGCCCCCGAAGCCAAGCCCTCCTCAGACGACCAACGTCGC 6611
QY      2224  AlaProSerSerAspSerLysAspPro----- 2232
Db      6612  CAACAGCTGGCCAGAGCGCGGACCCACCAACAGGACAGTGTTCCTGAATGGAGCC 6671
QY      2233  -----LeuAlaSerGlyProProAspSerMetalalaSerProSerPro 2247
Db      6672  CCTTGCCTGCACATCTGTGTCTAGCACCCCGCGCGGTGGCGGAGGACGCTCCCC 6731
QY      2248  LysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db      6732  AGACGCGCCCTGACTC-----CCGCCCCAGCATCACCT 6764

RESULT 15
US-08-455-543A-7
/ Sequence 7, Application US/08455543A
/ Patent No. 5792846
/ GENERAL INFORMATION:
/ APPLICANT: Harpold, Michael
/ APPLICANT: Ellis, Steven
/ APPLICANT: Williams, Mark
/ APPLICANT: Feldman, Daniel
/ APPLICANT: McCue, Ann
/ APPLICANT: Brenner, Robert
/ TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
/ TITLE OF INVENTION: METHODS
/ NUMBER OF SEQUENCES: 57
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Brown, Martin, Haller & McClain
/ STREET: 1660 Union Street
/ CITY: San Diego
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92101-2926
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FaalSEQ Version 1.5

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,543A
FILING DATE: May 31, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/223,305
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/482,384
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-52517
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7362 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 144..7163
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..143
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 7161..7362
US-08-455-543A-7

Alignment Scores:
Pred. No.: 1.17e-100 Length: 7362
Score: 1784.50 Matches: 637
Percent Similarity: 38.87% Conservative: 367
Best Local Similarity: 24.66% Mismatches: 836
Query Match: 14.99% Indels: 745
DB: 1 Gaps: 78

US-09-611-257A-37 (1-2266) x US-08-455-543A-7 (1-7362)
QY 27 GLYAlaGLYGLYArgProGLYProGLYSerAlaGLYAspProGLYSerAlaAspSer 46
Db 216 GGGGCGGGGGGGGGGGGGGGGGTCCCGGGGGCTGCAGCCCGCGCGGGTCTC 275
QY 47 GLUAlaGLUGLYLeuProTYRProAlaLeuAlaProValPhe----- 61
Db 276 TACAAGCAATCGATCGCGCAGCGCGCGCGGAGCCATGCGCGTACAAACCCATCCCGGTC 335
QY 62 -----PheTYRLeuSerGlnAspSerArgPro 70
Db 336 AAGCAGAACTGCTTCAACCGTCAACCGCTCGCTTCTTCAAGCGAGACAACGTCGTC 395
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QY 71 ArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIleSerMetLeuVal 90
Db 396 CGCAATACCGGAAGCGCATCACCGAGTGGCTCCATTGCAATATGATCTGGCCACC 455
QY 91 IleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAsp 110
Db 456 ATCATCGCAACTGCATCGTGTGGCCCTG-----GAGCAGCACCTCCCTGAT 503
QY 111 SerGlnArgCysArgIleLeuGlnAlaPheAspAsp-----PheIlePheAlaPhe 127
Db 504 GGGGACAAACGCCCATGTCCGAGCGGCTGGACGACAGAGCCCTATTTCATCGGGATC 563
QY 128 PheAlaValGluMetValValIleYMetValAlaLeuGly---IlePheGlyIleYsCys 146
Db 564 TTTTGTCTCGAGGCAAGGATCAAAATCATCGCTTGGGCTTTGTCTTCCACAAGGGCTCT 623
QY 147 TYRLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
Db 624 TACCTGCGGAACGGCTGGAACGTCAAGACTTCGTGTGCTGCTCACAGGATCTTGCC 683
QY 167 TYRser-----LeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArg 183
Db 684 ACGGCTGAACCTGACTTCGACCTGCGA-----ACACTGAGGGCTGTGCGT 728
QY 184 ValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeu 203
Db 729 GTGCTGAGGCCCTGAAGCTGTGTCTGGGATTCCAAAGTTGCAGGTGTCTCAAGTCC 788
QY 204 LeuLeuAspThrLeuPrometLeuGlyAsnValLeuLeuLeuCysPhePheValPhePhe 223
Db 789 ATCATGAAGGCCATGTGTTCCACTCTCTGCAGATTGGGCTGCTTCTTTCGCCATCTC 848
QY 224 IlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeu 243
Db 849 ATGTTGCCATCATGTGGCTGAGTTCTACATGGGCAAGTTCCACAAGGCTGTTC--- 905
QY 244 ProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTYRglInThrGluAsn 263
Db 906 -----CCCAACAGACAGATGCGGAG----- 926
QY 264 GluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArg 283
Db 926 ----- 926
QY 284 SerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeuAspTYRglu 303
Db 927 -----CCCGTG-----GTTGACTTCCCTGTGGCAAGAGGCCCA 962
QY 304 AlaTYRAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTYRtyrThrAsnCys 323
Db 963 GCCCGGCTGTGCGAGGCGACACTGAGTGC-----CGGAGTACTGGCCA----- 1007
QY 324 SerAlaGlyGluHisAsnProPheYsglyAlaIleAsnPheAspAsnIleGlyTYRAla 343
Db 1008 -----GGAACCAACTTTGGCATCCACCAACTTTGACAATATCTCTGTGGCC 1052
QY 344 TrpIleAlaIlePheGlnValIleThrLeuGluGlyTYRValAspIleMetTYRpheVal 363
Db 1053 ATCTTGACGGTGTTCAGTGATGCATCACATGAGGGCTGACTGATCATCTATAATACA 1112
QY 364 MetAsp---AlaHisSerPheTYRAsnPheIleTYRpheIleLeuLeuIleIleValGly 382
Db 1113 AAGCATGCGGCGGCAACACCTGGAAGTGGCTTACTTCATCTCTCATCATCATCGGC 1172
QY 383 SerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGluThrIys 402
Db 1173 TCCTTCTTCATGCTCAACCTGTGTGCGGCTGCTCTCGGGGAGTTTGCCAAGAGGCA 1232
QY 403 GlnArgGluSer-----GlnLeuMetArgGluGlnArgValArgPhe 416
Db 1233 GAGAGGGGTGAGAACCGCGGCTTCTCTGAAGCTGCGCGCGCAGACAGATCGAG--- 1289
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QY 417 LeuSerAsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeu 436
Db 1290 -----CGAGAGCTC 1298
QY 437 LeuLysTyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArg 456
Db 1299 AACGGGTACTGAGTGGATGATCTTCAAGCGGAGAGATCATGCTGGCCGAGGAGACAG 1358
QY 457 AlaAlaGlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThr 476
Db 1359 AATGCA-----GAGGAGAAAG 1373
QY 477 GlnProSerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHis 496
Db 1374 TCCCTTTGGACGTGCTGTAAGAGCGGCCACCAGAAGAGCAGAAATGACCTGATCCAC 1433
QY 497 HisHisHisHisHisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArg 516
Db 1433 ----- 1433
QY 517 AlaSerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProPro 536
Db 1434 ---GCAGAGAGGAGAGAGACCGGTTTGCAGAT----- 1463
QY 537 ProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPhe 556
Db 1463 ----- 1463
QY 557 TyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSerPro 576
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QY 577 SerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSer 596
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QY 617 ProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeu 636
Db 1463 ----- 1463
QY 637 GluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLys 656
Db 1464 -----CTGTGTGCTGTTGGATCCCCCTTCCGCCCGC 1493
QY 657 AlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGly 676
Db 1494 GCCAGCCTCAAGAGCGGAGAGACAGAGCTGTCATACTTCCGGAG----- 1541
QY 677 GluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPhe 696
Db 1542 -----AAGAGAAGATGTTCCGGTTT 1562
QY 697 ThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeu 716
Db 1562 ----- 1562
QY 717 GlyProAspAlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPhe 736
Db 1563 -----TTTATC 1568
QY 737 ArgLysIleValaAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsn 756
Db 1569 CGGCGCATGTGAAGGCTCAGAGCTTCTACTGGTGTGCTGTGCGTGCGCCCTGAAC 1628
QY 757 ThrLeuSerMetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGlu 776
Db 1629 ACACTGTGTGGCCATGTGCATTTACAACGCGCGGCTTACACGACCTGTAT 1688
QY 777 IleSerAsnIleValPheThrSerLeuPheAlaLeuGluMetLeuLysLeuVal 796

Db 1689 TTTGCAGAGTTTGTTTTCTCGGGTCTCTTCTCCACAGAGATGTCCCTGAAGATGTATGSC 1748
QY 797 TyrGlyProPheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValVal 816
Db 1749 CTGGGCCCCAGAAAGTACTTCCGGTCTCTCTCAACTGCTTGCACTTTGGGGTCACTGTG 1808
QY 817 IleSerValTrpGluIleValGlyGln-----GlnGlyGlyLeuSer 831
Db 1809 GGGAGCGTCTTTGAAGTGTGTGGCGGCCATCAAGCCGGGAAGCTCTTTGGGATCAGT 1868
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Db 1869 GTGCTGGGGCCCTCCGCTGTGAGGATCTTCAAGTCAAGAGTACTGAGCTCCCTG 1928
QY 852 GlnArgGlnLeuValValLeuMetLysThrMetAspAsnValAlaThrPheCysMetLeu 871
Db 1929 CGGAACCTGGTGGTGTCCCTGTGAACCTCCATGAATCCATCATCAGCCTGCTCTTG 1988
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Db 1989 CTCTTCTGTTCATTGTGTGCTTCCAGCTGCGCCGTGTGGGATGCAGCTGTTGGGGACAGTTG 2048
QY 892 AlaSerGluArgAspGlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrp 911
Db 2049 AACTTCCAGGATGAGACTCCACA-----ACCAACTTCGACACTTCCCTGCC 2096
QY 912 AlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsn 931
Db 2097 GCCATCTCACTGTCTTCCAGATCTGACGGAGAGACTGGAATGCATGATGATATCAC 2156
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Db 2157 GGGATCGAATCGCAAGCGCGCTCAGCAAAAGGCATGTTCTGCTCTTTAATTCAATTGTC 2216
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QY 982 -----LeuSerCysIleGln 986
Db 2337 AAGCTTGCTTGCAAAAGGCCAAGAAGTGCTGAAGTCAGCCCCCATGTCTGCCGGAAC 2396
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Db 2397 ATCTGCATCGCCGACGACAGAACTCGGCCAAGCGCGCTCGGTGTGGAGACAGCGG 2456
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Db 2457 GCCAGCAGCTACGCGTGCAGAACCTGCGGCGCAGCTGCGAGCGCTGTACAGCGAGATG 2516
QY 1027 Glu-----HisProGluLeuArgLys 1033
Db 2517 GACCCCGAGGAGCGGCTGCGCTTCCCACTACGCGCCCACTGCGGCCCGACATGAAGACG 2576
QY 1034 SerLeuLeuProProLeuIleIleHisThr-AlaAlaThrPrometSerLeuPro----- 1051
Db 2577 CACCTGACCGCGCGTGTGTGTGAAGCTGGCGCGGACGCGCGGGGGCCCGTGGGA 2636
QY 1052 -----LysSerThrSe 1055
Db 2637 GGCAAGCCCGACCTGAGGCTGCGGAGCGCCCGAGGGCGTGCACCTTCGCGCAGGCAC 2696
QY 1055 rThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThrSerSer----- 1071
Db 2697 CACCGGACCGCGACAAGACAAGACCCCGCGCGGGGAGCACGAGCAGACAGAGCC 2756
QY 1072 -----SerGlySerAlaGluProGlyAlaAlaHisGluMetLysSerProPr 1087

Db 2757 CCGAAGCGGAGACGGGGAGCCCGGTGCCCCGGAGAGCGCGCGCGCCGACCCGAC 2816
QY 1087 oSerAlaArg-----SerSerProHisSerProTrpSerAlaAlaSerSerTrpThrSe 1105
Db 2817 CACAGCAAGAGGCGCGCGGGCCCCCGGAGGGCGCGAGCGAGCGCGCGCGAGGGCCACGGC 2876
QY 1105 rArgArgSerSerArgAAsnSerLeuGlyArgAlaProSerLeuLySArgArgSerProSe 1125
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QY 1125 rGlyGlu----- 1127
Db 2931 CGGGAGCCCCGACGCCACCGCGCGCACCGGACCAAGATCCGAGCAAGAGTGCGCGCGC 2990
QY 1127 ----- 1127
Db 2991 GCCAAGGGCGAGCGCGCGCGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3050
QY 1128 -----ArgArgSerLeuSe 1133
Db 3051 GAGAGCGGGGAGAGCTTAC 3110
QY 1133 r-GlyGlyGln-GluserGlnAspGlnGluGluSerSerGlnGluGluArgAlaSer 1152
Db 3111 GAGGCTGTGAGAGAGACACGAGAGAGAGCGCACGAGAGAGAGGCTGAGATAGTG 3170
QY 1153 ProAlaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaLySerSerPhe 1172
Db 3171 GAAGCCGACAGAAAGAGAGCTCCGGAACCAACGCGCGGAGGCCACACTGTGACCTG 3230
QY 1173 AspleuProAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySer 1192
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QY 1221 GLyAspAspAlaAspAspGlnGlyAsnLeu-----SerLySgLyGluArg 1235
Db 3411 GAAGCCACGCTGCTCCCAAGTGGTAACGTGACCTGGAAAGCAAGCAGAGGGAAGAG 3470
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QY 1249 LeuGluArgAspSerTrpSerAlaTyrIlePheProGlnSerArgPheArgLeuLeu 1268
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QY 1269 CysHisArgIleIleThrHisLyMetPheAspHisValValLeuValIleIlePheLeu 1288
Db 3570 TGCCACTACATCGTGAACATGAGGTAAGTCTGAGGTGCTCATTTCTGCTCATCGCCTTG 3629
QY 1289 AsnCysIleThrIleAlaMetGluArgProLySileAspProHisSerAlaGluArgIle 1308
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Db 3687 GCTCTGAATAATACCTGGATTACATTTTCACTGGTCTTTTACCTTGAATGTTGATAAG 3746
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QY 1349 LeuAspGlyLeuLeuValLeuIleSerValIleAspIleLeuValSerMetVal---Ser 1367
Db 3807 CTGAGC-----TTCAATTGTGTCAAGTGGCGCCCTGTTGGCTTTTCTTCTCA 3854

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Db 3975 TCCCTGAAGATGCTCTCAACATCTTGATTGTCTACATGCTCTTCATGTTCAATTGCG 4034
QY 1428 IleLeuGlyValGlnLeuPheLySgLyLySPhenPheValCysGlnGlyGlu----- 1444
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QY 1445 -----AspThrArgAsn-----IleThrAsnLySerAspCysAlaGluAlaSer 1459
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QY 1460 TyrArg---TrpValArgHisLySLeuAspPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db 4155 CCCAGCGAGTGAAGAATAAGACTTTCATCAGCAATGTGCTCTGGCTGTGTCAGC 4214
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Db 4215 CTGTTCAAGTGTCCACGSGAGAGGCTGGCCATGGTGTGCTGAACAACACTCCGTGATGCC 4274
QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
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QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538
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QY 1539 AsnPheHisLySArgGlnHisGlnGluGluGluAlaArgArgArgGluGluLyS 1558
Db 4395 ACCTTC-----CAGAGCAGGGGAGCAAGGTATGTCTGAA----- 4430
QY 1559 ArgLeuArgArgLeuGlnLyLySArgArgLyAla-----GlnCysLyS 1573
Db 4431 -----TGCAGCCTGGAAGAAGAGAGGGCTTGACATTGACTTCCCATCAGCGCCAA 4484
QY 1574 ProTyr-----TyrSerAspTyrSerArg-----PheArgLeuLeuValHisIleLeu 1589
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QY 1590 CysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThr 1609
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Db 4605 CTGATGATGAAGTTCTATGATGACACCTATGATGACAGCTGATGCTGAATGCTGAAAC 4664
QY 1630 TyrIlePheThrValIlePheValLeuGluSerValPheLySLeuValAlaPheGlyPhe 1649
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QY 1670 MetGlyIleThrLeuGluGluIle---GluValAsnAlaSerLeuProIleAsnProThr 1688
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QY 1709 ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728
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QY 1789 IleMetLysAspThrLeuArgAsp-----CysAspGlnGlu-----SerThrCysTyr 1804
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QY 1805 AsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPheValLeu 1824
Db 5181 GGAAGTGACTTGCCTACTTCTACTCGTCTCTCTCATCTTCTGTGCTCTTCTGTATG 5240
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Db 5241 TTGAACCTCTTTGTGGCTGTGATCATGGACAATTTTGAGTACCTCACGGCGACTTTC 5300
QY 1834 -----LysHisLeuGlnGlu-SerAsnLysGluAlaLysGluGluLeu 1849
Db 5301 ATCTAGTCTCTACCACTTGAGTGAAGTTCATCCGGGCTGGGCTGAATACGACCCGGCT 5360
QY 1849 uGluAlaGluLeuGluLeuGluMetLysThrLeu-SerProGlnProHisSerProLeuG 1869
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GenCore version 5.1.6
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Run on: September 18, 2005, 18:24:02 ; Search time 2770.66 Seconds
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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	11815.5	99.3	7648	19 US-10-757-262-15	Sequence 15, Appl
3	11815.5	99.3	7825	22 US-10-756-149-31	Sequence 31, Appl
4	11815.5	99.3	7825	22 US-10-786-148-120	Sequence 120, App
5	11353	95.4	8116	17 US-10-062-674-2011	Sequence 2011, Ap
6	11111	93.3	7129	10 US-09-383-894-1	Sequence 1, Appli
7	11111	93.3	7285	10 US-09-383-894-3	Sequence 3, Appli
8	10945	91.9	6942	19 US-10-377-139-7	Sequence 7, Appli
9	6315.5	53.1	3993	21 US-10-930-301-51	Sequence 51, Appl
10	6215.5	52.2	7898	22 US-10-483-467-3	Sequence 3, Appli
11	5496.5	46.2	6990	19 US-10-377-139-8	Sequence 8, Appli
12	5492.5	46.1	6816	9 US-09-935-541-1	Sequence 1, Appli
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16	5418.5	45.5	6503	9 US-09-935-541-12	Sequence 12, Appl
17	5418.5	45.5	6503	16 US-10-425-800-12	Sequence 12, Appl
18	3959.5	33.3	5562	9 US-09-030-482B-18	Sequence 18, Appl
19	3867	32.5	6073	19 US-10-377-139-11	Sequence 11, Appl
20	3461.5	29.1	6933	22 US-10-450-763-10945	Sequence 10945, A
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38	1751.5	14.7	9695	21 US-10-486-706-207	Sequence 207, App
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45	1708	14.3	7477	19 US-10-322-696-177	Sequence 177, App

ALIGNMENTS

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: Publication No. US20040175761A1
: GENERAL INFORMATION:
: APPLICANT: Mackinnon, Roderick
: APPLICANT: Jiang, Youxiong
: APPLICANT: Lee Mackinnon, Alice
: APPLICANT: Ruta, Vanessa
: TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
: TITLE OF INVENTION: Uses Thereof
: FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
: CURRENT APPLICATION NUMBER: US/10/377,139
: CURRENT FILING DATE: 2003-03-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn version 3.1

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Db	4861	ATCGGGCTGAACGTGTGTCAACCATGGCCATGGAGCACTACCAAGACGCCCAAGATTCTGAT	4920
QY	1623	GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe	1642
Db	4921	GAGGCTCTGAAGATCTGCAACTACATCTTCACTGTTCATCTTGTCTTGAGTCAGTTTTC	4980
QY	1643	LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu	1662
Db	4981	AAACTTGTGCTTGTGTTCCGTGGTCTTCCAGGACAGGTGGAACCAAGCTGACCTG	5040
QY	1663	AlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGluIleGluValAsnAlaSer	1682
Db	5041	GCCATTGTGCTGCTGCATCATGGGCATCACGCTGAGGAATCGAGTCAACGCTCG	5100
QY	1683	LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu	1702
Db	5101	CTGCCCATCAACCCCACTCATCCGCATCATGAGGGTGTGCCGATTGCCCGAGTCTG	5160
QY	1703	LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu	1722
Db	5161	AAGCTGCTGAAGATGGCTGTGGGCATGCGGGCGCTGTGGAACAACGGTGATGCAGGCCCTG	5220
QY	1723	ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu	1742

Db	5221	CCCCAGGTGGGAACCTGGGACTTCTCTTCATGTTGTTTTCATCTTGCAGCTCTG	5280
QY	1743	GLYValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly	1762
Db	5281	GGCGTGGAGCTCTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTGAGGGCCTGGGC	5340
QY	1763	ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr	1782
Db	5341	CGTCATGCCACCTTTCGGAACCTTGGCATGGCCCTTCCTAACCCCTTCGAGTCTCCACA	5400
QY	1783	GLYAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr	1802
Db	5401	GGTGCATTTGAATGGCATTTATGAAGACACCCCTCCGGACTGTGACCAAGAGTCCACC	5460
QY	1803	CysTrpAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe	1822
Db	5461	TGCTACAAACACGGTCATCTCGCCTATCTACTTTGTGTCTTCGTGCTGACGGCCAGTTTC	5520
QY	1823	ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu	1842
Db	5521	GTGCTAGTCAACGTCGTGATTCGCCGTGTCGTATGAAGACCTGAGAGGACCAAGAGAG	5580
QY	1843	AlaLysGluGluAlaGluLeuGluAlaGluLeuGluGluMetLysThrLeuSerPro	1862
Db	5581	GCCAAGAGAGAGGCCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCTCAGCCCC	5640
QY	1863	GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer	1882
Db	5641	CAGCCCCACTCGCCACTGGGCGAGCCCCCTTCTCTGGCCTGGGGTCGAGGGCCCCGACAGC	5700
QY	1883	ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis	1902
Db	5701	CCCGACAGCCCCAAGCCTGGGGCTCTGCACCAAGCGGCCCAAGCGAGATCAGCTCCAC	5760
QY	1903	PheSerLeuGluHisProThr-----	1909
Db	5761	TTTTCCCTGGAGCACCCCAAGACAGCAGCTGTTGACACCATATCCCTGCTGATCCAG	5820
QY	1909	-----	1909
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QY	1909	-----	1909
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Db	6001	ACGAGTACTCTTTGCTGATGACATGCACACACTTACTTAGTGCCCTGGAGAGCAAT	6060
QY	1910	MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly	1929
Db	6061	ATGCAGCCCCACCCACGAGCTGCCAGACCACTTACTGACTGTGCGGAAGTCTGGG	6120
QY	1930	ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla	1949
Db	6121	GTCAGCGGAACGCACTCTTCCCAATGACAGCTACATGTGTCCGCAATGGAGCACTGCC	6180
QY	1950	GluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeu	1969
Db	6181	GAGGGGCTCTGGGACACAGGGGCTGGGGGCTCCCAAGCTCAGTCAAGCTCCGCTCTTG	6240
QY	1970	SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro	1989
Db	6241	TCCGTTCACTCCAGCCAGACAGATTACAGCTACATCTGCAGCTTCCCAAAGATGCACCT	6300
QY	1990	HisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProPro	2009

Db 6301 CATCTGCTCCAGCCCCACAGCGCCCCAACCTGGGGCACCATCCCCAAACTGCCCCACCA 6360
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Db 6361 GGACGCTCCCTTTGGCTCAGAGGCCACTCAGCGCCAGGACGACATTAAGACTGACTCC 6420
QY 2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049
Db 6421 TTGGACGTTACAGGCTCGGGCAGCCGGGAAGACTGCTGGCAGAGAGTGAGTGGCCCTCC 6480
QY 2050 ProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHis 2069
Db 6481 CCGCCCTGGCCCGGCTACTCTTCTGGGGCCAGTCAAGTACCCAGGCACAGCAGCAC 6540
QY 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089
Db 6541 TCCCGCAGCCACAGCAAGATCTCCAAGCACATGACCCCGCAGCCCTTGGCCACGAGCCCA 6600
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Db 6901 CGGCCCCAAGAAAAACTACGCCGCTAGTATCAACATAGACCCCCCGAGAGCCAAAGT 6960
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Db 6961 CCTCGGACCCCGCCAGCCCTGTATCTGCTCCGAGAGAGGCTCCGTCCAGCGACTCC 7020
QY 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLysLys 2249
Db 7021 AAGGATCCCTTGCCCTTGCCCTGCCCCCTGACAGCATGCTGCTCGCCCTCCCAAGAAA 7080
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; Sequence 15, Application US/10757262
; Publication No. US20040197825A1
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; APPLICANT: Karichehi, Venkateswarlu
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
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; PRIOR APPLICATION NUMBER: US 60/471,614
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; PRIOR APPLICATION NUMBER: US 60/491,156
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; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 7648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(7134)
US-10-757-262-15
Alignment Scores:
Pred. No.: 0 Length: 7648
Score: 11815.50 Matches: 2264
Percent Similarity: 95.29% Conservative: 1
Best Local Similarity: 95.25% Mismatches: 1
Query Match: 99.26% Indels: 111
DB: 19 Gaps: 2
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Db 61 CGGCTCAACGACTGTGCGGGGCGGGGGCCGGCCGGGGGGGTACAGAAAAGGAC 120
QY 41 ProGlySerAlaAspSerGlyAlaGlyGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 121 CCGGGCAGCGCGACTCCGAGGCGGAGGGCTGCCGTACCCGGGCTGGCCCGGTGTT 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 181 TTCTTCTACTTGAGCAGACAGACAGCCGCCGAGAGCTGTGTCTCCGACGCTGTAC 240
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 241 CCCTGTTTGAAGGCATCAGCATGTGTGTCATCTTCAACTGCGTGACCTGGGCATG 300
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
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QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 361 GATGACTTCATCTTGCCTTCTTTCGCGTGAAGATGTGTGAAGATGTGTGCTTGGGC 420
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160

Db 421 ATCTTTGGGAAAAAGTTACTTGGGAGACACTTGGAACCGGCTTGACTTTTTCATCGTC 480
QY 161 ILeaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 481 ATCGCAGGGATGCTGGAGTACTCGCTGGAACCTGCAGAACGTCAAGTCTTCAGCTGTCAAG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCCAAGCATGCCATCCTT 600
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 601 GTCAAGTTGCTGCTGGATAAGCTGCCCATGCTGGGCAACGTCTGCTGCTGCTTCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 661 GTCTTCTTCAATCTTCGGCATCGTGGCGCTCCAGCTGTGGGCAAGGCTGCTTCGGAACCGA 720
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
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QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 781 ACAGAGAACGAGATGAGAGACCCCTTCATCTGCTCCCAAGCACAAGAGAACGGCATGCGG 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyGlyProProCysGlyLeu 300
Db 841 TCCTGCAGAACGCTGCCCAAGCTGCCGGGGGACGGGGGGGTGGCCCACTTGCGGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
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QY 321 ThrAsnCysSerAlaGlyGlyHisAsnProPheGlyAlaIleAsnPheAspAsnIle 340
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QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlnGlyTrpValAspIleMet 360
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QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuIleIle 380
Db 1081 TACTTTGTGATGATGCTCATTTCTTCTACATTTTCATCTTCACTCCTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGATTGCCACGCAAGTTCTCAGAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluArgValArgPheLeuSerAsnAla 420
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QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGlnGluLeuLeuTyrLeu 440
Db 1261 AGCACCTGGCTAGCTTCTCTGAGCCCGGACGCTGCTATGAGAGAGCTGCTCAAGTACCTG 1320
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1321 GTGTACATCCTTCGTAAGCAGCCCGAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
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QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
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QY 521 ILeGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
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QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1801 ACGCTGAAGGAGAGGCACTAGTAGAGGTGGTGCACAGCTTGCGGCCCAACCTCAC 1860
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 1861 AGCTTCAACATCCACCCGGGCCCTTACAGCTTCATGCACAAGCTGTGGAAGACACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 1921 ACAGGTGCTGCCAAAGCTTGTCAAGATCTCAGCCCTTGCTTGAAAGCAGACAGTGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 1981 GCCTGTGCTCAGACAGCTGCCCTTACTGTGCCCCGGGCGGAGGGAAGGTGAGCTC 2040
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QY 1321 PheLeuAlaGluMetThrValLysValAlaAlaLeuGlyTrpCysPheGlyGlnAla 1340
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Db 3961 TTTCTGCTGAATGACAGTGAAGGTGGTGGCACTGGGCTGTGCTTCGGGGAGCAGCGG 4020
QY 1341 TyrrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
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Db 4021 TACCTCGGAGCAGTTGGAACGTGTGACAGCGGCTGTGTGCTCATCTCCGTCATCGAC 4080
QY 1361 ILeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
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Db 4081 ATTCTGTGTCCATGTGCTCTGACAGCGGCACCAAGATCTGGGCATGTGAGGGTGTG 4140
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLeu 1400
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Db 4141 CGGCTGCTGGGACCCCTGCGCCCGCTCAGGGTGATGATCAGCGCGGCGCAGGCGTGAAGCTG 4200
QY 1401 ValValGluThrLeuMetSerSerSerLeuLysProIleGlyAsnIleValValIleCysCys 1420
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Db 4201 GTGTGGAGACGCTGATGTCTCTACTGAAACCCTATCGGCAACATTGTAGTATCTGTCTGT 4260
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
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Db 4261 GCCTTCTTATCATATTTTCGCATCTTGGGGGTGCAGCTTTCAAAGGAAGTTCGTG 4320
QY 1441 CysGlnGlyLysPThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTyrr 1460
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Db 4321 TGCCAGGGCGAGATACAGAAACATCACCAATAATCGACTGTGCCAGGCCAGTTTAC 4380
QY 1461 ArgTrpValArgHisLysTyrrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
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Db 4381 CGGTGGTCCGGCAAGTACAACTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTTC 4440
QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyrrAspGlyLeuAspAlaValGly 1500
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Db 4441 GTTTTGCCCTCCAAAGATGTTGGGTGACATCATGTACGATGGGCTGATGCTGTGGGC 4500
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrrPheIleSerPhe 1520
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Db 4501 GTGACACGAGCCCATCATGAACCAACCCTGATGCTGCTGTACTTCATCTCGTTTC 4560
QY 1521 IleuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPhe 1540
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Db 4561 CTGCTCATTTGCGCCTTCTTGTCTGCAACATGTTGTGGGTGTGGTGAGAACTTC 4620
QY 1541 HisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluLysArgLeu 1560
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Db 4621 CACAAGTGTGGCAGCACCAAGAGAGAGAGAGGCCCGGGCGGGAAGAGAACGCCCTA 4680
QY 1561 ArgArgLeuGluLysLysArgArg----- 1568
|||||
Db 4681 CGAAGACTGGAAAAAAGAGAGGAATCTAATGCTGGAAGATGTAATTGCTTCCGGCAGC 4740
QY 1569 -----LysAlaGlnCysLysProTyrrTyrrSerAspTyrrSerArgPhe 1582
|||||
Db 4741 TCAGCCAGCGCTGCGTCAGAAAGCCAGTGCAAACCTTACTACTCCGACTACTCCCGCTTC 4800
QY 1583 ArgLeuLeuValHisHisLysLeuCysThrSerHisTyrrLeuAspLeuPheIleThrGlyVal 1602
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Db 4801 CGGCTCCTCGTCCACCACTTGTGCAACGACCACCTACTGGA CCTCTTCATCACAGGTGTC 4860

Qy 1603 ILeGIyleuAnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAsp 1622

Db 4861 ATCGGGCTGAACGTGTGCACCATGGCATTGAGACACTACGACAGCCCGAGATTCTGGAT 4920

Qy 1623 GluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPhe 1642

Db 4921 GAGGCTCTGAAGATCTGCACACTACATCTTCACTGTCACTTGTCTTGAGTCAGTTTTC 4980

Qy 1643 LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu 1662

Db 4981 AAACCTGTGGCTTTGGTTTCCGTGGTTCTTCCAGGACAGGTGGAACCAAGCTGGACCTG 5040

Qy 1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSer 1682

Db 5041 GCCATTGTGCTGCTGCTCCATCATGGGCATCAGCTGAGGAAATCGAGTCAACGCCCTCG 5100

Qy 1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702

Db 5101 CTGCCCATCAACCCACCATCATCCGCATCATGAGGTGCTGCGCATTGCCGAGTGCTG 5160

Qy 1703 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722

Db 5161 AAGTCGTGAAGATGGCTGTGGGCATCGGGCGCTGCTGACACGGTGATGACGGCCTG 5220

Qy 1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1742

Db 5221 CCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTGTTGTTTTCATCTTGGCAGCTCTG 5280

Qy 1743 GlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGly 1762

Db 5281 GCGGTGAGCTCTTTGGAGACCTGGAGTGTGACGAGACACACCCCTGTAGGGGCTGGGC 5340

Qy 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782

Db 5341 CGTCATGCCACCTTTCGGAACTTGGCATGGCCTTCTTAACCTCTTCCGAGTCTCCACA 5400

Qy 1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGluSerThr 1802

Db 5401 GGTGACAATTGAATGGCATTATGAAGACACCCCTCCGGACTGTGACCAGAGTCCACC 5460

Qy 1803 CysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnPhe 1822

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Qy 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGlu 1842

Db 5521 GTGCTAGTCAACGTGGTGATCGCCGTCTGATGAAGCACCTGGAGGAGAGCAACAGAG 5580

Qy 1843 AlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeuSerPro 1862

Db 5581 GCCAAGGAGAGGCCGAGCTAGAGCTGAGCTGAGCTGAGATGAAGACCCCTCAGCCCC 5640

Qy 1863 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSer 1882

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Qy 1909 ----- 1909

Db 5941 ATGAGGCTCTGTCTCTGACGTCAAGATTGTGTCTGAACCGCTCCTGTCTAGCTCTG 6000

Qy 1909 ----- 1909

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Db 6061 ATGACGCCCCACCCACGAGCTGCCAGAGCACTTACTGACTGTGCGGAAGTCTGGG 6120

Qy 1930 ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThraAla 1949

Db 6121 GTCAAGCCGAACGCACTCTGCCCCAATGACAGCTACATGTGCGCATGGGAGCACTGCC 6180

Qy 1950 GluGlyProLeuGlyHisArgGlyTrpGlyLeuProLysAlaGlnSerGlySerValLeu 1969

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Qy 1970 SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAlaPro 1989

Db 6241 TCCGTTCACTCCACGCCAGCATATCACACTATCTTGCAAGCTTCCCAAGAATGCACCT 6300

Qy 1990 HisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLeuProProPro 2009

Db 6301 CATCTGCTCCAGCCCAAGCGCCCAACCTGGGGCACCATCCCAACTGCCCCACCA 6360

Qy 2010 GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSer 2029

Db 6361 GGACGCTCCCTTTGGCTCAGAGCGCACTCAGGGCGCCAGGACAATPAGAACTGACTCC 6420

Qy 2030 LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer 2049

Db 6421 TTGAGCTTCAGGCTCTGGGACGCCGGAAGACTGTGCGAGAGGTGGGCCCTCC 6480

Qy 2050 ProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHis 2069

Db 6481 CCGCCCCCTGGCCCGGCTACTCTTCTGGGGCAGTCAAGTACCAGGACAGCAGCAC 6540

Qy 2070 SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro 2089

Db 6541 TCCCGACCCACAGCAAGATCTCCAAGCACATGACCCCGCAGCCCTTGGCCAGGCCCA 6600

Qy 2090 GluProAsnTrpGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu 2109

Db 6601 GAACCCAACCTGGGCAAGGCCCTCCAGAGACCAGAAAGCAGCTTAGAGTTGACACGGAG 6660

Qy 2110 LeuSerTrpIleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerPro 2129

Db 6661 CTGAGCTGGAATTCAGAGAACCTCTGCCCCCTGGCGGCCAGAGAGAGCCCATCCCA 6720

Qy 2130 ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer 2149

Db 6721 CGGACCTGAAGAAGTGTCTACAGCGTGGAGGGCCAGAGCTGCCAGCGCCCTACGTCC 6780

Qy 2150 TrpLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln 2169

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Qy 2170 ProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySer 2189

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Db 6901 CGGCCCAAGAAAAAAGTCAAGCCGCTAGTATCACCATAGACCCCCCGAGAGCCAAGGT 6960

Qy 2210 ProArgThrProProSerProGlyIleCysLeuArgArgArgAlaProSerSerAspSer 2229

Db 6961 CCTGGACCCCGCCAGCCCTGTGTATCTGCTCCGAGAGAGGCTCCGTTCCAGCACTCC 7020

QY 2230 LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProIysLeu 2249
Db 7021 AAGATCCCTTGCTGCTGCCCCCTGACAGCATGGCTGCCTGCCCTCCCAAGAAA 7080
QY 2250 AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7081 GATGTGCTGAGTCTCTCCGGTTATCCTTGACCCAGACAGACTGGAACCC 7131

RESULT 3

US-10-756-149-31
; Sequence 31, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 31
; LENGTH: 7825
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-756-149-31

Alignment Scores:

Pred. No.: 0 Length: 7825
Score: 11815.50 Matches: 2264
Percent Similarity: 95.29% Conservative: 1
Best Local Similarity: 95.25% Mismatches: 1
Query Match: 99.26% Indels: 111
DB: 22 Gaps: 2

US-09-611-257A-37 (1-2266) x US-10-756-149-31 (1-7825)

QY 1 MetAspGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 373 ATGACGAGAGAGAGATGAGCGGGCCGCGAGAGTCCGGACAGACCCCGAGCTTCATG 432
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyAlaArgProGlyProGlySerAlaGluLysAsp 40
Db 433 CGGCTCAACGACCTGTCGGGGGGCCGGGGCCGGGGCCGGGGTCAAGAAAAGAC 492
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 493 CCGGGCAGCGCGGACTCCAGAGCGGAGGGGTGCGTACCAGCGCGTCCCGGTGTT 552
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuAlaThrValCysAsn 80
Db 553 TTCTTCTACTTGAGCCAGGACAGCCGCCCGGAGCTGTGTCTCCGACGGTCTGTAA 612
QY 81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 613 CCTGTGTTGAGCGCATCAGCATGTGTGTCATCTTCTCAACTGCGTGAACCTGGGCA 672
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 673 TTCGGGCATGCGAGACATCGCTGTGACTCCAGCGCTGCCGATCTGCAAGCCCTTT 732
QY 121 AspAspPheIlePheAlaPhePheAlaValAlaGluMetValValLysMetValAlaLeuGly 140
Db 733 GATGACTTCATCTTTCCTTCTTGGCCGTGAGATGGTGAAGATGGTGGCCTTGGGC 792
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 793 ATCTTTGGGAAAAAGTGTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATCGTC 852
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 853 ATCGCAGGGATGCTGAGTACTCGCTGAGACCTGCAACGTCAGCTTTCAGCTGTCAAG 912

QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 913 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGGTGCCAGCATGCGCATCTT 972
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 973 GTACGTTGCTGTGATACGCTGCCCATGTCTGGGCAACGTCTGTGCTGTCTGCTTC 1032
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 1033 GTCTTCTTCACTTCGCGCATCGTCGGCGCTCCAGCTGTGGGCAAGGCTGCTTCCGAACCGA 1092
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 1093 TGCTTCTTACTGAGAAATTTCAGCTCCCTCCCTGAGCGGTGAACCTGAGCGCTATTACCA 1152
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 1153 ACAGAGAACGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAAGAACGCGATGCCG 1212
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 1213 TCCTGCAGAACGTGCCACCGCTGCGGGGAGCGGGGCGGTGCCACCTTGGGCTCTG 1272
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 1273 GACTATGAGGCTTACAACAGCTCCAGCAACACCACTGTGTCAACTGGAACCACTACTAC 1332
QY 321 ThrAsnCysSerAlaGlyGlyIleAsnProPheIleGlyAlaIleAsnPheAspAsnIle 340
Db 1333 ACCAAGCTGCTCAGCGGGGAGCAACCCCTTCAAGGGCGCCATCACTTGACACACTT 1392
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1393 GGCTATGCTTGATGCCCATCTTCCAGGTTCATCAGCTGAGAGGGCTGGTGCACATCATG 1452
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
Db 1453 TACTTTGTATGATGCTCATCTCTTCTTCAATTTCATTACTTCACTCTCTCATCATC 1512
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1513 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGATGTCACGCACTTCACAG 1572
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1573 ACCAAGCAGCGGGAAGCCAGCTGATGCGGAGAGCAGCGGTGCGGTCTCCACAGCC 1632
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1633 AGCACCTGGCTAAGTCTTCTGAGCCCGGACAGCTGCTATGAGAGAGCTGCTCAAGTACTG 1692
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIleGlyVal 460
Db 1693 GTGTACATCTTCTGTAAGCAGCCCGCAGCTGGCTCAGGTCTCTCGGGCAGCAGTGTG 1752
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1753 CGGGTGGGCTGTCAAGCAGCCAGCAACCTCGGGGGCCAGAGAACCCAGCCAGCAGC 1812
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1813 AGCTGCTCTCGCTCCACCGCGCTATCCGTCCACCACTGTGTGCAACCAACCAACCA 1872
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1873 CATCACCACTTACCACTGCGGCAATGGAGCGCTCAGGGCCCCCGGGCAGCCGGAG 1932
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 1933 ATCCAGACAGGAGATGCCAATGGGTCGCGCGGCTCATGTGTGCCAACCACTTCAGCGCT 1992

QY	541	AlAlauSerGIyAlaProProGIyGIyAlaGluSerValHisSerPheTyrHisAlaAsp	560
Db	1993	GGCCTCTCCGGGGCCCCCTGTGGCGAGAGTCTGTGCACAGCTTCTACCAATCCGAC	2052
QY	561	CysHisLeuGIuProValArgCysGlnAlaProProProArgSerProSerGIuAlaSer	580
Db	2053	TGCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTGAGCATCC	2112
QY	581	GIyArgThrValGIySerGIyLysValTyrProThrValHisThrSerProProGIu	600
Db	2113	GGCAGGACTGTGGGCGAGGGGAAGTGTATCCACCGTGCACACCAACCCCTCCACGGAG	2172
QY	601	ThrLeuLysGIuLysAlaLeuValGIuValAlaAlaSerSerGIyProProThrLeuThr	620
Db	2173	ACGCTGAAGAGAGAGCACTAGTAGAGGTGGCTGCCAGCTCTGGCCCCCAACCTCACC	2232
QY	621	SerLeuAsnIleProProGIyProTyrSerSerMetHisLysLeuLeuGIuThrGlnSer	640
Db	2233	AGCCTCAACATCCACCCGGGGCCCTACAGCTCCATGCACAAGCTGTGGAGACACAGAGT	2292
QY	641	ThrGIyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGIy	660
Db	2293	ACAGGTGCCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTGAAAGCAGACAGTGA	2352
QY	661	AlaCysGIyProAspSerCysProTyrCysAlaArgAlaGIyAlaGIyGIuValGIuLeu	680
Db	2353	GCCTGTGTCCAGACAGCTGCCCTACTGTGCCGGGCCGGGGCAGGGAGGTGAGCTC	2412
QY	681	AlaAspArgGIuMetProAspSerAspSerGIuAlaValTyrGIuPheThrGlnAspAla	700
Db	2413	GCCGACCGTGAATGCTGACTCAGACAGCGAGCGAGTTATGAGTTCACACAGATGCC	2472
QY	701	GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGIyProAspAla	720
Db	2473	CAGCACAGCGACCTCCGGGACCCCCACAGCCGGCGCAACGAGCCTGGGCCCAGATGCA	2532
QY	721	GluProSerSerValLeuAlaPheTyrPargLeuIleCysAspThrPheArgLysIleVal	740
Db	2533	GAGCCACAGCTCTGTGCTGGCCTTCTGAGGCTAATCTGTGACACCTTCCGAAGATTGTG	2592
QY	741	AspSerLysTyrPheGIyArgGIyIleMetIleAlaIleLeuValAsnThrLeuSerMet	760
Db	2593	GACAGCAAGTACTTGGCCGGGGAATCATGATCGCCATCTCTGTCAACACACTCAGCATG	2652
QY	761	GIyIleGIuTyrHisGIuGlnProGIuGIuLeuThrAsnAlaLeuGIuIleSerAsnIle	780
Db	2653	GGCATCGAATACCAAGCAGCAGCCGAGGAGCTTACCAAGCCCTAGAATCAGCAACATC	2712
QY	781	ValPheThrSerLeuPheAlaIleuGIuMetLeuLeuLysLeuLeuValTyrGIyProPhe	800
Db	2713	GTCTTCACCAAGCCTCTTGGCCCTGAGATGCTGCTGAAGCTGTGTATGTCTCCCTT	2772
QY	801	GIyTyrIleLysAsnProTyrAsnIlePheAspGIyValIleValValIleSerValTrp	820
Db	2773	GGCTACATCAAGAATCCCTACAACATCTTCGATGGTGTCTATGTGTGCATCAGCGTGG	2832
QY	821	GluIleValGIyGlnGlnGIyGIyLysLeuSerValLeuArgThrPheArgLeuMetArg	840
Db	2833	GAGATCGTGGCGCAGCGGGGGCGGCGCTGTGGTGTGGGACCTTCCGCTGATGCCGT	2892
QY	841	ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys	860
Db	2893	GTGCTGAAGCTGTGCGCTTCTGCGCGCTGCAGCGGCAGCTGTGTGTCTATGAAG	2952
QY	861	ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSer	880
Db	2953	ACCATGGAACAACGTGGCCACTTCTGCATGCTGCTTATGCTCTTCATCTTCATCTTACG	3012
QY	881	IleLeuGIyMetHisLeuPheGIyCysLysPheAlaSerGIuArgAspGIyAspThrLeu	900
Db	3013	ATCCTGGGCATGATCTCTTCCGCTGCAGATTGCTCTGAGCGGGATGGGGACACCTTG	3072
QY	901	ProAspArgLysAsnPheAspSerLeuLeuTyrPalaIleValThrValPheGlnIleLeu	920

Db	3073	CCAGACCGAAGATTGTGACTCCTTGCTCGGGCCATCGTCACTGCTTTCAGATCCTG	3132
QY	921	ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla	940
Db	3133	ACCCAGGAGGACTGGAAACAAGTCCCTCAACATGGTATGGCCCTCCACGTCGTCCTGGCG	3192
QY	941	AlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal	960
Db	3193	GCCCTTATTTCATTGCCCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTGCTGTC	3252
QY	961	AlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGly	980
Db	3253	GCCATTCTGTGGAGGGCTTCCAGGCGGAGAAATCAGCAACGGGAGATGCCAAGTCCGAA	3312
QY	981	GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGlu	1000
Db	3313	CAGTTAAGCTGATTTCAGCTGCTGTGCACTCCAGGGGGAGATGCCAACAAGTCCGAA	3372
QY	1001	SerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLeu	1020
Db	3373	TCAGAGCCCGATTCTTCTCACCCAGCCTGATGTGATGGGACAGGAAGAGTGTG	3432
QY	1021	AlaLeuValSerLeuGlyGluHisProGlnLeuArgLysSerLeuLeuProLeuIle	1040
Db	3433	GCCTTGGTGTCCCTGGAGAGCACCCGAGCTGCCGAAGAGCCTGTGCCGCTTCATC	3492
QY	1041	IleHisThrAlaAlaThrPrometSerLeuProLysSerThrSerThrGlyLeuGlyGlu	1060
Db	3493	ATCCACACGGCGCCACACCCATGTGCTGCCCAAGACACCAAGCACCGGGCTGGCGGAG	3552
QY	1061	AlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla	1080
Db	3553	GCGCTGGGCGCTGCGTCCGCCGACACAGCGGGTCCGACAGAGCCTGGGGCGGCC	3612
QY	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
Db	3613	CACGAGATGAGTCAACGCCAGCGCCCGCACTCTCCGACAGCCCTGGAGCGCTGCA	3672
QY	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120
Db	3673	AGCAGCTGGACCAAGCAGCGCGCTCCAGCCGGAACAAGCTCGGCCGTGCAACCCAGCTGAAG	3732
QY	1121	ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlyGlnGlnSerGln	1140
Db	3733	CGGAGAAGCCCAAGTGGAGAGCGCGCTCCCTGTGTCGGAGAGAAGCCAGAGACCAG	3792
QY	1141	AspGluGluGluSerSerGluGluGluArgAlaSerProAlaGlySerAspHisArgHis	1160
Db	3793	GATGAAGAGGAGACTCAGAAAGAGAGCGGCCAGCCCTCGGGCAGTGACCATCGCCAC	3852
QY	1161	ArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVal	1180
Db	3853	AGGGGCTCCCTGGAGCGGAGGCCAAGAGTTCCTTGAACCTGCCAGACACTGCAGGTG	3912
QY	1181	ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAsn	1200
Db	3913	CCAGGGCTGCATCGCACTGCCAGTGGCCGAGGTCTGCTTCTGAGCACCAAGACTGCAAT	3972
QY	1201	GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp	1220
Db	3973	GGCAAGTCGGCTTCAAGGGCGCCTGGCCCGGCCCTGGCTGATGACCCCACTGGAT	4032
QY	1221	GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle	1240
Db	4033	GGGATGACGCCGATGACGAGGGCAACCTGACCAAGGGGAACGGGTCCGCGCTGATC	4092
QY	1241	ArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePro	1260
Db	4093	CGAGCCCGACTCCCTGCTGCTGCTCGAGCGAGACTCCTGTTGACGCTACATCTTCCCT	4152
QY	1261	ProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHis	1280

Db 4153 CCTCAGTCCAGGTTCCGGCTCTCTGTGTACCCGGATCATCACCCACAAGATGTTGCACCAC 4212
QY 1281 ValValLeuValIleIlePheLeuAsnCyseIleThrIleAlaMetGluArgProLysIle 1300
Db 4213 GTGTCTCTTGTATCATCTTCCTTAACGTGCATCCATCGCCATGAGCGCCCCAAATTT 4272
QY 1301 AspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyriIlePheThrAlaVal 1320
Db 4273 GACCCCCACAGCGCTGAACGCATCTTCCTGACCCCTCCAATTACATCTTCACCCGACATC 4332
QY 1321 PheLeuAlaGluMetThrValIysValAlaLeuGlyTyTrpCysPheGlyGlyAlaIle 1340
Db 4333 TTTCTGGCTGAATGACAGTGAAGTGGTGGCATTGGCTGCTTCGGGAGCAGCGCG 4392
QY 1341 TyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAsp 1360
Db 4393 TACCTGCGGAGCAGTTGGAAAGCTGTGACCGGGCTGTGGTCTCATCTCCGTCATCGAC 4452
QY 1361 IleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLeu 1380
Db 4453 ATTCTGGTGTCCATGGTCTCTGACAGCGGCGCACCAAGATCCTGGGCATGCTGAGGGTGCTG 4512
QY 1381 ArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlyLeuLysLeu 1400
Db 4513 CGGCTGCTGCGGACCCCTGCGCCCGCTCAGGGTGATCAGCCGGCGCAGGGGCTGAAGCTG 4572
QY 1401 ValValGlyThrLeuMetSerSerLeuLysProIleGlyAsnIleValIleCysCys 1420
Db 4573 GTGTGGAGAGCGCTGATGTCTCTACGTGAACCCATCGGCAACATGTGATCATCTGCTGT 4632
QY 1421 AlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVal 1440
Db 4633 GCCTTCTTCATCATTTTCGGCATCTTGGGGGGTGCAGCTCTTCAAAGGGAAGTTTTCGTG 4692
QY 1441 CysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
Db 4693 TGCCAGGGCGAGATACGAGAAACATCACCAATTAATCGGACTGTGCCGAGGCCAGTTAC 4752
QY 1461 ArgTrpValArgHisLysTyTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPhe 1480
Db 4753 CGGTGGGTCCGGCACAGTACAACCTTTGACAACTTGCCAGGCCCTGATGTCCCTGTTC 4812
QY 1481 ValLeuAlaSerLysAspGlyTrpValAspIleMetTyTrpAspGlyLeuAspAlaValGly 1500
Db 4813 GTTTTGGCCTCCAAGATGGTGGGTGAGCATCATGTACGATGGGCTGATGCTGTGGGC 4872
QY 1501 ValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyPheIleSerPhe 1520
Db 4873 GTGGAACCAAGACCCCATCATGAACACACACCCCTGGATGCTGTACTTCATCTCGTTC 4932
QY 1521 LeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPhe 1540
Db 4933 CTGCTCATTTGTGGCTTTTGTCTGTAAACATGTTGTGGGTGTGGTGGAGAACTTC 4992
QY 1541 HisLysCysArgGlnHisGlnGlyGlyGluAlaArgArgArgGlyGlyLysArgLeu 1560
Db 4993 CACAAGTGTCCGACAGCACGAGAGAGAGAGAGCGCGCGGCGGAGAGAAAGCGCTTA 5052
QY 1561 ArgArgLeuGlyLysLysArgArg----- 1568
Db 5053 CGAAGACTGGAGAAAAAGAGAAGAAATCTAATGCTGGACGATGTAATTGCTTCCGGCAGC 5112
QY 1569 -----LysAlaGlnCysLysProTyTrpSerAspTyTrpSerArgPhe 1582
Db 5113 TCAGCCAGCGCTGCGTCAAGAACCCAGTGCAAACTTACTACTCCGACTACTCCGCTTC 5172
QY 1583 ArgLeuLeuValHisHisLeuCystrSerHisTyTrpLeuAspLeuPheIleThrGlyVal 1602
Db 5173 CCGGCTCTCGTCCACCACTTGTGCAACCAAGCACTTACCTGGAACCTCTTCAATCACAGGTGC 5232
QY 1603 IleGlyLeuAsnValValThrMetAlaMetGluHisTyGlnGlnProGlnIleLeuAsp 1622
Db 5233 ATCGGCTGAACGTGTGTACCATGGCCATGGAGCACTACAGCAGCCCGCAGATTCTGGAT 5292

QY 1623 GluAlaLeuLysIleCysAsnTyriIlePheThrValIlePheValLeuGluSerValPhe 1642
Db 5293 GAGGCTCTGAAGATGCAACTACATCTTCACTGTCAATCTTTGTCTTGAGTCACTTTTC 5352
QY 1643 LysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLeuAspLeu 1662
Db 5353 AAACCTGTGGCCTTTGGTTCCGTCGGTCTCTTCAGAGCAGGTGAACCAAGCTGACCTG 5412
QY 1663 AlaIleValLeuLeuSerIleMetGlyIleThrLeuGlyLysIleGlyValAsnAlaSer 1682
Db 5413 GCCATTGTGCTGCTGTCCATCATGGGCATCACGCTGAGGAATCGAGTCAACGCTCG 5472
QY 1683 LeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeu 1702
Db 5473 CTGCCCATCAACCCCAACCATCATCCGCATCATGAGGGTGTGGCATTTGCCAGTGTG 5532
QY 1703 LysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeu 1722
Db 5533 AAGCTGTGAAGATGGCTGTGGGCATGCGGGCGCTGCTGACACCGGTGATGCAGGCCCTG 5592
QY 1723 ProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaLeu 1742
Db 5593 CCCAGGTGGGAACCTGGGACTTCTTCACTGTGTGTTGTTTTCATCTTTGCAGCTCTG 5652
QY 1743 GlyValGlyLeuPheGlyAspLeuGlyCysAspGlyThrHisProCysGlyGlyLeuGly 1762
Db 5653 GGGGTGAGCTCTTTGGAGACCTGAGCTGTGACGAGACACACCCCTGTGAGGGCGCTGGC 5712
QY 1763 ArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThr 1782
Db 5713 CGTCATGCCACCTTTTCGGAACCTTGGCATGGCCTTCTTAACCTCTTCCGAGTCTCCACA 5772
QY 1783 GlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlySerThr 1802
Db 5773 GGTGACAATTGGAATGGCAATTATGAGGACACCCCTCCGGACTGTGAACAGAGTCCACC 5832
QY 1803 CysTyTrpAsnThrValIleSerProIleTyTrpPheValSerPheValLeuThrAlaGlnPhe 1822
Db 5833 TGCTACAACACCGGTCACTCGCCCTAATTACTTTGTGTCTTCGTGTGACGCGCCAGTTTC 5892
QY 1823 ValLeuValAsnValValIleAlaValLeuMetLysHisLeuGlyGluSerAsnLysGly 1842
Db 5893 GTGCTAGTCAACGTGGTGTATGCGGTGTGATGAAGCACTGGAGAGAGACAAACAAGAG 5952
QY 1843 AlaLysGlyGluAlaGlyLeuGlyAlaGlyLeuGlyLeuGlyMetLysThrLeuSerPro 1862
Db 5953 GCCAAGGAGGAGGCCGAGCTAGAGGCTGAGCTGGAGCTGGAGATGAAGACCTCAGACCCC 6012
QY 1863 GlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGlyGlyProAspSer 1882
Db 6013 CAGCCCCACTCGCCACTGGGCAGCCCCCTTCTCTGGCCTGGGGTTCAGAGGGCCCCGACAGC 6072
QY 1883 ProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis 1902
Db 6073 CCCGACAGCCCCAAGCCTGGGGCTGTGACCCAGCGGCCAGGAGATCAGCTCCAC 6132
QY 1903 PheSerLeuGluHisProThr----- 1909
Db 6133 TTTTCCCTGAGCACCCCAAGCAGCAGCAGCTGTTTGACACCATATCCCTGTGATCCAG 6192
QY 1909 ----- 1909
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QY	1909	-----	1909
DB	6373	ACGATGACTTTTGCCTGATGACATGCACACACTCTTAAGTGGCCCTGGAGACAAT	6432
QY	1910	MetGlnProHisProThrGluLeuProGlyProAspLeuLeuThrValArgIysSerGly	1929
DB	6433	ATGCAGCCCCACCCACGAGCTGCCAGACCACTTAAGTGTGCGGAAGTCTGGG	6492
QY	1930	ValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAla	1949
DB	6493	GTCAGCCGAACGCACTCTCTGCCAATGACAGCTACATGTGTCCGATGGAGCACTGCC	6552
QY	1950	GluGlyProLeuGlyHisArgGlyTyrGlyLeuProIysAlaGlnSerGlySerValLeu	1969
DB	6553	GAGGGCCCTGGGACACAGGGGCTGGGGCTCCCAAAGCTCAGTCAGGCTCCGCTTG	6612
QY	1970	SerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProIysAspAlaPro	1989
DB	6613	TCCGTTCACTCCACGACAGACAGATACAGTACATCCTGCAGCTTCCCAAAGATGCACCT	6672
QY	1990	HisLeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProIysLeuProProPro	2009
DB	6673	CATCTGCTCCAGCCCCACAGCGGCCCACTGGGGCACCATCCCCAAACTGCCCCACCA	6732
QY	2010	GlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAspSer	2029
DB	6733	GGACGCTCCCTTTGGCTCAGAGGCCACTCAGGGCCAGGCAACAATAAGACTGACTCC	6792
QY	2030	LeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSer	2049
DB	6793	TTGGACGTTCAAGGCTCTGGGCAGCCGGGAAGACCTGCTGGCAGAGGTGAGTGGGCCCTCC	6852
QY	2050	ProProLeuAlaArgAlaTyrSerPheTyrGlyGlnSerSerThrGlnAlaGlnGlnHis	2069
DB	6853	CCGCCCCCTGGCCCGGCTACTCTTTCTGGGGCCAAGTCAAGTACCAGGCACAGCAACAC	6912
QY	2070	SerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGlyPro	2089
DB	6913	TCCCGCAGCCACAGCAAGATCTCAAGACATGACCCCGCAGCCCTTGCCCAAGGCCCA	6972
QY	2090	GluProAsnTyrGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGlu	2109
DB	6973	GAACCCCACTGGGGCAAGGGCCCTCAGAGACCAGAAGAGCTTAGAGTTGGACACGGAG	7032
QY	2110	LeuSerTyrIleSerGlyAspLeuLeuProProGlyGlyGlnGluGluProProSerPro	2129
DB	7033	CTGAGCTGGAATTTCAAGAGACCTCTCTCCCTCGCGGCCACGAGAGCCCCCATCCCA	7092
QY	2130	ArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSer	2149
DB	7093	CGGGACCTGAAGAAGTCTACAGCGGTGGAGGCCACAGAGCTGCCAGCGCGCTTACGTCC	7152
QY	2150	TyrLeuAspGluGlnArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGln	2169
DB	7153	TGGCTGATGAGCAGAGAGACACTTATCGCCGTACGTGCTGGACAGCGGCTCCAA	7212
QY	2170	ProHisLeuGlyThrAspProSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySer	2189
DB	7213	CCCCACCTGGGCACAGACCCCTCTTAACCTTGGGGCCAGCCTCTTGGGGGCGCTGGGAGC	7272
QY	2190	ArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerGlnGly	2209
DB	7273	CGGCCCAAGAAAAAAGTCAAGCCCCGCTAAGTATCAACCATAGACCCCCCGAGAGCAAGGT	7332
QY	2210	ProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer	2229
DB	7333	CCTCGGACCCCGCCAGCCCTGTATCTGCTCCGGAGGAGGCTCCGTCCAGCCTCC	7392
QY	2230	LysAspProLeuAlaSerGlyProProAspSerMetAlaIleSerProSerProLysLys	2249
DB	7393	AAGATCCCTTGCCCTCTGGCCCCCTGACAGCATGCTGCTGCCCTCCCAAAGAAA	7452
QY	2250	AspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro	2266

DB	7453	GATGCTGAGTCTCTCCGTTTATCCTTGACCCAGACAGACCTGAGCCCC	7503
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; Sequence 120, Application US/10786148			
; Publication No. US20050191634A1			
; GENERAL INFORMATION:			
; APPLICANT: LIN, SHIU-RU			
; APPLICANT: WANG, JAW-YUAN			
; TITLE OF INVENTION: GENES FOR DIAGNOSING COLORECTAL CANCER			
; FILE REFERENCE: BHT/3230-85			
; CURRENT APPLICATION NUMBER: US/10/786,148			
; CURRENT FILING DATE: 2004-02-26			
; NUMBER OF SEQ ID NOS: 142			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 120			
; LENGTH: 7825			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
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Score: 11815.50			
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Query Match: 99.26%			
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QY	1	MetAspGluGluGluAspGlyAlaGlyAlaGluGlnSerGlyGlnProArgSerPheMet	20
DB	373	ATGCAGAGGAGGAGGATGAGCGGGCCCGAGAGTCCGGACAGCCCGGAGCTTCATG	432
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyLysArgProGlySerAlaGluLysAsp	40
DB	433	CGGCTCAACGACCTGTGGGGGCCGGGGCCGGCCGGGGCGGGGTACAGAGAAAAGAC	492
QY	41	ProGlySerAlaAspSerGluAlaGlyLeuProTyrProAlaLeuAlaProValVal	60
DB	493	CCGGGACGCGCGACTCCGAGGCGGAGGGCTGCCGTACCCGCGCTGCCCGCGTGT	552
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn	80
DB	553	TTCTTCTACTTGAGCCAGACAGACGCCGCCGAGCTGTGTCTCCGACCGTCTGTAAC	612
QY	81	ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	613	CCCTGCTTGAAGCGCATCAGCATGTTGTCATCTTCTCAACTGCGTGAACCTGGGCATG	672
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	673	TTCCGCCATGCGAGGACATCGCCTGTGACTCCAGCGCTGCCGATCTGCAGGCCCTT	732
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	733	GATGACTTCACTTGTGCTTCTTGTGCCGTGAGATGTGTGAAGATGTGGCTTGCGC	792
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleVal	160
DB	793	ATCTTGGGAAAAAGTGTTAACCTGGGAGACACTTGAACCGGCTTGACTTTTCATCGT	852
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	853	ATCGCAGGATGCTGAGACTCGCTGGAACCTGAGAACGTCAGCTTCTCAGCTGTCAAG	912
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	913	ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAAACGGGTGCCCAGCATGCCATCTT	972
QY	201	ValThrLeuLeuLeuAspThrLeuPrometLeuGlyAsnValLeuLeuLeuCysPhePhe	220

Db 973 GTACAGTTGCTGATAGCTAGCTGCCATGCTGGGCAACGCTCTGCTGCTCTTC 1032
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 1033 GTCTTCTCATCTTCGGCATCGTCGGCGTCCAGCTGTGGCAGGGCTGCTTCGGAACGA 1092
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 1093 TGCTTCCTACCTGAGAAATTTCAGCCTCCCCCTGAGCGTGACCCTGGAGCGCTATTACCA 1152
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 1153 ACAGAGAACGAGATGAGAGCCCTTCATCTGCTCCAGCCACGCGAGAACGGCATGCGG 1212
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 1213 TCCTGCAGAAAGCGTGCCACGCTGCGGGGACGGGGCGGTGGCCCACTTGCGGTCTG 1272
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 1273 GACTATGAGCGCTACACAGCTCCAGCAACACCACTGTGTCACTGGAAACAGTACTAC 1332
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheGlyAlaIleAsnPheAspAsnIle 340
Db 1333 ACCAACTGCTCAGCGGGGGAGCACAAACCCCTTCAAGGGCGCCATCACTTTGACAA 1392
QY 341 GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1393 GGCTATGCTGGATCGCATCTTCCAGGTATCAAGCTGGAGGGCTGGGTGACATCATG 1452
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1453 TACTTTGTGATGATGCTCATCTCTTCTCAAAATTTCATCTACTTCACTCTCATCATC 1512
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1513 GTGGGCTCCTTCTTCATGATCAACCTGTGCGTGGTGATTGCCACGCACTTCTCAGAG 1572
QY 401 ThrIysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1573 ACCAAGCAGCGGGAAGCCAGCTGATGCGGGAGCAGCGTGTGCGTCTCCAACGCC 1632
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLeu 440
Db 1633 AGCAACCTGGCTAGCTTCTTGAGCCCGGCGAGCTGCTATGAGAGAGTGTCAAGTACC 1692
QY 441 ValTyrIleLeuArgGlyAlaIleArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1693 GTGTACATCCTTCGTAAAGCAGCCCGCAGAGCTGGCTCAAGTCTCTGGGCAAGGTGTG 1752
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1753 CGGGTTGGGCTGCTCAGCAGCCCAAGCAACCCCTCGGGGGCCAGAGAACCCAGCAGAC 1812
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisIleLeuValHisHisHisHis 500
Db 1813 AGCTGCTCTCGTCCCAACCCCGCTATCCGTCCACCACTGTGACCAACCAACCAAC 1872
QY 501 HisHisHisHisTyrHisIleGluGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1873 CATCAACCACTACCACTGGGGCAATGGAGCTCAGGGGCCCGGGGCCAGCCCGGAG 1932
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSerThrPro 540
Db 1933 ATCCAAGACAGGATGCCAATGGGTCCCGCGGCTCATGTGCCACCACTTCAGCGCT 1992
QY 541 AlaIleuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1993 GCCCTCTCCGGGGCCCCCCTGGTGGCGCAGAGTGTGCACAGCTTCTACATGCCGAG 2052
QY 561 CysHisIleuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580

Db 2053 TGCCACTTAGAGCCAGTCCGCTGCCAGGCGCCCCCTCCAGGTCCCATCTGAGGCATCC 2112
QY 581 GlyArgThrValGlySerGlyIysValTyrProThrValHisThrSerProProProGlu 600
Db 2113 GGCAGAGACTGTGGGCAGCGGGAAGGTATCCCAACCGTGCACACAGCCCTCCAGCGGAG 2172
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 2173 ACGCTGAAGGAGAAAGCACTAGTAGAGGTGGCTGCCAGCTCTGGGGCCCCCAACCTCACC 2232
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisIlysLeuLeuGluThrGlnSer 640
Db 2233 AGCCTCAACATCCACCCGGGCCCTTACAGCTCCATGCACAACTGCTTGAGACACAGAGT 2292
QY 641 ThrGlyAlaCysGlnSerSerCysIysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 2293 ACAGGTGCTGCCAAAGCTCTTGCAAGATCTCCAGCCCTTGCTGAAAGCAGACAGTGA 2352
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyLysValGluLeu 680
Db 2353 GCCTGTGTCAGACAGCTGCCCTTACTGTGCCCGGGCCAGGGAGGTGAGCTC 2412
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2413 GCCGACCGTGAATGCCCTGACTCAGACAGCAGGCAAGTTATGAGTTACACACAGATGCC 2472
QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2473 CAGCACAGCGACTCCGGGACCCCAAGCCGGCGGCAACGGAGCCTGGGCCAGATGCA 2532
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
Db 2533 GAGCCAGCTGTGTGCTGGCCTTCTGAGAGCTAATCTGTGACACTTCGAAAGATGTG 2592
QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
Db 2593 GACAGCAAGTACTTTGGCCGGGAATCATGATGCCATCCTGGTCAACACACTCAGCATG 2652
QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
Db 2653 GGCAATCAATACCAAGAGCAGCCCGAGAGCTTACCAACGCCCTTAGAAATCAGCAACATC 2712
QY 781 ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPhe 800
Db 2713 GTCTTCAACGACTTTTGGCCTGAGATGCTGTGAAGCTGCTTGTATGTGCCCTTT 2772
QY 801 GlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerValTrp 820
Db 2773 GGCTACATCAAGAAATCCCTACAACATCTTCATGTGTGTCATGTGTCATCAGCGTGG 2832
QY 821 GluIleValGlyGlnGlnGlyGlyLysSerValLeuArgThrPheArgLeuMetArg 840
Db 2833 GAGATCGTGGGCCAGAGGGGGCGGCTGTGGTGCTGCGACCTTCGCGCTGATGCGT 2892
QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
Db 2893 GTGCTGAAGCTGTGGCTTCTTGCCCGGCTGCAAGCGGCAAGCTGTGCTCATGAG 2952
QY 861 ThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
Db 2953 ACCATGACAACGTGCCACCTTCTGCAATGCTTATGTCTTCACTTTCATCTTCAGC 3012
QY 881 IleLeuGlyMetHisIleuPheGlyCysLysPheAlaSerGluArgAspGlyAspThrLeu 900
Db 3013 ATCTGGGCATCATCTTTCGGCTGCAAGTTTGCTTGAGCGGAGTGGGACACACCTG 3072
QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
Db 3073 CCAGACCGGAAGAATTGACTCTGTGCTGGGCCATCGTCACTGTCTTTCAGATCCTG 3132
QY 921 ThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAla 940
Db 3133 ACCCAGGAGGACTGAACAAGTCTCTACATGTTATGGCTTCACAGTGTCTCTGGGCG 3192

QY 941 AlaleuTyrPheIleAlaleuMetThrPheGlyAsnTyrValLeuPheAsnLeuVal 960
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Db 3193 GCCCTTATTTCATTGCCCCCTCATGACCTTCGGCAACTACGTGCTCTTCAATTTCCTGGTC 3252

QY 961 AlaleuValGluGlyPheGlnAglGluIleSerLysArgGluAspAlaSerGly 980
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Db 3253 GCCATTCTGTGAGGGCTTCAGCGCGAGGAATCAGCAAACGGGAAGATGCGAGTGGA 3312

QY 981 GlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAlaAsnLysSerGlu 1000
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Db 3313 CAGTTAAGCTGATTCAGCTGCTGTGCACTCCAGGGGGAGATGCCAACAGTCCGAA 3372

QY 1001 SerGluProaspPhePheSerProSerLeuAspGlyAspGlyAspArgLysCysLeu 1020
| | | | |
Db 3373 TCAGAGCCCATTTCTTCTCACCCAGCCTGGATGGGACAGGAAGAGTGCTTG 3432

QY 1021 AlaleuValSerLeuGlyGlnHisProGluLeuArgLysSerLeuLeuProProLeuIle 1040
| | | | |
Db 3433 GCCTTGGTGTCCTGGAGAGCACCCGGAGCTGCGGAAGACCTGCTGCCCTCTCATC 3492

QY 1041 IleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyGlu 1060
| | | | |
Db 3493 ATCCACACGGCCGCCACACCCCATGTGCTGCCAAGAGCACACAGCGGCTTGCGCGAG 3552

QY 1061 AlaleuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAla 1080
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Db 3553 GCGCTGGGCCCTCGCTGCGCGCGCACAGCAGCGGGTCCGACAGACCTGGGCGGCC 3612

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QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGlnSerGln 1140
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Db 3733 CGGAGAAAGCCCAAGTGGAGAGCGCGGCTCTCTGTGTCGGGAGAAAGGCCAGAGAGCCAG 3792

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Db 3793 GATGAAGAGAGAGCTCAGAAGAGAGCGGGCCAGCCTTGCGGGCAGTGACCATCGCCAC 3852

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QY 1181 ProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGlnHisGlnAspCysAsn 1200
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QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAsp 1220
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QY 1221 GlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
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Db 4033 GGGGATGACCGCATGACGAGGGCAACTGAGCAAAAGGGAAACGGGTCCGCGCTGGATC 4092

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RESULT 5
US-10-062-674-2011
; Sequence 2011, Application US/10062674


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; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 2011
; LENGTH: 8116
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 404183.1
; LOCATION: (1) ... (8116)
; OTHER INFORMATION: a, t, c, g, or other
; US-10-062-674-2011

Alignment Scores:
Pred. No.:      0      Length:      8116
Score:          11353.00  Matches:      2204
Percent Similarity: 93.48%  Conservative: 19
Best Local Similarity: 92.68%  Mismatches: 20
Query Match:     95.37%      Indels:      135
DB:              17          Gaps:         5

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QY      41 ProGlySerAlaAspSerGlyAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
DB      533 CCGGGCAGCGCGGACTCCGAGCGCGAGGGGCTGCCGTACCCTGCGCCCGGTGTT 592
QY      61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
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QY      81 ProTyrPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
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DB      713 TTCCGGCCATGCGAGACATCGCCTTGACTCCAGCGCTGCCGATCCTGCAGGCTTT 772
QY      121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
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QY      141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
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QY      161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
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QY      181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
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QY      221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
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QY      421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluLysLeuLysTyrLeu 440
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QY      461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
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DB      1973 ATCCAGACAGGATGCAATGGGTCCCGCGGCTCATGTGCCACCACTTCAGACGCT 2032
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Db	2153	GGCAGGACTGTGGCGCAGCGGAGAGGTGTATCCACCGTGCAACACGCTCCACCGGAG	22122
Qy	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
Db	2213	ACGCTGAAGAGAGGACACTAGTAGAGGTGGCTGCCAGCTTGGGCCCCCAACCTTACC	22722
Qy	621	SerLeuAsnIleProProGlyProTyrSerSerSerMetHisLysLeuLeuGluThrGlnSer	640
Db	2273	AGCCTCAACATCCACCCGGGCCCTACAGCTCCATGCACAGCTGTGGAGACACAGAGT	23322
Qy	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
Db	2333	ACAGGTGCCTGCCAAGCTCTTGCAAGATCTCCAGCCCTTGCTTGAAGCAGACAGTGA	23922
Qy	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680
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Qy	681	AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla	700
Db	2453	GCCGACCGTGAATGCTGACTGACAGACAGCAGGAGTATTGAGTTACACAGAGATGCC	25122
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Db	2513	CAGCACAGCGAAGCTTCGGGAACCCCAAAAGCGGGGCGACAGGAGCTGGGCCAGATGC	25722
Qy	720	AspProSerSerValLeuAlaPheThrPArgLeuIleCysAspThrPheArgLysIleVal	740
Db	2573	AGAGCCCAAGCTGTGTGCTGGCCTTCTGAGGCTAATCTGTGACACTTCCGAAAGATTGT	26322
Qy	740	IAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMe	760
Db	2633	GGACAGCAAGTACTTTGGCCGGGAATCATGATGCCATCCGTGTCAACACACTCAGCAT	26922
Qy	760	PglIleValGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnI	780
Db	2693	GGGCATCGAATACCAAGCAGCAGCCGAGAGACTTACCAACGCCCTAGAATCAGCAACAT	27522
Qy	780	ValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPh	800
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Qy	800	eglTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValAlaIleSerValTr	820
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Db	2873	GGAGATCGTGGGCCAGCAGGCGGGCGGCTGTCCGTCTGCCGACTTCCGGCTGATGCG	29322
Qy	840	GValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLy	860
Db	2933	TGTGCTGAAGCTGGTGCCTTCTCCGCGCTGCAGCGGACGCTGTGTCTCATATGAA	29922
Qy	860	srThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePheSe	880
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Db	3053	CATCCTGGGCATGCATCTCTCGGCTGCAAGTTTGCTCTGAGCGGGAATGGGACACCCCT	31122
Qy	900	uProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLe	920
Db	3113	GCCAGACCGGAAGAATTTTGACTCTTGTCTGGGCCATCGTCACTGTCTTCAAGATCCT	31722
Qy	920	uThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAl	940

Db	3173	GACCCAGAGAGACTGAAACAAGTCCCTTACAATGGTATGGCCCTCACGTCGTCCTGGGC	3232
Qy	940	aAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuVa	960
Db	3233	GGCCCTTATTTCATTTGCCCCCTCATGACCTTCGGCACTACGTGCTCTTCAATTGCTGGT	3292
Qy	960	lAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerG	980
Db	3293	CGCCATTCTGGTGAGGGCTTCCAGCGGAG-----	3323
Qy	980	yGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerG	1000
Db	3324	-----GGAGATGCCAACAACTCCGA	3343
Qy	1000	uSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCysLe	1020
Db	3344	ATCAGAGCCCGATTCTTCTTCACCCAGCCTGGATGGTGAATGGGACAGAGAAGAGTGTCT	3403
Qy	1020	uAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProProLeuIl	1040
Db	3404	GGCCTTGCTGTCCCTGGAGAGCACCCGAGCTGCGGAAGAGCCTGCTGCCCTCTCAT	3463
Qy	1040	eIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGlyG	1060
Db	3464	CATCCACACGGCCGCCACACCCCATGTGCTGCCCAAGACACACAGACGGGCTGGCGCA	3523
Qy	1060	uAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAlaAl	1080
Db	3524	GGCGCTGGCCCTGCGTCGCGCCGACACAGACAGAGCGGGTCCGACAGCCTGGGGCGGC	3583
Qy	1080	aHisGluMetLysSerProProSerAlaArgSerSerProHisSerProTTrpSerAlaAl	1100
Db	3584	CCACGAGATGAAGTACCCGCCACGCCCGCAGCTCTCCGCACAGCCCTGGACCGCTGC	3643
Qy	1100	aSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLy	1120
Db	3644	AAGCAGCTGGACACAGAGCGGCTCCAGCCGGAACAGCTCGGCCGTGCACCCAGCTGAA	3703
Qy	1120	sArgArgSerProSerGlyGluArgArgSerSerLeuLeuSerGlyGlyGlnGlnSerG	1140
Db	3704	GGGAGAGACCCCAAGTGAGAGCGCGGTCCCTGTTGTGGGAAGAAGCCAGAGAGCCA	3763
Qy	1140	nAspGluGluLysSerSerGluGluArgAlaSerProAlaGlySerAspHisArgHi	1160
Db	3764	GGATGAAGAGAGAGCTCAGAAAGAGAGCGGCCAGCCCTCGGGCAGTGACCATCGCCA	3823
Qy	1160	sArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnVa	1180
Db	3824	CAGGGGTCCCTGGAGCGGAGGCCAAGATTCTTTGACTGCCAGACACACTGCAGGT	3883
Qy	1180	lProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAspCysAs	1200
Db	3884	GCCAGGGCTGCATCGCACTGCCAGTGGCCGAGGGTCTGCTTGAAGACACAGACTGCAA	3943
Qy	1200	nGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeuAs	1220
Db	3944	TGGCAAGTCGGCTTCAAGGCGCTTGGCCCGGCCCTGATGACCCCCCACTGGA	4003
Qy	1220	pGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIl	1240
Db	4004	TGGGATGACGCCGATGACGAGGCAACTGAGCAAAAGGGAAAGGGTCCGCGCTGGAT	4063
Qy	1240	eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr	1260
Db	4064	CCGAGCCCGACTCCCTGCTGCTGCTCGAGCGAGACTCTGTGTCAGCCTACATCTTCCC	4123
Qy	1260	oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi	1280
Db	4124	TCCTCAGTCCAGGTTCCGCTCTGTGTCAACCGATCATCAACCAAGATGTTGACCA	4183
Qy	1280	sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIl	1300

Db 4184 CGTGGCTCTGTATCATCTTCCTTAACGTGCATCACCATCGCCATGGAGCGCCCAAAAT 4243
QY 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVa 1320
Db 4244 TGACCCCCACAGCGCTGAACGCATCTTCCTGACCCCTCCCAATTACATCTTCACCGCA 4303
QY 1320 lPheLeuAlaGluMetThrValLysValValAlaLeuGlyTTrpCysPheGlyGluGlnAl 1340
Db 4304 CTTTCTGGCTGAATGACAGTGAAGGTGGTGGCACTGGGCTGGTCTTCGGGGAGCAGGC 4363
QY 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360
Db 4364 GTACCTGCGGAGCAGTTGGAACTGCTGGACGGGCTGTTGGTCTCATCTCCGTCAATCGA 4423
QY 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380
Db 4424 CATTCTGGTCCATGGTCTCTGTACAGCGGCACCAAGATCTGGGCATGTGAGGGTGCT 4483
QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysIle 1400
Db 4484 GCGGCTGCTGGGAGACCCCTGCGCCGCTCAGGGTGATCAGCCGGGCGCAGGGGCTGAAGCT 4543
QY 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420
Db 4544 GGTGGTGGAGACGCTGATGTCTCTCACTGAAAACCCATCGGCAACATTGTATCTGTGCTG 4603
QY 1420 sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
Db 4604 TGCTTCTTCAATCATTTTCGGCATCTTGGGGGTGCAGCTCTTCAAAAGGAGTTTTCGT 4663
QY 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460
Db 4664 GTGCCAGGGCGAGGATACCAGGAACATCACCAATAAATCGACTGTGCCGAGGCCAGTTA 4723
QY 1460 rArgTrpValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480
Db 4724 CCGGTGGTCCGACCAAGTACAACTTTGACAACCTTGGCCAGGCCCTGATGTCCCTGTT 4783
QY 1480 eValLeuAlaSerLysAspGlyTTrpValAspIleMetTyrAspGlyLeuAspAlaValG 1500
Db 4784 CGTTTGGCTCCAAAGATGGTTGGGTGGACATCATGTAGATGGGCTGATGCTGTGGG 4843
QY 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh 1520
Db 4844 CGTGAACCAAGCCCATCATGAACCAAAACCCCTGGATGCTGTACTTCACTTCGTT 4903
QY 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGluAsnPh 1540
Db 4904 CCTGCTCATGTGGCTTCTTGTGTCTGAACAATGTTGTGGGTGTGGTGGAGAACTT 4963
QY 1540 eHisLysCysArgGlnHisGlnGlnGluGluAlaArgArgArgGlu-GluLysArgL 1560
Db 4964 CCACAAGTGTGGGACAGCACAGGAGAAGAGAGCCCGGGCGCGGAGCCAGAAAGCGCC 5023
QY 1560 euArgArgLeuGluLysLysArgArg-----LysAlaGlnCysL 1573
Db 5024 TACGAAGACTGGCGAAAAAGAGAGCGAGCTAGAGAAAGAGATGGCTGAAGCCCAAGTGA 5083
QY 1573 ySPProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisHisLeuCysThrSerH 1593
Db 5084 AACCTTACTACTCCGACTACTCCCGCTTCCGGCTCCTGTCACCACTTGTGACCAAGCC 5143
QY 1593 iSTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetG 1613
Db 5144 ACTACCTGGAACCTTTCATCAACAGGTGTCAATCGGCTGAACGTGGTCAACCATGGCCATGG 5203
QY 1613 luhISTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIlePheT 1633
Db 5204 AGCACTACCAAGAGCCCGAGATTCGATGAGGCTCTGAAGATCTGCAACTACATCTTCA 5263
QY 1633 hrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPheP 1653
Db 5264 CTGTCACTTTGTCTTGGAGTCAGTTTCAAACTTGTGGCTTGGTTCCGTGGTTCCT 5323

QY 1653 heGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleT 1673
Db 5324 TCCAGGACAGGTGGAAACCACTGGACCTGGCCATTGTGCTGTCTTCATCATGGGCATCA 5383
QY 1673 hrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleM 1693
Db 5384 CGCTGAGGAATCGAGGTCAACGCCCTGCTGCCATCAACCCCAACCATTCATCCGATCA 5443
QY 1693 eArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgA 1713
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QY 1713 lAlLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheM 1733
Db 5504 CGCTGTGAGACACGATGATGCAAGGCCCTGCCCAAGTGGGAACTGGGACTTCTTCA 5563
QY 1733 eTLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCysA 1753
Db 5564 TGTGTGTTGTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTGGAGACCTGGAATGTG 5623
QY 1753 sPGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetA 1773
Db 5624 ACGAGACACACCCCTGTGAGGGCTGGGCCCTGCATGCCACCTTCCGAACCTTGGCATGG 5683
QY 1773 lAPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspT 1793
Db 5684 CCTTCTTAACCTCTTCCGAGTCTCCACAGGTGAACAATTGGAATGGCATTAAGAAGACA 5743
QY 1793 hrLeuArgAspCys--AspGlnGluSerThrCysTyrAsnThrVal-----IleSerP 1810
Db 5744 CCCTCGGGAGCTGCACCCACGACGAGCGCAGCTGCTGAGCAGCCTGATGTTGTGCGC 5803
QY 1810 roIleTyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleA 1830
Db 5804 CGCTGTACTTCGTGAGCTTCGTGCTCACCGCGCAGTTCGTCTCATCAACGTGTGTGG 5863
QY 1830 lAValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuG 1850
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QY 1850 lAlaGluLeuGluLeuGluMetLysThrLeuSerProGlnProHisSerProLeuGlyS 1870
Db 5924 ATGCCAGCTCGAGCTGGAGATGAAGACCTCAGCCCCAGCCCCACTGCGCACTGGGCA 5983
QY 1870 exProPheLeuTrpProGlyValGluGlyProAspSerProAspSerProLysProGlyA 1890
Db 5984 GCCCTTCTCTGCTGGCTGGGGGTGAGGGCCCCGACAGCCCCGACAGCCCCAAAGCTGGGG 6043
QY 1890 lAlLeuHisProAlaAlaHisAlaArg-SerAlaSerHisPheSerLeuGluHisProThr 1909
Db 6044 CTGTGACCCCAAGCGCGCCACGCGAGATCAGCTCCCACTTTTCCCTGAGACACCCACAG 6103
QY 1909 ----- 1909
Db 6104 GACAGCAGCTGTTTGACACCATATCCCTGCTGATCCAGGGCTCCCTGGAGTGGAGCTG 6163
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QY 1909 ----- 1909
Db 6224 AGCCTGGAGGCTCCGACCAAGATCCCTTAAGCTGAGATGAGGCTGTGCTGTGACG 6283
QY 1909 ----- 1909
Db 6284 TCAGAGATTGTGTGAACCGTCTGCTCTTAAGCTCTGACGAGATGACTTTGGCCTGAT 6343
QY 1910 -----MetGlnProHisProThrGlu 1916
Db 6344 GACATGCACACACTTACTTAAGTGCCCTGGAAGCAATATGACAGCCCAACCCACGAGAG 6403

QY 1917 LeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeu 1936
Db 6404 CTGCCAGGACCACTTACTGACTGTGCGGAAGTCTGGGGTCAGCCGAAACGCACTCTCTG 6463
QY 1937 ProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArg 1956
Db 6464 CCAATGACAGCTACATGTGTGGCATGGAGCACTGCCGAGGGGCCCCCTGGGACACAGG 6523
QY 1957 GlyTyrGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAla 1976
Db 6524 GGCTGGGGGCTCCCAAGCTCAGTCAGGCTCCGTCTGTCCGTTCACTCCAGCCAGCA 6583
QY 1977 AspThrSerTyrIleLeuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSer 1996
Db 6584 GATACCAGCTACATCCTGCAGCTTCCCAAAGATGCACCTCATCTGCTCCAGCCCCACAGC 6643
QY 1997 AlaProThrTyrGlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGln 2016
Db 6644 GCCCCAACCTGGGGCACCATCCCAAACTGCCCAACCCACAGGACGCTCCCTTGGCTCAG 6703
QY 2017 ArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGly 2036
Db 6704 AGGCACACTCAGGCGCCAGGACCAATTAAGACTGACTCCTTGACGTTTCAAGGTTGGGC 6763
QY 2037 Ser-ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyr 2056
Db 6764 AGCCCGGGAAGACCTGTGGGACAGAGTGAGTGGGCCCTCCCGCCCTGGGCCCGGCTTA 6823
QY 2056 rSerPheTyrGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIle 2076
Db 6824 CTCTTTCTGGGGCCAGTCAAGTACCAGGACAGACGACTCCCGCAGCCACAGCAAGAT 6883
QY 2076 eSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGly 2096
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Db 6944 CCCTCCAGAGACAGAGAGACTTGAAGTGGACAGAGCTGAGCTGATTTCAAGGAGA 7003
QY 2116 pheLeuLeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysLysCysTyr 2136
Db 7004 CCTCCTGCCCCCTGGCGGCAGAGAGGCCCATCCCAAGGACTGAAGAAGTGTCTA 7063
QY 2136 rSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGlnArgAr 2156
Db 7064 CAGCGTGGAGGGCCAGAGCTGCCAGCGCGCTACGTCTGGCTGATGAGCAGAGAG 7123
QY 2156 gHisSerIleAlaValSerCysLeuAspSerGly-SerGlnProHisLeuGlyThrAsp 2176
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QY 2176 roSerAsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeu 2196
Db 7184 CCTCTAACCTTGGGGCCAGCCTCTTGGGGGCTGGGAGCCGGCCCAAGAAAAAACTCA 7243
QY 2196 eRProProSerIleThrIle-AspProProGluSerGlnGlyProArgThrProProSer 2215
Db 7244 GCCCGCTAGTATCACCAATTAGACCCCCCGAGAGCCAAGTCTCGGACCCCGCCAGC 7303
QY 2216 Pro-GlyIleCysLeuArgArgAlaProSerSerAspSerLysAspProLeuAlaSe 2235
Db 7304 CCTGGGTTNTCTGCTCCGAGGAGAGGCTCCGTCCAGCGACTCCAAAGATCCCTTGGCCTC 7363
QY 2235 rGlyProPro--AspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeu 2254
Db 7364 TGGGGCCCCCTGAACAGCATGGCTGCTGCCCTCCCAAGAAAGATGTGCTGAGTCTC 7423
QY 2255 SerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 7424 TCCGGTTTATCTCTGACCCAGACAGACTGGAACCCC 7459

RESULT 6

US-09-383-894-1
; Sequence 1, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383,894
; EARLIER FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,004
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/117,399
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7129
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-383-894-1

Alignment Scores:
Pred. No.: 0
Score: 11111.00
Percent Similarity: 94.80%
Best Local Similarity: 93.27%
Query Match: 93.34%
DB: 10
Matches: 7129
Conservative: 35
Mismatch: 95
Indels: 24
Gaps: 5
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QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
Db 1 ATGACGAGAGAGAGATGAGCGGGCCCGAGAGTCCGGACAGCCCGTAGCTTCAGC 60
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 61 CAGCTCAACGACTGTCCGGGGCCGGGGCCGGCAGGGGGCCGGGGTTCAGCGAAAGGAC 120
QY 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 121 CCGGGCAGCGCGGACTCCGAGGCGGAGGCTGCCGTACCCGCGCTAGCCCGTGTTC 180
QY 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn 80
Db 181 TTCTTCTACTTGAGCCAGACAGACCGCCCGGAGCTGTGTCTCCGACGCTGTATAC 240
QY 81 ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet 100
Db 241 CCGTGTTCGAGCGAGTCAATATGTCTTCTTCACTGTGTGACTCTGGGTATG 300
QY 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 301 TTCAAGCCGTTGTGAGACATTGCTGTGATCCAGCGCTGCGGATCTGCAGGCTTTC 360
QY 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 361 GATGACTTCATCTTGCCTTCTTGTGTGGAATGTGTGAAGATGTGGCTTGGGC 420
QY 141 IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal 160
Db 421 ATCTTGGGAAGAATGTATACCTGGAGACACTTGAAACCGGCTTGACTTTTCATTGTC 480
QY 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 481 ATTGCAGGAGATGCTGAGTATTCGTGACCTGCAGACGTCAGCTTCCGACGTACAG 540
QY 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
Db 541 ACAGTCCGTGTGTGCGACCGCTCAGGGCCATTAAACGGGTGCCAGCATGCGCAATTCTC 600
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220

Db 601 GTCACTACTGCTGGACACCTTGCTATGCTGGCAACGTCCTGCTGCTGTTCTTC 660
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 661 GTCTTTTTCATCTTTGGCATCGTGGGGGTCCAGCTGTGGGAGAGACTGCTTCGCAACCGA 720
QY 241 CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 721 TGCTTCCTCCCGAGAAGCTTCAAGCTCCCTTGAGCGTGAGCTGGAGCCTTATTAACAG 780
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 781 ACAGAGAATGAGGACGAGAGCCCTTCATCTGCTCTCAGCCTCGGGAATGGCATGAGA 840
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 841 TCCTGACGAGTGTGCCACACACTGCGTGGGGAAGCGGTGTGGCCACCCCTGCAGTCTG 900
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrCysValAsnTrpAsnGlnTyrTyr 320
Db 901 GACTATGAGACCTATAACAGTTCAGCAACACCACTGTGTCAACTGGAACCACTACTAT 960
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheGlyAlaIleAsnPheAspAsnIle 340
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QY 341 GlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1021 GGCTATGCTTGATCGCCATCTTCAGGTCAACACTGGAGGGCTGGGTGCACATCATG 1080
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIle 380
Db 1081 TACTTGTAAATGACGCTCACTCCTTCTCAAACTTCATCTACTTCACTTCTTCATCATC 1140
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGATGGCCACGCACTTCTCCAG 1200
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1201 ACCAAACAGCGGAGAGTACGCTGATGGGGAAGCAGCGTGTACGATTCTGTCCAATGCT 1260
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu 440
Db 1261 AGCAACCTGGCAAGCTTCTGTGAGCCAGGCAAGCTGTATGAGAGCTACTCAAGTACTG 1320
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1321 GTGTACATCTCCGAAAAGCAGCCCGAAGGCTGGCCCAAGTCTCTAAGGCTATAGGCGTG 1380
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
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QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1441 AGCTGCACTCGCTCACACCGTGTCTGTCTGTCCACCACTGTGCCACCACTACACAC 1500
QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
Db 1501 CACCATCACCACTACCACTGGGTAATGGAGCGCTCAGAGTTCCTCCGGGCGAGCCAGAG 1560
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 1561 ATCCAGGACAGGAGTGCCAATGGGTCTTCGCCGGCTCATGTCTACCAACCACTCTACACC 1620
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
Db 1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGGAGTCTGTACACAGCTTCTACCATGTGTAC 1680
QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 1681 TGCCACTTGGAGCAGTCCGTTGCCAGGCACCCCCTCCAGATGCCCATCGAGGCACTCT 1740

QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
Db 1741 GGTAGCACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAAGCCCTCCACCAAG 1800
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 1801 ATACTGAAGATAAAGCACTAGTGAGGTGGCCCCCAGCCCTGGGGCCCCCACTCAC 1860
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 1861 AGCTTCAACATCCCACTGGGCCCTTCAGCTCCATGCACAAAGCTCTTGAGACACAGAGT 1920
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
Db 1921 ACGGAGCCTGCCATAGCTTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGACAGACGTGA 1980
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
Db 1981 GCCTGGGGGGCGGACAGTGTCCCTCACTGTGCCCGACAGAGACAGACCAAGAGTCC 2040
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2041 GCTGACCATGTCAATGCTTCACTCAGACAGACGAGCTGTATGAGTTACACAGACGCT 2100
QY 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719
Db 2101 CAGCAGAGTGAACCTCCGGATCCCAACAGCCGGCGGCGACAGCGAGCCTGGGGCCAGAT 2160
QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
Db 2161 GCAGAGCCTAGTTCTGTGGCTTCTGTGAGGCTGATCTGTACACATTCGGAAGATC 2220
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 2221 GTAGATAGCAATACTTTGGCGGGGAATCATGATGCCATCCTGGTCAATACACTCAGC 2280
QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 2281 ATGGGATCGAGTACCACGAGCAGCCGAGAGCTCACCAACGCCCTGGAATACAGCAAC 2340
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyPro 799
Db 2341 ATGTCCTTCAACCAAGCCTTTCGCCCTTGAGATGCTGCTGAACCTGCTTCTACCGTCCC 2400
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerVal 819
Db 2401 TTGGCTACATTAAGAATCCTTCAACATCTTGTGATGTGTCAATTGTGTATCATCAGTGTG 2460
QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
Db 2461 TGGAGATTGTGGCCAGCAGGGAAGTGGCTGTGGTGTCTGCGACCTTCGCGCTGATG 2520
QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
Db 2521 CGGGTGTGAAGCTGTGTGCCCTTCTGCGCGCCCTGCAGCGCCAGCTCGTGGTGCATG 2580
QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879
Db 2581 AAGACCATGGAACAACGTGGCACTTCTGCATGTCTCTCATGTCTTCACTTCACTTTC 2640
QY 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899
Db 2641 AGCATCTGGGCATGCATCTTGTGTGCAAGTTGCAATCGAACGGGATGGGAGACAG 2700
QY 900 LeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIle 919
Db 2701 TTGCCAGACCGGAAGATTGCACTCCCTGCTGTGGGCCATGCTCACTGTCTTCAGATT 2760
QY 920 LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939
Db 2761 CTGACTCAGGAAGACTGGAATAAAGTCTCTTACACGGCATGGCCTCCACATCGTCTTG 2820

QY	940	AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu	959
Db	2821	GCTGCTCTTAACCTCATCGCCCTCATGACTTTGGCAACTATGTGCTCTTAAACCTGCTG	2880
QY	960	ValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAlaSer	979
Db	2881	GTGGCCATTCTTGTGGAAGGATTCCAGGCGAAGAAATCCGCAACGGGAAGATGCGAGT	2940
QY	980	GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSer	999
Db	2941	GGACAGTTAAGCTGTATTACAGCTGCTGTCAACTCTCAGGGGGAGATGCCAAGTCT	3000
QY	1000	GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys	1019
Db	3001	GAGTCAGAGCCTGATTTCTTTTCGCCAGTGTGATGTGATGGGACAGAAAGAACGCC	3060
QY	1020	LeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeuLeuProLeu	1039
Db	3061	TTGGCCCTGTGGCTTTGGGAGAACAACGGGAATCAAGAAAGACCTTTGGCAACCCCTC	3120
QY	1040	IleIleHisThrAlaAlaThrPrometSerLeuProLysSerThrSerThrGlyLeuGly	1059
Db	3121	ATCATCCATACGGCTGCCACCAATGTCACTACCAAGAGCTCCAGCACAGGTGTGGGG	3180
QY	1060	GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla	1079
Db	3181	GAAGCACTGGGCTCTGGCTCTCGACGTACCAAGTACAGTGGGTCCGCTGAGCTTGAAGT	3240
QY	1080	Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer	1098
Db	3241	GCCCAACCATGAGTGAATCTCCGCCAAGTGCCTCCGACAGTCCCTGGAGT	3300
QY	1099	AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer	1118
Db	3301	GCGGCAAGCAGCTGACCAAGCAGCGCTCCAGCAGGAACAGCTGGGCCGGGCCCCAGC	3360
QY	1119	LeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGlu	1138
Db	3361	CTAAAGCGAGAGGCCGAGCGGGAGCGAGGTCTCTGCTGTGAGAGGGCCAGAGAG	3420
QY	1139	SerGlnAspGluGluGluSerSerGluGluArgAlaSerProAlaGlySerAspHis	1158
Db	3421	AGTCAGGATGAGGAGAAAGTTCAAGAGAGGACCGGGCCAGCCAGCAGCAGTGAACAT	3480
QY	1159	ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu	1178
Db	3481	CGCCACAGGGGTTCTTGGAACTGAGGCCAAGAGTTCCTTGACCTGCTGACACTCTG	3540
QY	1179	GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp	1198
Db	3541	CAGGTGCCGGGGCTGACCGCACAGCCAGCGGCGGAGCTCTGCCTGAGCACCAGAAC	3600
QY	1199	CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro	1218
Db	3601	TGTAATGGCAAGTCGGCTTCAAGCGGCTTGGCCCGCACTGAGAGCTGATGACCCCA	3660
QY	1219	LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla	1238
Db	3661	CTGATGGGATGATGACAATGATGAGGGAATCTGAGCAAAAGGGGAACGATACAAAGCC	3720
QY	1239	TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle	1258
Db	3721	TGGGTCAAGATCCCGGCTTCTGCTGTGCCGAGCGAGATTCTGTGTCGCTATATATC	3780
QY	1259	PheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe	1278
Db	3781	TTTCCTCTCAGTCAAGTTTCGTCTCTGTGTCAACGGATCATCACCACAAGATGTTT	3840
QY	1279	AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro	1298
Db	3841	GACCATGTGTCCTCGTCATCATCTTCTCAACTGTATACCATCGCTATGAGCGGCC	3900
QY	1299	LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr	1318

Db	3901	AAATTTGACCCCGACAGCGCTGAGCGCATCTTCTGACCCCTCTCCAACTACATCTTCACG	3960
Qy	1319	AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGlu	1338
Db	3961	GCAGTCTTTCTAGCTGAATATGACAGTGAAGGTGTGGCACTGGGCTGGTGTGGGAG	4020
Qy	1339	GlnAlaTyrLeuArgSerSerTyrAsnValLeuAspGlyLeuLeuValLeuIleSerVal	1358
Db	4021	CAGGCTTACCTGGCAGACAGCTGGAATGTGTGACGGCTGTGTGTCTCATCTCCGTC	4080
Qy	1359	IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg	1378
Db	4081	ATCGACATCTGTGTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGTGAGG	4140
Qy	1379	ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu	1398
Db	4141	GTGCTCGGGCTGCTGCGGACCCCTGCGTCCACTCAGGGTCATCAGCCGGGCCAGGACTG	4200
Qy	1399	LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle	1418
Db	4201	AACTGGTGTGAGACTCTGATGTATCCTCAAAACCATTTGGCAACATTGTGTCAAT	4260
Qy	1419	CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe	1438
Db	4261	TGCTGTGCCTTCTTCATCATTTTGGAAATTCGCGGGTGACGCTCTCAAGGGAAGTTC	4320
Qy	1439	PheValCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla	1458
Db	4321	TTGCTGTGTACGGGTGAGGACACCAAGAACATCACTAACAAATCCGACTGCGGTGAGGC	4380
Qy	1459	SerTyrArgTyrValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer	1478
Db	4381	AGCTACCGATGGGTCCGGACAAGTACAACTTTGCAACCTGGGCCAGGCTGTGATGTC	4440
Qy	1479	LeuPheValLeuAlaSerLysAspGlyTyrPheValAspIleMetTyrAspGlyLeuAspAla	1498
Db	4441	CTGTTTGTGTGCTGAGCTTCAAGATGGTGGTTGATCATCATGTATGATGGCTGATGCT	4500
Qy	1499	ValGlyValAspGlnGlnProIleMetAsnHisAsnProTyrMetLeuLeuTyrPheIle	1518
Db	4501	GTGGGTGTGATCAGCAGCCCATCATGAACACCAACCCCTGGATGCTGCTATCTTCATC	4560
Qy	1519	SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValValGlu	1538
Db	4561	TCCTTCTCTCATCGTGGCTTCTTTGTCTTGACATGTTGTGGCGGTGTGTGGAG	4620
Qy	1539	AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgArgGluGlyLys	1558
Db	4621	AACTCCATAAGTCAGACAGACACAGAGAGAGAGAGCGAGCGCGTGAGAGAAAG	4680
Qy	1559	ArgLeuArgArgLeuGluLysLysArgArg-----	1568
Db	4681	CGACTACGGAGGCTGGAGAAAAAGAGAGAAATCTAATGTTGACGATGTAAATTCCTCC	4740
Qy	1569	-----LysAlaGlnCysLysProTyrTyrSerAspTyrSer	1580
Db	4741	GGCAGCTCAGCCAGCGCTGCGGTCAAGAACCCAGTGCAGCCCTACTACTGTGACTACTCG	4800
Qy	1581	ArgPheArgLeuLeuValHisHisLysLeuCysThrSerHisTyrLeuAspLeuPheIleThr	1600
Db	4801	AGATTCCGGCTCTTGTCCACCACTGTGTACCAAGCACTAAGCTTGTCACTCACT	4860
Qy	1601	GlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIle	1620
Db	4861	GGTGTTCATCGGGCTGACGTGTCTCACTATGCGCATGGAACATTAACAGACGCCGAGATC	4920
Qy	1621	LeuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSer	1640
Db	4921	CTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCACTTGTGTCTTGAGTCA	4980
Qy	1641	ValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLeu	1660

Db 4981 GTTTCAAACTTGTGGCCTTGGCTTCCGCCGTTTCTTCCAGGACAGGTGAAACGACCTG 5040
QY 1661 AspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluIleGluValAsn 1680
Db 5041 GACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGAGATGAGTCAAT 5100
QY 1681 AlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg 1700
Db 5101 GCTTCGCTGCCATCAACCCCAACCATCATCCGTATCATGAGGGTGCTCCGATTGCTCGA 5160
QY 1701 ValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGln 1720
Db 5161 GTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGGACACCGGTGATGCAG 5220
QY 1721 AlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPheIlePheAla 1740
Db 5221 GCCCTGCCCAAGGTGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTCATCTTTGCA 5280
QY 1741 AlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGly 1760
Db 5281 GCTGTGGCGGTGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCCTGTGAGGGC 5340
QY 1761 LeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVal 1780
Db 5341 TTGGGTCCGCATGCCACCTTAGAACCTTTGATAGCCCTTTCGACCCCTCCGAGTC 5400
QY 1781 SerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCysAspGlnGlu 1800
Db 5401 TCCACTGGTGACAACGTGAATGGTATTATGAAGACACCCCTCCGGGACTGTGACCAAGAG 5460
QY 1801 SerThrCysGlyTrpAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAla 1820
Db 5461 TCCACCTGCTACACAACGTGTCATCTCCCCCTATCTACTTTGTGTCTTCGTGTCAGGCC 5520
QY 1821 GlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuGluGlnSerAsn 1840
Db 5521 CAGTTTGTGTGGTCAACGTTGTCATAGCTGTGCTGATGAGCACCTGGAAGAAACCAAC 5580
QY 1841 LysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMetLysThrLeu 1860
Db 5581 AAAGAGGCCAAGAGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAACGCTC 5640
QY 1861 SerProGlnProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyPro 1880
Db 5641 AGCCCGCAGCCCCACTCCCGCTGGCGACCCCTTCTGCGCCCGGGGTGAGGGGTGC 5700
QY 1881 AspSerProAspSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAla 1900
Db 5701 AACAGTCTCTGACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCACATTGGAGCAGCC 5760
QY 1901 SerHisPheSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro----- 1918
Db 5761 TCGGGCTTCTCCCTTGAGCACCCCAAGATGGTACCCCAACCCGAGGAGGTGCCAGTCCCC 5820
QY 1919 ---GlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937
Db 5821 CTAGGACCAGACTGCTGACTGTGAGGAAGTCTGGTGCAGCCGAGCACTTCTGCC 5880
QY 1938 AsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGly 1957
Db 5881 AATGACAGCTACATGTGCCGCAATGGGAGCACTGTGAGAGATCCCTAGGACACAGGGGC 5940
QY 1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977
Db 5941 TGGGGGCTCCCAAGCCCAAGTCAAGGCTTCATCTGTCCGTTCACTCCCAACCAAGAGAC 6000
QY 1978 ThrSerTyrIleLeuGlnLeuProLysAspAlaProHisIleLeuGlnProHisSerAla 1997
Db 6001 ACCAGCTGCATCTTACAGCTTCCCAAGATGTGACTATCTGCTCCAGCCTCATGGGGCC 6060
QY 1998 ProThrTrpGlyThrIleProLysLeuProProProGlyArgSerProLeuAlaGlnArg 2017
Db 6061 CCCACCTGGGGCGCATCCCTAAACTACCCCACTGCGCGTCCCTCTGTGCTCAGAGG 6120

QY 2018 ProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySer 2037
Db 6121 CCTCTCAGGCGGCCAGGCAATAAGACTGACTCCCTGGATGTGCAGGGCCTGGTAGC 6180
QY 2038 ArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSer 2057
Db 6181 CGGGAAGACCTGTTGTACAGAGGTAGTGGGCCCTCTGCCCTCTGACCCGGTCTCATCC 6240
QY 2058 PheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSer 2077
Db 6241 TTCTGGGGCGGTGAGCATCCAGGTGCAGTCAGCAGCGCTCCGGCATTCAGACAAAGTCTCC 6300
QY 2078 LysHisMetThrProProAlaProCysProGlyProGluProAsnTrpGlyLysGlyPro 2097
Db 6301 AAGCACATCCGCCTGCGCAGCCCTTGCCCAAGCCTGGAACCAAGCTGGGCCAAGACCT 6360
QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
Db 6361 CCAGAGACCAGAAGCAGCTTAGAGCTGGACACGAGCTGAGCTGATTCAGAGACCTC 6420
QY 2118 LeuProProGlyGlyGlnGluGluProProSerProArgAspLeuLysCysTyrSer 2137
Db 6421 CTT---CCCAAGACGCCAAGAAACCCCTGTCCCAAGGAGCTGAAGAGTGTACAGT 6477
QY 2138 ValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHis 2157
Db 6478 GTAGAGACCAGAGCTGCAGCGCGCAGCCCTGGGTCTGCTAGATGAACACGCGAGACAC 6537
QY 2158 SerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSer 2177
Db 6538 TCCATTGCTGTCAAGTGTGTGACAGCGGCTCCCAACCCGCTTATGTCCAAGCCCTCA 6597
QY 2178 AsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerPro 2197
Db 6598 AGCCTGGGGGGCCAACTCTTGGGGGTCTGTGGAGCCGGCCTAAGAAATAAATCAGCCCA 6657
QY 2198 ProSerIleThrIleAspProProGluSerGlnGlyProArgThrProProSerProGly 2217
Db 6658 CCCAGTATCTCTATAGACCCCGGAGAGACGAGGCTCTCGGCCCAATGCAGTCTGTGT 6717
QY 2218 IleCysLeuArgArgArgAlaProSerSerAspSerLysAspProLeuAlaSerGlyPro 2237
Db 6718 GTCTGCTCAGGAGAGGGGCGCGCCAGTAGTACTTAAGATCCCTCGGTCTCCAGCCCC 6777
QY 2238 ProAspSerMetAlaAlaSerProSerProLysLysAspValLeuSerLeuSerGlyLeu 2257
Db 6778 CTTGACAGCAGCGCTGCTTCACTCCCAAGAAAGACACGCTGAGTCTCTGTGTTG 6837
QY 2258 SerSerAspProAlaAspLeuAspPro 2266
Db 6838 TCTTGTGACCCCAACAGACATGGAACCC 6864

RESULT 7
US-09-383-894-3
; Sequence 3, Application US/09383894
; Publication No. US20030125269A1
; GENERAL INFORMATION:
; APPLICANT: Li, Ming
; TITLE OF INVENTION: T-Type Calcium Channel
; FILE REFERENCE: 004.00191
; CURRENT APPLICATION NUMBER: US/09/383, 894
; EARLIER APPLICATION NUMBER: 1999-08-26
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: US 60/098, 004
; EARLIER FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 7285
; TYPE: DNA
; ORGANISM: Rattus sp.

US-09-383-894-3

Alignment Scores:			
Pred. No.:	0	Length:	7285
Score:	1111.00	Matches:	2135
Percent Similarity:	94.80%	Conservative:	35
Best Local Similarity:	93.27%	Mismatches:	95
Query Match:	93.34%	Indels:	24
DB:	10	Gaps:	5

US-09-611-257A-37 (1-2266) x US-09-383-894-3 (1-7285)

QY	1	MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20
DB	157	ATGGACGAGGAGGAGATGGAGCGGGCCGAGAGTCCGGACAGCCCCGTAGCTTCA	216
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyAlaArgProGlyProGlySerAlaGluLysAsp	40
DB	217	CAGCTCAACGACTGTTCGGGGCCGGGGCCGGCAGGGGCCGGGGTGCACGAAAGGAC	276
QY	41	ProGlySerAlaAspSerGlyAlaGluGlyLeuProTyrProAlaLeuAlaProVal	60
DB	277	CCGGCAGCGCGGACTCCGAGCGGAGGGCTGCCGTACC	336
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80
DB	337	TTCTTCTACTGTAGCCAGACAGACCGCCCGGAGCTGTGTCTCCGACCGGTCTGTAC	396
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
DB	397	CCGTGGTTCGAGCGAGTCAAGTATGCTGTGATTTCTTCACTGTGTGACTCTGGGTATG	456
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
DB	457	TTCAAGCCCGTGTGAGGACATTGCTGTGACTCCACGCGCTGCCGATCTCGAGGCCCTTC	516
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140
DB	517	GATGACTTCATCTTGCTTCTTCTTCTGTGTGAAATGGTGTGAGATGGTGGCCTTGGGC	576
QY	141	IlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleVal	160
DB	577	ATCTTTGGGAAGAAATGTACCTGGGAGACACTTGAAACCGGCTGACTTTTTCATTGTC	636
QY	161	IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg	180
DB	637	ATTGCAGGGATGCTGGAGTATTCGCTGACTGCAGACGTCAAGCTTCTCCGACGTCAAG	696
QY	181	ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu	200
DB	697	ACAGTCCGTGTGTGCGACCGCTCAAGGGCCATTAAACGGGTGCCACGATGCGCATTTCTC	756
QY	201	ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe	220
DB	757	GTCACATTACTGTGACACCTTGCTATGTGGCAACGTCTGCTGTGTTTCTTC	816
QY	221	ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg	240
DB	817	GTCCTTTTCATCTTGGCATCGTGCGTCCAGCTGTGGCAGAGACTGCTTCGCAACCGA	876
QY	241	CysPheLeuProGluAsnPheSerLeuProLeuSerValAspLeuGluArgTyrTyrGln	260
DB	877	TGCTTCTCCCGAGAACTTCAAGCTCCCCCTGAGCGTGACCTGAGCCTTATTACAG	936
QY	261	ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg	280
DB	937	ACAGAGAATGAGGACGAGACCCCTTCATCTGTCTCAACCTCGGAGAAATGGCATGAGA	996
QY	281	SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu	300
DB	997	TCCTGCAGAGAGTGTGCCCACTGCGTGGGGAAGCGGTGTGGGCCCACTTGCAAGTCTG	1056
QY	301	AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr	320

DB	1057	GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCACTAT	1116
QY	321	ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle	340
DB	1117	ACCAACTGCTCTGCGGGCGAGCAACACCTTCAAAAGGCGCCATCAACTTGAACAATT	1176
QY	341	GlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAspIleMet	360
DB	1177	GGCTATGCCCTGGATCGCCATCTTCCAGGTCACTACACTGAGGGCTGGTGCATCATG	1236
QY	361	TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle	380
DB	1237	TACTTCGTAATGAGCGCTCACTCTTCTTCAACTTCATCTTCACTTCTTCATCATC	1296
QY	381	ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu	400
DB	1297	GTGGGCTCTTCTTCATGATCAACCTGTGCTGTGTGATTTGCCACGACGATTCTCCAG	1356
QY	401	ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla	420
DB	1357	ACCAAAACGGGGAGAGTCAAGTGTGCGGAGCAGCGGTGTACGATTCTGTCCAAATGCT	1416
QY	421	SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLysTyrLeu	440
DB	1417	AGCACCTGGCAAGCTTCTCTGAGCCAGGACGCTGCTATGAGAGACTACTCAAGTACCTG	1476
QY	441	ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal	460
DB	1477	GTTGATACCTCTCCGAAAAGCAGCCCGAAGGCTGGCCCAAGTCTTAAGGCTATAGCGGTG	1536
QY	461	ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer	480
DB	1537	CGGGCTGGCTGCTCAGACGCCACGTGGCCCGTAGTGGCAGAGAGCCCAAGCCAGTGCC	1596
QY	481	SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis	500
DB	1597	AGCTGACCTGCTCACACCGTGTGTGTGTGTCCACCACCTGTGTCCACCACCATCACAC	1656
QY	501	HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu	520
DB	1657	CACCATCACCACTAACCACTGGGTATGGAGCGCTCAGAGTTCCCGGGCAGCCCAAG	1716
QY	521	IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro	540
DB	1717	ATCCAGGACAGGATGCCAATGGGTCTGCCGGCTCATGCTAACCAACCACTTACACCC	1776
QY	541	AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp	560
DB	1777	ACTCCCTCTGGGGGCCCTCCGAGGGGTGGAGTCTGTACACAGCTTCTACCATGTGTAC	1836
QY	561	CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer	580
DB	1837	TGCCACTTGAGCCAGTCCGTTGCCAGGCAACCCCTCCAGATGCCATCGAGGATCT	1896
QY	581	GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu	600
DB	1897	GGTAGACTGTGGGTAGTGGAAGGTGTACCCCACTGTGCATACCAAGCCCTCCACCAAG	1956
QY	601	ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr	620
DB	1957	ATACTGAAGATAAAGCACTAGTGAGGTGGCCCCCAAGCCCTGGGCCCCCAACCTCAC	2016
QY	621	SerLeuAsnIleProProGlyProTyrSerSerSerMetHisLysLeuLeuGluThrGlnSer	640
DB	2017	AGCTTCAACATCCCACTGGGCCCTTTCAGCTTCATGCACAAGCTCTTGAGACACAGAGT	2076
QY	641	ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly	660
DB	2077	ACGGAGCCTGCTATGCTCTGTCAAAATCTCAAGCCCTTGTCTCCAAGGCAAGACAGTGA	2136
QY	661	AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu	680

Db 2137 GCCTGGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGACGAGAGCCAGACTCC 2196
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
Db 2197 GCTGACCATGTCATGCTGACTGACAGACGAGGCTGTATGAGTTCACACAGGACGCT 2256
QY 701 GlnHisSerAspLeuArgAspProHisSer--ArgArgGlnArgSerLeuGlyProAsp 719
Db 2257 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCACAGCGGAGCCTGGGCCAGAT 2316
QY 720 AlaGluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgIle 739
Db 2317 GCAGAGCCTAGTTCGTGCTGGCTTTCTGGAGGCTGATCTGTACACATTCCGGAAGATC 2376
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
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QY 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 2437 ATGGGCAATCGAGTACCAAGAGCGCCGAGGAGCTCACCAAGCCCTGGAATCAGCAAC 2496
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799
Db 2497 ATCGTCTTACCAAGCCTCTTCGCTTGAGAGATGCTGTGAALACTGCTGTCTACGGTCCC 2556
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819
Db 2557 TTGGCTACATTAAGAATCCCTACCAACATCTTGATGGTGTCAATTGTGTCACTCAGTGTG 2616
QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
Db 2617 TGGAGATTGTGGCCAGCAGGAGGTGGCCTGTCCGTGCTGCGGACCTTCCGCTGATG 2676
QY 840 ArgValIleuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
Db 2677 CGGCTGTGAAGCTGGTGGCTTCTTCGCGCTTCGCCGCCAGCCAGCTCGTGTGCTCATG 2736
QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuMetLeuPheIlePheIlePhe 879
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QY 920 LeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939
Db 2917 CTGACTCAGAAAGACTGGAATAAGTCTCTCAACCGCATGGCCTCCACATGCTCTTGG 2976
QY 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959
Db 2977 GCTGCTCTTACTTCATCGCCCTCATGACTTTTGGCACTATGTGCTCTTAACTGCTG 3036
QY 960 ValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSer 979
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QY 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019
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QY 1040 IleIleHisThrAlaAlaThrPrometSerLeuProLysSerThrSerThrGlyLeuGly 1059
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QY 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079
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QY 1080 Ala---HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098
Db 3397 GCCCACCATGAGATGAATCTCCGCCAAGTGCCCGCAGCTCCCGCACAGTCCCTGAGT 3456
QY 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118
Db 3457 GCGGCAAGCAGCTGGACAGCAGCGGCTCCAGCAGGAACAGCCTGGCGCGGGCCCCAGC 3516
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QY 1159 ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu 1178
Db 3637 CGCCACAGGGGTTCTTGGAACGTGAGGCCAAGAGTCTTTGACCTGCTGACACTCTG 3696
QY 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198
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QY 1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAla 1238
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QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
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QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538
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QY 1569 -----LysAlaGlnCysLysProTyrTyrSerAspTyrSer 1580
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Db 4897 GGCAGCTCAGCCAGCGCTGCGTCAAGAGCCCAAGCCCTACTACTCTGACTACTCG 4956
QY 1581 ArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleThr 1600
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Db 5197 GACCTGGCTATGTGCTTCTGTCCATCATGGGCATCACACTGAGAGGATTGAGGTCAT 5256
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QY 1958 TrpGlyLeuProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAsp 1977
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Db 6097 TGGGGGCTCCCCAAAGCCAGTCAAGCTCCATCTTGTCCGTTCACTCCCAACAGCAGAC 6156
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Db 6337 CGGGAAGACCTGTTGTCAAGAGTGAGTGGGCCCTCCTGACCCGCTCCTCATCC 6396
QY 2058 PheTrpGlyGlnSerSerThrGlnaGlnGlnHisSerArgSerHisSerLysIleSer 2077
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Db 6397 TTCTGGGGCGGGTGAAGCATCCAGGTGACGACGCGTTCCGGCATCCAGACAAAGTCTCC 6456
QY 2078 LysHisMetThrProAlaProCysBProGlyProGluProAsnTrpGlyLysGlyPro 2097
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QY 2098 ProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu 2117
| | | | |

Db 6517 CCAGAGACCAGAGCCTTAGAGCTGGACACGAGCTGAGCTGATTTTCAGAGACCTC 6576
Qy 2118 LeuProGluGlyGlnGluGluProProSerProArgAspLeuLysLysCysTyrSer 2137
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Qy 2138 ValGluAlaGlnSerCysGlnArgArgProThrSerTyrLeuAspGluGlnArgHis 2157
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Qy 2158 SerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSer 2177
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Qy 2178 AsnLeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLeuSerPro 2197
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Db 6814 CCCAGTATCTATAGACCCCGGAGAGCCAGGCGCTCGGCCCCCATGACATCGCTGGT 6873
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Db 6874 GTCTGCCTCAGAGAGGAGGGCGCCGCACTGACTTAAGATCCCTCGGTCTCCAGCCCC 6933
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RESULT 8
US-10-377-139-7
; Sequence 7, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: Jiang, Youxing
; APPLICANT: Lee Mackinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 6942
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-377-139-7

Alignment Scores:
Pred. No.: 0 Length: 6942
Score: 10945.00 Matches: 2107
Percent Similarity: 93.99% Conservative: 34
Best Local Similarity: 92.49% Mismatches: 101
Query Match: 91.94% Indels: 36
DB: 19 Gaps: 6

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Qy 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp 40
Db 174 CAGCTCAACGACCTGTCCGGGGCGGGGGCCGGCAGAGGGCCGGGTGCGACGAAAAAGAC 233

Qy 41 ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal 60
Db 234 CCGGCGACGCGCGACTCCGAGCGCGGAGGGGGTGTCCGTACCCGCGCTAGCCCCGGTGT 293
Qy 61 PhePheTyrLeuSerGlnAspSerArgProArgSerTyrCysLeuArgThrValCysAsn 80
Db 294 TTTCTTACTTGAAGCCAGACAGCCGCCCGGAGCTGTGTCTCCGACGGTCTGTAAAC 353
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Db 354 CCGTGGTTCGAGCGAGTCAGTATGCTGTGATCTTCTCAACTGTGTACTCTGGTATG 413
Qy 101 PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe 120
Db 414 TTCAGGCCGTGTGAGGACATTCCTGTGATCCAGCGCTGCCGATCCTGACGCCCTTC 473
Qy 121 AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly 140
Db 474 GATGACTTCATCTTGGCTTCTTGTGCTGTGGAATGTGTGTAAGATGTGGCCTTGGGC 533
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Qy 161 IleAlaGlyMetLeuGluTyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 594 ATTGACGGATGTGAGTATTCGCTGACCTGCAGAAACGTACAGCTTCTCCGACGTACG 653
Qy 181 ThrValArgValLeuArgProLeuArgAlaIleAsnArgValProSerMetArgIleLeu 200
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Qy 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArg 240
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Qy 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIle 340
Db 1074 ACCAACTGCTTCGGGGGAGCACAAACCTTCAAAAGCGCCATCACTTTGACAACATT 1133
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QY 501 HisHisHisHisTyrHisHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGlu 520
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QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
1674 ATCCAGGACAGGAGATGCCAATGGGTCTCGCGGCTCATGTACCAACCACTCTACACCC 1733
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
1734 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGAGTCTGTACACAGCTTCTACCATGTGAC 1793
QY 561 CysHisLeuGluProValAlaArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
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QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProProGlu 600
1854 GGTAAGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCACTCCACACAG 1913
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
1914 ATACTGAAGATAAAGCACTAGTGAGGTGGCCCCAGCCCTGGGCCCCACCCCTCAC 1973
QY 621 SerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSer 640
1974 AGCTTCAACATCCCACCTGGGCCCTTCAGCTTCATGCACAAGCTCCTGGAGACACAGAGT 2033
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
2034 ACGGAGCCTGCAATAGCTCTGCMAAATCTCCAGCCCTTGCTCCAGGCAAGACAGTGA 2093
QY 661 AlaCysGlyProAspSerCysProTyrCysAlaArgAlaGlyAlaGlyGluValGluLeu 680
2094 GCCTGCGGCGGACAGTGTCTCTACTGTGCCCGGACAGAGCAGAGCAGAGCAGAGTCC 2153
QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
2154 GCTGACCATGTGATGCTGACTCAGACAGCGAGGCTGTATGATGATCACAAGAGCGCT 2213
QY 701 GlnHisSerAspLeuArgAspProHisSer---ArgArgGlnArgSerLeuGlyProAsp 719
2214 CAGCACAGTGACCTCCGGGATCCCAACAGCCGCGGCGGACAGCGGAGCTGGGCCAGAT 2273
QY 720 AlaGluProSerSerValLeuAlaPheTyrArgLeuIleCysAspThrPheArgLysIle 739
2274 GCAGAGCCTAGTCTGTGTGCTGGCTTCTGTGAGGCTGATCTGTGACACATTCGGGAAGATC 2333
QY 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
2334 GTAGATAGCAAAATACTTGGCCGGGAATCATGATCCCATCTGTGTCAATACACTCAGC 2393
QY 760 MetGlyIleGlyTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779

Db 2394 ATGGGCAATGAGTACCACGAGACGCCGAGAGACTCACCAACGCCCTGAAATCAGCAAC 2453
QY 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799
2454 ATCGTCTTACCAAGCCTCTTGCCCTTGAGATGTGTGAAACTGCTGTGTACGGTCCC 2513
QY 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValValIleSerVal 819
2514 TTGGCTACATTAAGATCCCTACACATCTTGATGGTGTCAATTGTGTCACTAGTGTG 2573
QY 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
2574 TGGGAGATTGTGGCCAGCAGGAGGTGGCTGTGCGGTCTGCGGACCTTCGCGCTGATG 2633
QY 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValLeuMet 859
2634 CGGGTGTGAAGCTGTGCGCTTCTGCGGCCCTGCAAGCCGACGCTCGTGTGCTCATG 2693
QY 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheIlePhe 879
2694 AAGACCATGACAACGCTGGCCACTTCTGCATGTCTTCATGTCTGTTCACTTCATCTTC 2753
QY 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAspGlyAspThr 899
2754 AGCATCCTGGGCATGCATCTCTTGTTGTCAGAGTTCGCATCTGAAACGGATGGGACACG 2813
QY 900 LeuProAspArgLysAsnPheAspSerLeuLeuThrPalaIleValThrValPheGlnIle 919
2814 TTGCCAGACCGGAAGAAATTTCCACTCCCTGCTCTGGGCCATCGTCACTGTCTTCAGATT 2873
QY 920 LeuThrGlnGluAspTyrPasnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrp 939
2874 CTGACTCAGGAAGACTGGAATAAAGTCTCTACAAACGGCATGGCCCTCCACATCGTCTTG 2933
QY 940 AlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuLeu 959
2934 GCTGCTCTTAATCTCATCGCCCTCATGACTTTGGCACTATGTGCTCTTAACTGTGCTG 2993
QY 960 ValAlaIleLeuValGluGlyPheGlnAlaGluLysSerLysArgGluAspAlaSer 979
2994 GTGGCATTCTTGTGAAGATTCCAGGCAGAG----- 3026
QY 980 GlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSer 999
3027 -----GGAGATGCCACCAAGTCT 3044
QY 1000 GluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspArgLysLysCys 1019
3045 GAGTCAGAGCCTGATTTCTTTTCGCCAGTGTGATGTGATGGGACAGAAAGAACGCC 3104
QY 1020 LeuAlaLeuValSerLeuGlyLysHisProGluLeuArgLysSerLeuLeuProProLeu 1039
3105 TTGGCCCTGTGGCTTTGGAGAAACACCGGAACCTACGAAGAGCCTTTTGGCACCCCTC 3164
QY 1040 IleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerThrGlyLeuGly 1059
3165 ATCATCCATACGGCTGCAGACCAATGTCAACACCCCAAGAGCTCCAGACAGAGTGTGGG 3224
Db 1060 GluAlaLeuGlyProAlaSerArgArgThrSerSerSerGlySerAlaGluProGlyAla 1079
3225 GAAGCACTGGGCTGTGGCTCTCGACGTACCAAGTAGCAGTGGGTCCGCTGAGCCTGAGCT 3284
QY 1080 Ala--HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSer 1098
3285 GCCCACCATGAGATGAATGTCCGCAAGTGCCTCCGACGCTCCCGCAAGTCCCTGAGT 3344
QY 1099 AlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSer 1118
3345 GCGGCAAGCAGCTGACCAAGAGCGCTCCAGCAGGAACAGCCTGGGCCGCGCCCAAGC 3404
QY 1119 LeuLysArgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyGlyGlnGlu 1138

Db 3405 CTAAGCGAGAGACCCGAGCGGGAGCGGAGTCCCTGCTGTCTGAGAGGGCCAGAG 3464
QY 1139 SerGlnAspGluGluGluSerSerGluGluValArgAlaSerProAlaGlySerAspHis 1158
Db 3465 AGTCAGGATGAGGAGGAAGTTCAGAGAAGGACCGGGCCAGCCCAAGAGGAGTGAACCAT 3524
QY 1159 ArgHisArgGlySerLeuGluArgGluAlaIlySerSerPheAspLeuProAspThrLeu 1178
Db 3525 CGCCACAGGGGTTCTTGGAACGTGAGGCCAAGATTCTTTGACCTGCTGACACTCTG 3584
QY 1179 GlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerGluHisGlnAsp 1198
Db 3585 CAGGTGCCGGGGCTGCACCCGACAGCCGCGGAGCTTGCTCTGAGCACCAAGAC 3644
QY 1199 CysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProPro 1218
Db 3645 TGTAAATGGCAAGTCGGCTTCAGGGCGTTTGGCCCGCACCTGAGAGACTGATGACCCCAA 3704
QY 1219 LeuAspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyLysArgValArgAla 1238
Db 3705 CTGATGGGGATGATGACAATGATGAGGGAATCTGAGCAAAAGGGGAACGCATCAAGCC 3764
QY 1239 TrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIle 1258
Db 3765 TGGGTCAGATCCCGGCTTCCTGCTGTGGCCGAGCGGAGATTCCTGCTCGGCTATATC 3824
QY 1259 PheProProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPhe 1278
Db 3825 TTTCCTCCTCAGTCAAGGTTTCGTCTCTGTGTACCCGATCATCACCAAGATGTTT 3884
QY 1279 AspHisValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgPro 1298
Db 3885 GACCATGGTCTCTGTCATCATCTTCTCACTGTATCACCATCGTATGAGCGGCCCC 3944
QY 1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr 1318
Db 3945 AAAATTGACCCCAAGCGCTGAGGCATCTTCCTGACCTCTCCAACTACATCTTCACG 4004
QY 1319 AlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCysPheGlyGlu 1338
Db 4005 GCAGTCTTCTAGCTGAATGACAGTGAAGTGTGGCACTGGGCTGTGCTTGGGGAG 4064
QY 1339 GlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValIleSerVal 1358
Db 4065 CAGGCCCTACTGCGCAGCAGCTGGAATGTCTGACGGCTTGCTGCTCATCTCCGTC 4124
QY 1359 IleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArg 1378
Db 4125 ATGCACATCTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGTGAGG 4184
QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398
Db 4185 GTGCTGCGGCTGTCGGGACCTGCTCCACTCAGGGGTCAACCGGGCCAGGGACTG 4244
QY 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIle 1418
Db 4245 AAGCTGGTGAAGACTCTGATGTCACTCAAAACCAATTGGCAACATTTGTGTCAATT 4304
QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438
Db 4305 TGCTGTGCCTTCTTCATCATTTTGGAAATCTCGGGGTGAGCTCTTCAAAAGGAAGTTC 4364
QY 1439 PheValCysGlnGlyGlyLysAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAla 1458
Db 4365 TTCGTGTGTACGGGTGAGGACACCAAGAAATCACTAACAAATCCGACTGCGCTGAGGCC 4424
QY 1459 SerTyrArgTyrValArgHisLysTyrAsnPheAspAsnLeuGlyGlnAlaLeuMetSer 1478
Db 4425 AGCTACCGATGGGTCCGGCACAAATCAACTTGAACAACCTGGGCGAGGCTTGATGTCC 4484
QY 1479 LeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAla 1498
Db 4485 CTGTTTGTGTGGCTCCAAAGGATGTTGGGTGACATCATGTATGATGGGCTGATGCT 4544

QY 1499 ValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIle 1518
Db 4545 GTGGTGTGATCAGACGCCCATCATGAACCAACACCCTGGATGCTGTATCTCATC 4604
QY 1519 SerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGlu 1538
Db 4605 TCCTTCCCTCATCGTGCGCTTCTTGTCTGAACATGTTTGGGCGTGGTGGAG 4664
QY 1539 AsnPheHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLys 1558
Db 4665 AACTTCCATAAGTGACAGACAGCACAGAGAGAGAGCGAGCGGCGTGAGAGAAAG 4724
QY 1559 ArgLeuArgArgLeuGluLysLysArgArg-----LysAlaGln 1571
Db 4725 CGACTACGGAGGCTGAGAAAGAGAGAGTAAGAGAGAGAGAGAGAGATGGCCGAAGCCAG 4784
QY 1572 CysLysProTyrTyrSerAspTyrSerArgPheArgLeuLeuValHisIleuCysThr 1591
Db 4785 TGCAAGCCCTACTACTGTGACTACTCGAGATTCCGGCTCTTGTCCACCACTGTGTACC 4844
QY 1592 SerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAla 1611
Db 4845 AGCCACTACCTGAGCCCTTCATCACTGGTGTGATCGGGCTGAACGTGTCACTATGGCC 4904
QY 1612 MetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCysAsnTyrIle 1631
Db 4905 ATGGAACATTACCAGCAGCCCAAGATCCTGGAGAGGCTCTGAAGATGTCAATTACATC 4964
QY 1632 PheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArg 1651
Db 4965 TTTAACGTCATCTTGTCTTTGAGTCAGTTTCAACTTGTGGCCTTGGCTCCGCCGT 5024
QY 1652 PhePheGlnAspArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGly 1671
Db 5025 TTCTTCCAGGACAGGTGAACACAGCTGAGCCTGGCTATTGTGCTTCTGTCCATCATGGGC 5084
QY 1672 IleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArg 1691
Db 5085 ATCACACTGGAGGAGATTGAGGTCAATCTGTGCTGCCCATCAACCCCATCATCCGT 5144
QY 1692 IleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMet 1711
Db 5145 ATCATGAGGGTGTCCGCAATTGCTCGAGTCTGAAGCTGTTGAAGATGGTGTGGCATG 5204
QY 1712 ArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeu 1731
Db 5205 CGGGCACTGCTGCACACGGGTGATGACAGGCCCTGCCAGGTGGGAACTGGGACTTCTC 5264
QY 1732 PheMetLeuLeuPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGlu 1751
Db 5265 TTCATGTATTATTGTTTTCATCTTTGACGCTCGGGCGTGAGCTCTTGGAGACTGGAG 5324
QY 1752 CysAspGluThrHisProCysGluGlyLeuGlyLysArgHisAlaThrPheArgAsnPheGly 1771
Db 5325 TGTGATGAGACACACCCTTGTGAGGGCTTGGGTGGCATGCCACCTTGAAGACTTGGT 5384
QY 1772 MetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLys 1791
Db 5385 ATGGCCTTCTGACCCCTTTCGAGTCTCCACTGTGTGAACACTGGAACTGTAATTATGAAG 5444
QY 1792 AspThrLeuArgAspCysAspGlnGlnLeuSerThrCysTyrAsnThrValIleSerProIle 1811
Db 5445 GACACCTCCGGAGCTGTGACAGAGTCCACTGTCTACAAACACTGTCACTCCCTATC 5504
QY 1812 TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaVal 1831
Db 5505 TACTTTGTGTCTTGTGTGTGACGGCCAGTTTGTGCTGTCGAACGTGTCACTAGCTGTG 5564
QY 1832 LeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAla 1851
Db 5565 CTGATGAAGCACTGGAAGAAAGCAACAAGAGGCCCAAGAGAGCGGAGCTCGAGGCC 5624

QY	1852	GIuLeuGIuLeuGIuMetLysThrLeuSerProGlnProHisSerProLeuGIySerPro	1871
Db	5625	GAGCTGAGCTGAGATGAAGAAGCGCTCAGCCCGCAGCCCCACTCCCGCTGGGCAAGCCC	5684
QY	1872	PheLeuTrpProGIyValGIuGIyProAspSerProAspSerProIyAlaLeu	1891
Db	5685	TTCTCTGGCCCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGTCCA	5744
QY	1892	HisProAlaAlaHisAlaArgSerAlaSerHisPheSerLeuGIuHisProThrMetGln	1911
Db	5745	CACACCACCTGCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCACGATGGTA	5804
QY	1912	ProHisProThrGluLeuPro-----GIyProAspLeuLeuThrValArgLysSer	1928
Db	5805	CCCCACCCCGAGAGGTGCCAGTCCCCCTAGGACCAAGCCTGTGACTGTGAGGAAGTCT	5864
QY	1929	GIyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGIySerThr	1948
Db	5865	GGTGTACCGCGGACGCACTCTGCCCCATGACAGTACATGTGCCCAATGGAGCACT	5924
QY	1949	AlaGIuGIyProLeuGIyHisArgGIyTyrGIyLeuProLysAlaGlnSerGIySerVal	1968
Db	5925	GCTGAGAGATCCCTAGACACAGGGGCTGGGGCTCCCAAGCCAGTCAGGCTTCATC	5984
QY	1969	LeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAspAla	1988
Db	5985	TTGTCCGTTCACTCCCAACACAGACACACAGCAGTCATCTTACAGCTTCCCAAGATGTG	6044
QY	1989	ProHisLeuLeuGlnProHisSerAlaProThrTrpGIyThrIleProLysLeuProPro	2008
Db	6045	CACATATCTGCTCCAGCCTCATGGGGCTCCACACCTGGGGGCCATCCCTAAACTACCCCA	6104
QY	2009	ProGIyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAsp	2028
Db	6105	CCTGGCCGCTCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAATAGGACTGAC	6164
QY	2029	SerLeuAspValGlnGIyLeuGIySerArgGIuAspLeuLeuAlaGluValSerGIyPro	2048
Db	6165	TCCCTGATGTGACGGGCTGGGTAGCCGGGAAGACCTGTGTGCAGAGGTGAGTGGGCC	6224
QY	2049	SerProProLeuAlaArgAlaTyrSerPheTrpGIyGlnSerSerThrGlnAlaGlnGln	2068
Db	6225	TCCTGCCCTTGACCCGGTCTCATCTTCTGGGGGGTGCAGCATCCAGTGCAGCAG	6284
QY	2069	HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGIy	2088
Db	6285	CGTTCGGGCATCCAGAGCAAAGTCTCCAAGCACATCCGCTGCCAGCCCTTGCCCAAGC	6344
QY	2089	ProGIuProAsnTrpGIyLysGIyProProGIuThrArgSerSerLeuGIuLeuAspThr	2108
Db	6345	CTGGAACCCAGCTGGGCGCAAGACCCTCCAGAGACCAGAAGCACTTAGAGCTGACACG	6404
QY	2109	GIuLeuSerTrpIleSerGIyAspLeuLeuProProGIyGIyGlnGIuGIuProProSer	2128
Db	6405	GAGCTGAGCTGGATTTCAGAGACCTCCTT--CCAGCAGCCAGGAAGAACCCCTGTTTC	6461
QY	2129	ProArgAspLeuLysLysCysTyrSerValGluAlaGlnSerCysGlnArgArgProThr	2148
Db	6462	CCACGGGACCTGAAAGAGTGCTTACAGTGTAGAGACCAGAGCTGCAGGGCGCAGGCTGGG	6521
QY	2149	SerTrpLeuAspGIuGlnArgArgHisSerIleAlaValSerCysLeuAspSerGIySer	2168
Db	6522	TTCTGGCTAGATGAACAGCGGACACTCCATTGCTGTCACTGTCTGGACAGCGGCTCC	6581
QY	2169	GlnProHisLeuGIyThrAspProSerAsnLeuGIyGIyGlnProLeuGIyGIyProGIy	2188
Db	6582	CAACCCCGCCTATGTCGAAGCCCTCAAGCCTCGGGGCAACCTTGGGGTCTCTGGG	6641
QY	2189	SerArgProLysLysLysLeuSerProProSerIleThrIleAspProProGIuSerGln	2208
Db	6642	AGCGGCGCTAAGAAAAACTCAGCCCAACCAAGTATCTCTATGACCCCCCGAGAGCCAG	6701
QY	2209	GIyProArgThrProProSerProGIyIleCysLeuArgArgArgAlaProSerSerAsp	2228

Db 6702 GGCTCTCGCCCCCAATGCAGTCTGTGTCTGCTCAGGAGGAGGGCGCCGCACTGAC 6761

QY 2229 SerLysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSerProLys 2248

Db 6762 TCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACAGCAGGCTGCCTCACCCCTCCCAAG 6821

QY 2249 LysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266

Db 6822 AAAGACACGCTGAGTCTCTGTGTTGTCTTGTGACCCCAACAGACATGACCCCC 6875

RESULT 9

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US-10-930-301-51
: Sequence 51, Application US/10930301
: Publication No. US20050026207A1
: GENERAL INFORMATION:
: APPLICANT: Issa, Jean-Pierre
: TITLE OF INVENTION: CAGNAIG POLYNUCLEOTIDE POLYPEPTIDE AND
: TITLE OF INVENTION: METHODS OF USE THEREFOR
: FILE REFERENCE: JHU1590
: CURRENT APPLICATION NUMBER: US/10/930,301
: CURRENT FILING DATE: 2004-08-30
: PRIOR APPLICATION NUMBER: US/09/398,522
: PRIOR FILING DATE: 1999-09-15
: NUMBER OF SEQ ID NOS: 120
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 51
: LENGTH: 3993
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: CAGNAIG - a gene encoding a T-type calcium channel
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (373)...(3993)
US-10-930-301-51

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Alignment Scores:

Pred. No.:	0	Length:	3993
Score:	6315.50	Matches:	1207
Percent Similarity:	98.13%	Conservative:	0
Best Local Similarity:	98.13%	Mismatches:	0
Query Match:	53.05%	Indels:	23
DB:	21	Gaps:	1

US-09-611-257A-37 (1-2266) x US-10-930-301-51 (1-3993)

QY	1	MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet	20
Db	373	ATGCACGACGAGGAGGATGGAGCGGGCCCGACGAGAGTCGGACAGCCCGGAGCTTCATG	432
QY	21	ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyProGlySerAlaGluLysAsp	40
Db	433	CGGCTCAACGACCTGTGCGGGGGCCGGGGCCGGGGCCGGGGTCAAGAAAGAGAC	492
QY	41	ProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAlaLeuAlaProValVal	60
Db	493	CCGGGACGCGGACTCCGAGGCGGAGGGCTGCCGTACCCGGCGTGGCCCCGGTGTT	552
QY	61	PhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsn	80
Db	553	TTCTTCTTACTTGAGCCAGGACAGCCGCCCGGAGAGCTGGTCTCCGACGGTCTGTAAAC	612
QY	81	ProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMet	100
Db	613	CCCTGGTTTGAGCGGCATCAGCATGTTGTTCATCTTCTCAACTGCCTGACCCCTGGGCATG	672
QY	101	PheArgProCysGluAspIleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPhe	120
Db	673	TTCCGGCCATGCGAGGACATGCGCTGTGACTCCAGCGCTGCCGATCCTGCAGGCCCTTT	732
QY	121	AspAspPheIlePheAlaPhePheAlaValGluMetValValLysMetValAlaLeuGly	140

Db 733 GATGACTTCATCTTTGCTTCTTTGCCGTGGAGATGGTGTGAAGATGTTGGCCTTGGGC 792
QY 141 ILePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleVal 160
Db 793 ATCTTTGGGAAAAAGTGTACCTGGGAGACACTTGAAACCGGCTTGACTTTTCATCGTC 852
QY 161 ILeAlaGlyMetLeuGluTyrSerIleuAspLeuGlnAsnValSerPheSerAlaValArg 180
Db 853 ATCGCAGGGATGCTGGAGTACTCGCTGGACCTGCAGAAACGTCAAGCTTCTCAGCTGTCAAG 912
QY 181 ThrValArgValLeuArgProLeuAlaIleAsnArgValProSerMetArgIleLeu 200
Db 913 ACAGTCCGTGTGCTGCAGACCGCTCAGGGCCATTAAACGGGTGCCCAGCATGCGCATCCTT 972
QY 201 ValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePhe 220
Db 973 GTCACGTTGCTGGATACGCTGCCATGCTGGCAACGTCCTGCTGCTGCTTCTTC 1032
QY 221 ValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArg 240
Db 1033 GTCTTCTTCATCTTCGGCATCGTCGGGCTCCAGCTGTGGGAGGGGCTGCTTCGGAACCGA 1092
QY 241 CysPheLeuProGluAsnPheSerIleuProLeuSerValAspLeuGluArgTyrTyrGln 260
Db 1093 TGCTTCCTACTGAGAATTTCAGCCTCCCTGAGCGTGGACCTGGAGCGCTATTACCAAG 1152
QY 261 ThrGluAsnGluAspGluSerProPheIleCysSerGlnProArgGluAsnGlyMetArg 280
Db 1153 ACAGAGAACGAGATGAGAGACCCCTTCATCTGCTCCAGCCAACGAGAACGGCATGCGG 1212
QY 281 SerCysArgSerValProThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu 300
Db 1213 TCCTGCAGAAAGCGTCCACCGCTGCGGGGAGCGGGCGGTGGCCACCTTGCGGTCTG 1272
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThrCysValAsnTrpAsnGlnTyrTyr 320
Db 1273 GACTATGAGGCTACAACAGCTCCAGCAACACACCTGTGTCAACTGGAAACCACTACTAC 1332
QY 321 ThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyValIleAsnPheAspAsnIle 340
Db 1333 ACCAAGTGTCAAGCGGGGAGACAAACCCCTTCAAGGGCGGCATCACTTGACAACATT 1392
QY 341 GlyTyrAlaIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAspIleMet 360
Db 1393 GGCTATGCTGGATCGCCATCTTCCAGGTCAACGCTGGAGGGCTGGTGCACATCATG 1452
QY 361 TyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeuIleIle 380
Db 1453 TACTTTGTGATGATGCTCATTTCTTCACAATTTCATCTTCACTTCACTCCTCATATC 1512
QY 381 ValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPheSerGlu 400
Db 1513 GTGGGCTCCTTCTCATGATCAACCTGTGCTGTGGTGAATTGCCACGCACTTCAGAG 1572
QY 401 ThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSerAsnAla 420
Db 1573 ACCAAGCAGCGGGAAGCCAGCTGATGGGGAAGCAGCGTGTGGCTTCTGTCCAAGCC 1632
QY 421 SerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGlnLeuLeuLysTyrLeu 440
Db 1633 AGCAACCTGGCTAGCTTCTCTGAAGCCCGCAGCTGTGATAGAGAGCTGTCAAGTACTG 1692
QY 441 ValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAlaGlyVal 460
Db 1693 GTGTACATCTTCTGTAAGCAGCCCGCAGGCTGGCTCAGGTCTCTCGGGCAGCAGGTGTG 1752
QY 461 ArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSer 480
Db 1753 CGGGTTGGGCTGTCAAGCAGCCAGCAACCTCGGGGCGCAGAGAACCCAGCCAGCAGAC 1812
QY 481 SerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHisHisHis 500
Db 1813 AGCTGCTCTGCTCCCAACGCGCGCTATCCGTCCACCAACCTGTGCAACCAACCAACAC 1872

QY 501 HisHisHisHisTyrHisLeuGlyAsnGlyThrLeuAlaAlaProArgAlaSerProGlu 520
Db 1873 CATCAACCACTACTACCTGGGCAATGGAGCGCTCAGGGCCCCCGGGCCAGCCCGAG 1932
QY 521 IleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSerThrPro 540
Db 1933 ATCAGAGACAGGATGCCAATGGGTCCCGCGGCTCATGCTGCACCAACCTCGACGCCT 1992
QY 541 AlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHisAlaAsp 560
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QY 561 CysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGluAlaSer 580
Db 2053 TGCCACTTAGAGCCAGTCCGCTGCCAGCGCCCTCCAGGTCCCACTGAGGCATCC 2112
QY 581 GlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProProGlu 600
Db 2113 GGCAGAGCTGTGGGACGGGGAAGGTGATCCCAACGTGCACACAGCCCTCCACCGAG 2172
QY 601 ThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThrLeuThr 620
Db 2173 ACGTGAAGAGAGAGGCACTAGTAGAGTGGTCCAGCTCTGGGCCCCCAACCTCAC 2232
QY 621 SerLeuAsnIleProProGlyProTyrSerSerSerMetHisLysLeuLeuGluThrGlnSer 640
Db 2233 AGCTCAACATCCCAACCGGGCCCTTACAGCTCCATGCACAAGCTGCTGAGACACAGAGT 2292
QY 641 ThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAspSerGly 660
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QY 681 AlaAspArgGluMetProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAla 700
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QY 701 GlnHisSerAspLeuArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAla 720
Db 2473 CAGCAGACGACCTCCGGGACCCCAAGCCGGCGCAACGAGCCTGGGCCCAGATGCA 2532
QY 721 GluProSerSerValLeuAlaPheTrpArgLeuIleCysAspThrPheArgLysIleVal 740
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QY 741 AspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMet 760
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QY 761 GlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIle 780
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QY 841 ValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLys 860
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QY 861 ThrmcAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSer 880
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QY 881 IleLeuGlyMetHisLeuPheGlyCysIysPheAlaSerGluArgAspGlyAspThrLeu 900
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QY 901 ProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeu 920
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QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGluSerGln 1140
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; Publication No. US20050164161A1
; GENERAL INFORMATION:
; APPLICANT: Kath, Gary S.
; APPLICANT: McManus, Owen
; APPLICANT: Galyantes, Tina
; APPLICANT: Bennett, Paul B., Jr.
; APPLICANT: Imredy, John P.
; APPLICANT: Augustine, Paul R.
; APPLICANT: Bugianesi, Randal M.
; TITLE OF INVENTION: ELECTRICAL FIELD STIMULATION OF
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 20794YP
; CURRENT APPLICATION NUMBER: US/10/483,467
; CURRENT FILING DATE: 2004-01-12
; PRIOR APPLICATION NUMBER: PCT/US02/22161
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/304,955
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7898
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-483-467-3
Alignment Scores:
Pred. No.: 0 Length: 7898
Score: 6215.50 Matches: 1368
Percent Similarity: 65.29% Conservative: 212
Best Local Similarity: 56.53% Mismatches: 518
Query Match: 52.21% Indels: 322
DB: 22 Gaps: 60
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QY 27 G1YAlaG1YArgProGlyPro-GlySer----- 36
Db 350 GGGCGCGGAGCGGAGCGGAGCGGGGTCCAGACTCGGCGTGTCACTCCGAGAGCCC 409
QY 37 ----AlaGluLysAspProGlySerAlaAspSerGluAlaGluGlyLeuProTyrProAl 55
Db 410 GCGCGCGGAGCGCGCGCGGAGCTGGGTGCCAGCAGAGAGCAGCGCGTCCCGTACCGGCG 469
QY 55 aLeuAlaProValAlaPhePheTyrLeuSerGlnAspSerArgProArgSerTrpCysLe 75
Db 470 CTTGGCGGCCACGGTCTTCTTCTGCTCGTCAAGACCAAGCGCGCGCGCAGCTGTGCT 529
QY 75 uArgThrValCysAsnProTrpPheGluArgIleSerMetLeuValIleLeuLeuAsnCy 95
Db 530 CCGGCTGTGTGCAACCATGTGTTGAGCAGCTGAGCATGTGTTAATCATGTCTAACTG 589
QY 95 sValThrLeuGlyMetPheArgProCysGluAspIleAlaCysAspSerGlnArgCysAr 115
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QY 115 gIleLeuGlnAlaPheAspAspPheIlePheAlaPhePheAlaValGluMetValValLy 135
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QY 135 smetValAlaLeuGlyIlePheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLe 155
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QY 855 uValValLeuMeLysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPh 875
Db 2963 CGTGGTGTGTGAAGACCATGACCAACGTGGCTACCTTCTGCACGCTGCTCATGTCTTT 3022
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QY 895 gAsp---GlyAspThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaileVa 914
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QY 974 sArGluAspAlaSerGlyGlnLeuSerCysileGlnLeuProValAspSerGlnGlyl 994
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QY 994 yAspAlaAsnLysSerGluSerGluProAspPheSerProSerLeuAspGlyAsp-- 1013
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QY 1014 -----GlyAspArgLysLysCysLeuAlaLeuValSerLe 1025
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QY 1163 rLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeu----- 1178
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QY 1192 rAlaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuAlaArgAlaLe 1212
Db 3962 TGCAGCCGAGCTTGACGACGACTCGGAGGACAGACGTGTGCTCCCGCTGCATTAAGTCT 4021
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Db 4022 GGAGCCCTTACAAGCCC----- 4037
QY 1232 sGlyGluArgValArgAlaTrpIleArgAlaArgLeuProAlaCysTyrLeuGluArgAs 1252
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Db 4058 GGCCTGGGCCCTTACCTCTTCTCCCAAGAACCGGTCGGCTCTCCTGCCAAGAGT 4117
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QY 1312 uSerAsnTyrIlePheThrAlaValPheLeuAlaGluMetThrValLysValAlaAla 1332
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QY 1332 uGlyTyrPheGlyGlyGlnAlaTyrLeuArgSerSerTrpAsnValLeuAspGlyLe 1352
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QY 1352 uLeuValLeuileSerValileAspIleLeuValSerMetValSerAspSerGlyThrLy 1372
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QY 1432 nLeuPheLysGlyLysPhePheValCysGlnGlyGluAspThrArgAsnileThrAsnLy 1452
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QY 1452 sSerAspCysAlaGluAlaSerTyrArgTrpValArgHisLysTyrAsnPheAspAsnle 1472
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Db 4778 GTAAGACGGGCTGATGCGGTGTGTCAGACAGCAGCTGTGAGAAACCAACCCCTGT 4837
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Db 4898 CGTGGCGGTGTGTGAGAACTTCCACAAGTGC CGCGCAGCACCAAGAGCGGAGAGGC 4957
QY 1552 aArgArgArgGluGluLysArgLeuArgGluGluLysLysArgArg----- 1568
Db 4958 GCGCGCGGAGAGAGAGCGGCTGCGCGCTAGAGAGAGGCGCAGAGCACTTCCC 5017
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Db 5198 GTACTGCAACTACGTCTTCAACCATCGTGTGTTGCTTCGAGGCTGCACGTGAAGCTGTAGC 5257
QY 1646 aPheGlyPheArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValIle 1666
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Db 5318 GCTGTCACTCATGGGCATCACGCTGAGAGATAGAGATGAGCGCGCTGCCATCAA 5377
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Db 5858 ACGGAGGATGCGGAGCTGACGCGCAGATCGAGCTGAGATG----- 5900
QY 1863 nProHisSerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerPr 1883
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QY 1936 uProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyPro----- 1952
Db 6029 GCCCAACGACAGCTACATGTTACAGGCCCGTGTGCTGCTCGGCGGCCCA CCGCGCC 6088
QY 1953 -----LeuGlnHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySe 1967
Db 6089 GCTGCAGGAGGTGAGATGAGACCTATGGGCGCGCACCC-----TTGGGCTC 6139
QY 1967 rValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAs 1987
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Db 6195 -----CTGGTGTGTCTGCCAGCCAGAGAGCGGAGCCCTCCACGCCCTGTG 6244
QY 2007 oProProGly-----ArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaI 2025
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QY 2025 eArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeu-----Al 2043
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QY 2043 aGluValSerGlyProSerPro-----ProLeuAlaArgAlaTyrSerPheTyrGly-- 2060
Db 6362 AGAGCTGTGAGAAACCCCGGTGAGGCGCGGTGACCCAGGGGGGCTCCCTGCAGTCCC 6421
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Db 6422 ACCACGCTCCCAAGCGCCGCCAGCGTCCGACATCGTAAGCATACC--TTCGACAGCA 6478
QY 2079 sMetThrProProAlaPro---CysProGlyProGluProAsnTyrGlyLysGlyProPr 2098
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Db 6516 -GAGCGGAGGCTCTCGAGCCAGCCAGCGAGGATCAAGCATCACCACTCCGCTG 6574
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QY 2208 nGlyProArgThrProProSerPro-----GlyIleCysLeuArgArgArgAlaPr 2225

Db 6851 GGGCTTCGGCGGCCCTCCGCGGACAGGGCGGACACCACTGAGCGCAGACCCC 6910
Qy 2225 oSer-----SerAspSerLysAspProLeu-----AlaSe 2235
Db 6911 GTCCTGTGAGGCCACGCCCTCACAGGACTCCCTGGAGCCCCACAGAGGGCTCAGGCCGCG 6970
Qy 2235 rGlyProProAspSerMetAla-----AlaSerProSerProLysLysAspValLe 2252
Db 6971 GGGGACCCCTGCAGCCCAAGGGGAGCGCTGGGGCCAGGCTCCTGCGCGGCTGAGACCT 7030
Qy 2252 uSerLeuSerGlyLeuSerSerAspProAlaAspLeu-----AspPro 2266
Db 7031 GACCGTCCCAAGCTTTGCTTGTAGCCGCTGACCTCGGGGTCCCAAGTGAGACCTT 7088

RESULT 11
US-10-377-139-8

Sequence 8, Application US/10377139
Publication No. US20040175761A1
GENERAL INFORMATION:
APPLICANT: Mackinnon, Roderick
APPLICANT: Jiang, Youxing
APPLICANT: Lee Mackinnon, Alice
APPLICANT: Ruta, Vanessa
TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
CURRENT APPLICATION NUMBER: US/10/377,139
CURRENT FILING DATE: 2003-03-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 6990
TYPE: DNA
ORGANISM: Homo sapiens
US-10-377-139-8

Alignment Scores:
Pred. No.: 0 Length: 6990
Score: 5496.50 Matches: 1244
Percent Similarity: 60.31% Conservative: 216
Best Local Similarity: 51.38% Mismatches: 525
Query Match: 46.17% Indels: 437
DB: 19 Gaps: 60

US-09-611-257a-37 (1-2266) x US-10-377-139-8 (1-6990)

Qy 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
Db 73 CAGCCCGGACCCCGGAGCCCCCATCTCCCGCCAGCGCTGAGAGAGCTCTGATGA 132
Qy 51 -----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln 66
Db 133 GCTGATCCTCATGTCCACACCCAGACCTGGCGCTATTGCCCTTCTTGCTGCGACAG 192
Qy 67 AspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGluArgIle 86
Db 193 ACCACCAAGCCCCCGGAAGTGTGCATCAAGATGCTGTCAACCCGCTTGAATGTGTC 252
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 253 AGCATGCTGTGATCTGCTGAAGTGCATGCACTTGCGATGTACCAAGCGGTGCGACGAC 312
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
Db 313 ATGAGACTGCCTGTCCGACCGCTGCAAGATCCTGCAGGTCTTTGATGACTTCACTTTATC 372
Qy 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys 146
Db 373 TTCTTTGCCATGAGATGGTCTCAAGATGTGGCCCTGGGATTTTGGCAAGAAGTGC 432
Qy 147 TyrLeuGlyAspThrTyrAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166

Db 433 TACCTGGGGACACATGGAACCGCCTGGATTCTTTCATGCTCATGCGAGGAGTGTGAG 492
Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 493 TACTCCTTGGAACCTTCAGAACATCAACCTGTCAAGCATCCGACCGTGGCGTCTGAGG 552
Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
Db 553 CCCCTCAAGCCATCAACCGCGCTGCCAGTATGCGGATCTGTGAACCTGCTCTTGAC 612
Qy 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226
Db 613 ACATGCCCCATGTGGGAATGCTGTGCTGCTGCTTGTGCTTGTCTTCACTTTTGGC 672
Qy 227 IleValGlyValGlnLeuTyrAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
Db 673 ATCATAGTGTGACAGCTGTGGCGGGCTGTGCGTAAACCGCTGCTTCCGTGAGAGAAC 732
Qy 247 PheSerLeuProLeuSerValaAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
Db 733 TTCACCATACAAAGGGGATGTGGCTTGCCCCCATATCAACCAACCGGAGAGATGATGAG 792
Qy 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
Db 793 ATGCCCTTCACTGTCTCCCTGTGCGGCGCAATGGGATTAAGGCTGCCATGATCCCC 852
Qy 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 853 CCGCTCAAGAGACAG-----GCCGTGAGTGTGCTGTCCAAAGACGACGTCTAC 903
Qy 301 AspTyrGluAlaTyrAsnSerSerAsnThrThr-----CysValAsnTyrAsnGln 318
Db 904 GACTTTGGGGGGGGCGCCAGACCTCAATGCCAGCGGCTGTGTCAACTGAACCGT 963
Qy 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
Db 964 TACTACAATGTGTGCCGACGGGCGCAACCCCAAGGGTGCCATCAACTTGAC 1023
Qy 339 AsnIleGlyTyrAlaTyrPheAlaIlePheGlnValIleThrLeuGluGlyTyrValAsp 358
Db 1024 AACATCGGTATGCTTGGATTGTCACTTCCAGGTGATCACTGGAAGGCTGGGTGAG 1083
Qy 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
Db 1084 ATCATGTACTAGTGTGATGATGCTCACTCTTCTACAACCTTCATCTCACTTCTGCTT 1143
Qy 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
Db 1144 ATCATAGTGGGCTCTTCTTCATGATCAACCTGTGCTGCTGTGCATAGCAGCCAGTTC 1203
Qy 399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
Db 1204 TCGAGACCAAGCAACGGGAGCACCGGCTGATGCTGAGCAGCGGACCGCTACCTGCC 1263
Qy 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLeuLys 438
Db 1264 --TCCAGCACGGTGGCCAGCTACGCCGAGCCTGGCGACTGCTACGAGAGATCTTCAG 1320
Qy 439 TyrLeuValTyrIleLeuValGlyAlaIleArgArgLeuAlaGlnValSerArgAlaAla 458
Db 1321 TATGTCTGCACATCTGCGCAAGGCCAAGCGC-----CGCGCCCTG 1362
Qy 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478
Db 1363 GGCTCTACAGGCCCTGCAGAGCGCGGCCAGGCCCTGGGCCGAGGCCCGGCCCC 1422
Qy 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisHisLeuValHisHis 498
Db 1423 GCCAAACCT-----GGGCCCCAC 1440
Qy 499 HisHisHisHisHisHisTyrHis-----LeuGlyAsnGlyThrLeuArgAlaPro 515
Db 1441 GCCAAGAGCCCCGGCACTACCATGGGAAGACTAAGGTCAGGA----- 1485

Qy 516 ArgAlaSerProGluIleGlnAspArgAspAlaAsn---GlySerArgArgLeuMet--- 533
Db 1486 -----GATGAAGGAGACATCTCGGAAGCCGGCATTTGCCAGACT 1524
Qy 534 LeuProProProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerVal 553
Db 1525 TTGCATGGGCTTCCTCCCT-----GGAATGATCACTCGGAGAGAG----- 1569
Qy 554 HisSerPheTyrHisAlaAspCysHisLeuGluProValArgCysGlnAlaProProPro 573
Db 1570 -----CTGTGC-----CCGCAA 1581
Qy 574 ArgSerProSerGluAlaSerGlyArgThrValGlySerGlyLysValTyrProThrVal 593
Db 1582 CATAGCCCCCTGGATGCGACGCCCAACCCCTG----- 1614
Qy 594 HisThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSer 613
Db 1615 ---GTGAGCCCCATCCCGCCACGCTG----- 1638
Qy 614 SerGlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHis 633
Db 1638 ----- 1638
Qy 634 LysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerPro 653
Db 1638 ----- 1638
Qy 654 CysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg--- 672
Db 1639 -----GCTTCGATCCCGCCAGCTGCCCTTGCTGCCAGCATGAG 1677
Qy 673 -----AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAsp 687
Db 1678 GACGCGCGCGGCCCTCGGCGCTGGGACGACCGAC---TCGGGCCAAGAGGGCTCGGGC 1734
Qy 688 SerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAsp 707
Db 1735 TCCGGGAGCTCCGCTGGTGGCGAG-----GACGAGCGGATGGGACGGGGCCCGGAGC 1788
Qy 708 ProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeu-- 726
Db 1789 AGCGAGACGAGCCTCTCAGAACTGGGGAAGAGAGAGAGAGAGAGAGAGCGGAT 1848
Qy 727 -----AlaPheTrpArgLeuIleCysAspThrPheArgLysIle 739
Db 1849 GGGCGGCTGTGGCTGTGCGGGGATGTGTGGCGGAGACGCGAACCAAGCTGCGCGCATC 1908
Qy 740 ValAspSerLysTyrPheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSer 759
Db 1909 GTGACAGACGACTACTCAACCGGGCATCATGATGGCATCTGTCAACACCGTCAAGC 1968
Qy 760 MetGlyIleGluTyrHisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsn 779
Db 1969 ATGGGCATGACGACCAACGAGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2028
Qy 780 IleValPheThrSerLeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyPro 799
Db 2029 GTGCTTCACCAACGATGTTTGCCCTGAGATGATCTGAAGCTGGCTGCATTGGGGCTC 2088
Qy 800 PheGlyTyrIleLysAsnProTyrAsnIlePheAspGlyValIleValIleSerVal 819
Db 2089 TTGACATCCTGCGTAACCCCTACACATCTTCGACAGCATATTGTCATCATCAGCATC 2148
Qy 820 TrpGluIleValGlyGlnGlnGlyGlyLeuSerValLeuArgThrPheArgLeuMet 839
Db 2149 TGGGAGATCGTGGGGGACGCGGAGCGTGGGCTGTCCGTGCTGCGGACCTTCCGGGCTG 2208
Qy 840 ArgValLeuLysLeuValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMet 859
Db 2209 CGCGTGTGAACCTGGTGGCTTCATGCTTGCCTGCGCGCGCCAGACTCGTGTGCTCATG 2268

Qy 860 LysThrMetAspAsnValAlaThrPheCysMetLeuLeuMetLeuPheIlePhe 879
Db 2269 AAGACCATGACACACCGGCCACCTTCTGCATGCTGCTCATGCTTCATCTTCATCTTC 2328
Qy 880 SerIleLeuGlyMetHisLeuPheGlyCysLysPheAlaSerGluArgAsp---GlyAsp 898
Db 2329 AGCATCCTTGGGATGCAATATTTTGGCTGCAAGTTCAAGCTCCGCAAGGACACTGGAGAC 2388
Qy 899 ThrLeuProAspArgLysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGln 918
Db 2389 ACGGTGCCCGACAGAGAACTTCGACTCCCTGCTGTGGCCATCGTCACTGTGTCCAG 2448
Qy 919 IleLeuThrGlnGluAspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSer 938
Db 2449 ATCCTCACCCAGAGAGACTGGAACGTGTTCTTCAATGGCATGGCTTCCACTTCTCCC 2508
Qy 939 TrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeu 958
Db 2509 TGGGCTCCCTCTACTTTGTGCGCCCTCATGACTTCGGCAACTATGTGCTTCAACCTG 2568
Qy 959 LeuValAlaIleLeuValGluGlyPheGlnAlaGluIleSerLysArgGluAspAla 978
Db 2569 CTGCTGGCCATCCTGGTGAAGGCTTCCAGGCGAG----- 2604
Qy 979 SerGlyGlnLeuSerCysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLys 998
Db 2605 -----GGTGAAGCCCAATGCG 2619
Qy 999 SerGluSerGluProAspPheSerProSer----- 1009
Db 2620 TCCTACTCGGACGAGGACGAGACTCATCCAACTAGAAGATTGATTAAGCTCCAGGA 2679
Qy 1010 ---LeuAspGlyAspGlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHis 1028
Db 2680 GGCCTGGAACAGCAGCGGAGATCCCAAGCTCTGCGCAATCCCATGACCCCCCAATGGGAC 2739
Qy 1029 ProGluLeuArgLysSerLeuLeuProProLeuIleIleHisThrAlaAlaThrPromet 1048
Db 2740 -----CTGAGCCCC----- 2748
Qy 1049 SerLeuProLysSerThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArg 1068
Db 2749 AGTCTCCCACTGGGTGGCACTTAGTCTGTGCGGCTGCGGAGACTGCCCCGACTC 2808
Qy 1069 Thr-----SerSerSerGlySerAla 1075
Db 2809 TCACTGACCGCGACCCCATGCTGTGGCCCTGGGCTCCCGAAGAGAGAGTGCATGTCT 2868
Qy 1076 GluProGlyAlaAlaHisGluMetLysSerProProSerAlaArgSerSerProHisSer 1095
Db 2869 CTAGGAGGATGAGCTATGACCAACGAGCTCCCTGTCCAGCTCCCGAGCTCTACTACGGG 2928
Qy 1096 ProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArg 1115
Db 2929 CCATGGGGCGGACGCGGCTGGGCGAGCCGTGCTCCAGCTGAAC----- 2976
Qy 1116 AlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerSerLeuSerGlyGlu 1135
Db 2977 -----AGCCTCAAGCAACAGCCGCTCGGCGGAGCATGAGTCCCTGCTCTCGGAG 3030
Qy 1136 ---GlyGlnGluSerGlnAspGluGluGluSerSerGluGlu-----GluArgAlaSer 1152
Db 3031 CGGCGCGGCGGCGCCGCGGTGCGAGGTTCGCGCGGACGAGGGCGCGCGCGCGCA 3090
Qy 1153 ProAlaGlySerAspHis----- 1158
Db 3091 CCCCTGCAACACCCACACGAGCCCAACCATTCATCAAGGGCCCATCTGAGCCACGCCAC 3150
Qy 1159 ---ArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThr 1177
Db 3151 CGCCACCAACCGCGGAGCGTGTCTCGACAAAGGGAAGTCCGTGGAAGCTGGCCGAGCTG 3210
Qy 1178 LeuGlnValProGlyLeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGlu 1195

Db 3211 GTGCCCCGGTGGCGCCACCACCCCGCGCCTGGAGGGCGGCAGCCCGCCCGCGG 3270
QY 1196 HlSGlnAspCySaSnglYlYsSerAlaSerGlYArgLeuAlaArgAlaLeuArgProAsp 1215
Db 3271 CATGAGGACTGCAATGGCAGGAT-GCCCCAGCATCGC--CAAGAAGCTCTTCACCAAGAT 3326
QY 1216 AspProProLeu-AspGlyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyLuar 1235
Db 3327 GGGCGACCGCGGGGATCGCGGGAGGATGAGAGAAATCGACTACACCCTGTGCTTCG 3386
QY 1235 gValArgAlaTrpIleArgAlaArgLeuProAlaCysTrYrLeuGluArgAspSerTrpSe 1255
Db 3387 CGTCCGAAGATGATCGACGTCTATAAGCCCGACTGTGTGCGAGGTCCGCGAAGACTGTG 3446
QY 1255 rAlaTrYrIlePheProProGlnSerArgPheArgLeuLeuCyShIsArgIleIleThrAlaMe 1275
Db 3447 TGTCTACCTCTCTCTCCGAGAACAGGTTCCGGGTCTGTGTGACACCATATTGCCCA 3506
QY 1275 sLysMetPheAspHisValValLeuValIleIlePheLeuAsnCySileThrIleAlaMe 1295
Db 3507 CAAACTCTTCGACTACGTCTGTCTGCGCCTTCATCTTCTCACTGACATCACCATCGCCCT 3566
QY 1295 tGluArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTy 1315
Db 3567 GGAGCGGCTCAGATCGAGCGCGGACCGGACCGAAGCATCTTCTCACCCTGTCCAACTA 3626
QY 1315 rIlePheThrAlaValPheLeuAlaGluMetThrValLysValValAlaLeuGlyTrpCy 1335
Db 3627 CATCTTCACGGCCCATCTTCTGTGGCGAGATGACATTGAAGGTAGTCTCGCTGGCCTGTA 3686
QY 1335 sPheGlyGluGlnAlaTrYrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValle 1355
Db 3687 CTTCGGGAGCAGCGCGTACCTACGACAGCTGGAACGTGTGATGGCTTCTTGTCCT 3746
QY 1355 uIleSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGl 1375
Db 3747 CGTGTCCATCATCGACATCGTGTGTCTCCGTGCGCTCAGCCGGGGAGCCAAAGATCTTGGG 3806
QY 1375 yMeLeuArgValLeuArgLeuLeuArgTrpLeuArgProLeuArgValIleSerArgAl 1395
Db 3807 GGTCTCCGAGTCTTGTGGGCTCTGCGCACTTACGCCCTGTGTCATCAGCCGGGCG 3866
QY 1395 aGlnGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnI 1415
Db 3867 GCCGGGCTGAAGCTGTGTGTGAGACACTATCTCTCCCTCAAGCCCATCGGCAACAT 3926
QY 1415 eValValIleCySaAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLy 1435
Db 3927 CGTGTCTCATCTGTGTGCTCTTCTTCATCATCTTTGGCATCTCTGGAGATGACGCTCTTCAA 3986
QY 1435 sGlyLysPhePheValCySglnGlyLysAspThrArgAsnIleThrAsnLysSerAspCy 1455
Db 3987 GGGCAAGTTCTACCACTGTCTGGGCGTGAGACACCGCAACATCACCAACCGCTCGGACTG 4046
QY 1455 sAlaGluAlaSerTrYrArgTrpValArgHisLysTrYrAsnPheAspAsnLeuGlyGlnAl 1475
Db 4047 CATGGCCGCCAACTACCGCTGGGTCCATCACAAATACAACCTTCGACAACCTGGGCCAGGC 4106
QY 1475 aLeuMetSerLeuPheValLeuAlaSerLysAspGlyTrpValAspIleMetTrYrAspGl 1495
Db 4107 TCTGATGTCCCTCTTGTCTGTGGCATCCAAGGATGGTTGGGTGAACATCATGTACAATGG 4166
QY 1495 yLeuAspAlaValGlyValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLe 1515
Db 4167 ACTGGATGCTGTGTGTGACACGAGCCTGTGACCAACCAACCCCTGGATGCTGCT 4226
QY 1515 uTrYrPheIleSerPheLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyVa 1535
Db 4227 GTACTTCATCTCTCTCTGCTCATCGTCAGCTTCTTTGTGCTCAACATGTTGTGGGTGT 4286
QY 1535 lValValGluAsnPheHisLysCySaArgGlnHisGlnGluGluGluAlaArgArgAr 1555

Db 4287 CGTGTGAGAACTTCCACAAGTCCCGGACAGCAGAGAGGCTGAAGAGGACGCGCGCG 4346
QY 1555 gGluGluLysArgLeuArgArgLeuGluLysLysArgArgLysAlaGlnCyLysProTy 1575
Db 4347 TGAGGAGAAGCGGCTGCGCGGCTTGAGAGAAGAGCGCGGAAGGCCAGCGGCTGCCCTA 4406
QY 1575 rTrYrSerAspTrYrSerArgPheArgLeuLeuValHisIleLeuCyThrSerHisTrYrle 1595
Db 4407 CTATGCCACTATTGTACACACCGGGCTGTCTCATCTCATCTGATGTGCACCAGCACTACCT 4466
QY 1595 uAspLeuPheIleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTy 1615
Db 4467 GGACATCTTCATCACCTTCATCATCTGCTCAACGTGTCAACCATGTCCCTGGAGCACTA 4526
QY 1615 rGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCyAsnTrYrIlePheThrValIl 1635
Db 4527 CAATCAGCCCACTCCCTGGAGACAGCCCTCAAGTACTGCAACTATATGTTACCACTGT 4586
QY 1635 ePheValLeuGluSerValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAs 1655
Db 4587 CTTGTGTCTGAGGCGTGTGCTGAAGCTGTGGCATTTGTGTGAGGCGCTTCTTCAAGGA 4646
QY 1655 pArgTrpAsnGlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGl 1675
Db 4647 CCGATGAACCAAGCTGAGCTGGCCATTGTGTCTACTGTGATCATGGGCATCACCTTGA 4706
QY 1675 uGluIleGluValAsnAlaSerLeuProIleAsnProThrIleIleArgIleMetArgVa 1695
Db 4707 GGAGATCGAGATCAATGCGGCGCTGCGCCATCAATCCACCATCATCCGATCATGAGGGT 4766
QY 1695 lLeuArgIleAlaArgValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLe 1715
Db 4767 TCTGCGCATGCGCGAGTGTGAAGCTGTTGAAGATGGCCACAGAATGCGGGCCTGCT 4826
QY 1715 uAspThrValMetGlnAlaLeuPProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLe 1735
Db 4827 GGACACGGGTGTCGAAGCTTTGCCAGGTGGGCAACCTGGCCCTCTTCATGCTGTCT 4886
QY 1735 uPhePheIlePheAlaAlaLeuGlyValGluLeuPheGlyAspLeuGluCySaAspGluTh 1755
Db 4887 CTTCCTCATCTATGTCTCTCTCGGGGTGAGCTCTTTGGGAAGCTGTGTGCAACGACA 4946
QY 1755 rHisProCySglnGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPhele 1775
Db 4947 GAACCCGTGCGAGGCATGAGCCGGCATGCCACCTTCAGAACTTCGGCATGGCCTTCTCT 5006
QY 1775 uThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuAr 1795
Db 5007 CACACTCTTCAGAGTCTCCACGGGTACAACTGGAACGGGATCATGAAGACACGCTGCG 5066
QY 1795 gAspCyS---AspGlnGluSerThrCySTyrAsnThrVal-----IleSerProIleTy 1812
Db 5067 GGACTGCACCCACGACGAGCGCAGCTGCTGAGCAGCCTGCACTTGTGTGCGCGCTGTA 5126
QY 1812 rPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValValIleAlaValle 1832
Db 5127 CTTCGTGAGCTTGTGTCTCACCGCGCATTCGTCTCATCAACGTGTGTGCTGTGCT 5186
QY 1832 uMetLysHisLeuGluGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGl 1852
Db 5187 CATGAAGCACCTGACGACAGCAAGAGAGCGGACGAGAGCGCCGAGATGATGCCGA 5246
QY 1852 uLeuGluLeuGluMet---LysThrLeuSerProGlnProHisSerProLeuGlySerPr 1871
Db 5247 GCTCGAGCTGAGATGGCCCATGGCTGGGCCCTGCGCCGAGGCTGCTACCGGCTGCC 5306
QY 1871 oPheLeuTrpProGlyValGlyLysProAsp----- 1881
Db 5307 GGGCGCC---CCTGGC---CGAGGGCGGGAGGGCGGGCGGCGGCGACACCGAGGG 5360
QY 1882 -----SerPro----- 1883
Db 5361 CGGCTTGTGCGGCGCTGTACTCGCTGCCCGCAGAGAACTGTGGCTGGAACAGCTCTC 5420

QY 1884 -----AspSerProlySProGl 1889
Db 5421 TTTAATCATCAAGGACTCCTTGAGGGGGAGCTGACCATCATCGACAACCTGTGGGCTC 5480
QY 1889 yAlaLeuHis-----ProAlaAla----- 1895
Db 5481 CATCTTCCACCACTACTCCTCGCTGGCTGCAGAAAGTGTCAACGACAGCAAGA 5540
QY 1896 -----HisAlaArgSerAlaSer----- 1901
Db 5541 GGTGACAGCTGGCTGAGACGAGGCTTCTCCCTGAACCTCAGACAGTCTCCTCGTCCATCCT 5600
QY 1902 -----HisPheSerLeuGlnHisProThrmGlnPro----- 1913
Db 5601 GCTGGGTGACGACCTGAGTCTCGAGAACCCACAGCCTGCCCCAAGACAG 5660
QY 1913 sProThrGlnLeuProGlyProAlaSerLeuThrValArgLysSerGly----- 1929
Db 5661 CAAGGCTGAGCTGGAACCCACCTGAGCCCATGCGTGTGGAGAACCTGGCGAATGCTTCTT 5720
QY 1930 ----ValSerArgThrHisSerLeuProAsn--AspSerTyrMetCysArgHisGlySe 1947
Db 5721 CCCCTTGTCTCTTAACGGCCGCTGCGCGGATCCAGAGAACTTCTGTGTAGATGAGGA 5780
QY 1947 rThrAlaGlnGlyProLeuGlnHisArgGlyTyrGlyLeuProLysAlaGlnSerGlySe 1967
Db 5781 GATCCCATTCACAACCTGTC-----CGGTCTGTG-----CTGAACATGACAGAGTCA 5828
QY 1967 rValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuProLysAs 1987
Db 5829 AGCACCCCCCAAGTCCCTTCTCCCGGATGCTCCAGCCCTCTCCTGCCATGCCAGCCGA 5888
QY 1987 pAlaProHis-----LeuLeuGlnProHisSerAlaProThrTyrGl 2001
Db 5889 GTTCTTCCACCTGCACTGTCTGCCACCCAGAAAGGCCAGAAAGGGCACTGGCACTGG 5948
QY 2001 yThrIleProLysLeuProProProGly-----ArgSerProLeuAlaGl 2016
Db 5949 AACCTTCCCAAGATTGCGCTGACGGGCTCTGGGATCTTGCCTGACCAAGGGTCAA 6008
QY 2016 nArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGl 2036
Db 6009 CTGTACCCCTCTCTCGGCGAGGCCAGCGGAGCGACACGTCGCTGAC----- 6054
QY 2036 ySerArgGlnAspLeuLeuAlaGlnValSerGlyProSerProProLeuAlaArgAlaTy 2056
Db 6055 -----GCCAGCCCCAGCAGCTCCGCGGCGAGCCTTGCA 6086
QY 2056 rSerPheTyrGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIl 2076
Db 6087 GACCACGCTCGAGGACAGCCTGACCTGAGCGACAGACCCCGCGCTGCC----- 6135
QY 2076 eSerLysHisMetThrProProAlaProCysProGlyProGlnProAsnTyrGlyLysGl 2096
Db 6136 -----CTGGGGCGCGCGCGCTGCTCCAGGACCCCGGCGCGCTGTCC----- 6180
QY 2096 yProProGlnThrArgSerSerLeuGlnLeuAspThrGlnLeuSerTyrIleSerGlyAs 2116
Db 6181 ----CCCGCGCGCTCGCGCGCGCTGAGCCTG----- 6207
QY 2116 pLeuLeuProProGlyGlyGlnGlnGlnProProSerProAlaArgAspLeuLysCysTy 2136
Db 6208 -----CGCGCGCGCGCGCTTTCAGCCTGCG 6233
QY 2136 rSerValGlnAlaGlnSerCysGlnArgArgProThrSerTyrLeuAspGlnArgAr 2156
Db 6234 GGGGCTGGGGCG-----CATCAGCGCAG 6257
QY 2156 gHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspPr 2176
Db 6258 CCACAGCAGCGGGGGCTCC--ACCAAGCCCGGGCTGCACCAACCAAGACTCCATGAGACC 6314

QY 2176 oSerAsn-----LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLy 2193
Db 6315 CTCGACGAGAGAGGCGCGGCTGGCGCGGCGCGGGCGCGGCGAGCACTCGGA 6374
QY 2193 sLysLeuSerProProSerIleThr-----IleAspProProGlnSerGlnGlyPr 2210
Db 6375 GACCTCAGACGACCTCTCGCTACCTCCCTCTTGCCCCCGCC----- 6420
QY 2210 cArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAspSer-- 2229
Db 6421 ----CCGCGCGCAGCCCCCGGCTCAGCGCCCGCGAGAAAGTTACAGCAGCAGCAGCCT 6476
QY 2230 -----LysAspProLeuAlaSerGlyProProAspSerMetAlaAlaSerProSe 2246
Db 6477 GCGCGCCCCCGCGCGCGCCCAACCGCGCGCTGGGCCACAGGCTGGCGCGGAGCCCTC 6536
QY 2246 rProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPr 2266
Db 6537 GTGGCGCGCGGAC-----CGCAGCAAGAGACCCCGCGGCGGCGACC 6578
QY 2266 o 2266
Db 6579 G 6579

RESULT 12

US-09-935-541-1
; Sequence 1, Application US/09935541
; Patent No. US20020150911A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGiven, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/09/935,541
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 09/404,650
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-09-935-541-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 9 Gaps: 55

US-09-611-257A-37 (1-2266) x US-09-935-541-1 (1-6816)

QY 31 ArgProGlyProGlySerAlaGlnLysAspProGlySerAlaAspSerGlnAlaGlnGly 50
Db 264 CAGCCCGGACCCCGGAGCCCGCATCTCCCGCGAGGCTTGAGAGAGCTTGATGGA 323
QY 51 -----LeuProTyrProAlaLeuAlaProValAlaPhePheTyrLeuSerGln 66
Db 324 GGTGATCTCATGTCCACACCCAGACCTGGCGCTATTGCTTCTTGCTGCGACAG 383
QY 67 AspSerArgProArgSerTyrCysLeuArgThrValCysAsnProTyrPheGlnArgIle 86
Db 384 ACCACGAGCCCCCGGAAGTGTGATCAAGATGTGTGCAACCCGTGTGATGTGTG 443
QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGlnAsp 106

Db 444 AGCATGCTGTGATCTCTGTAAGTCCGTGACACTTGGCATGTACCAAGCCGTGCGAGC 503
QY 107 ILeAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspPheIlePheAla 126
Db 504 ATGACTGCTGTGTCGACCGCTGCAGAGATCTTGAGTTCATCTTATC 563
QY 127 PhePheAlaValGluMetValValIysMetValAlaLeuGlyIlePheGlyLysLysCys 146
Db 564 TTCTTTGCCATGAGATGGTGCTCAAGATGGTGGCCCTGGGATTTTGGCAAGAGTGC 623
QY 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIleAlaGlyMetLeuGly 166
Db 624 TACCTCGGGACACATGGAACCGCCTGGATTCTTCATCGTCATGGCAGGATGTCGAG 683
QY 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 684 TACTCCCTGACCTTCAGAAATCAACCTGTCAAGCCATCCGCACCGCTGCCCTGTGAG 743
QY 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuAsp 206
Db 744 CCCCTCAAGCCATCAACCGCGTGCAGTATGCGGATCCTGGTGAACCTGCTCCTGAG 803
QY 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226
Db 804 ACACTGCCCATGTCTGGGAATGTCTGTCTGTCTGTCTTGTCTTCTTCACTTGTGC 863
QY 227 ILeValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
Db 864 ATCATAGTGTGACGCTCTGGCGCGCTGTGCGTAACCGCTGCTTCTTGAGAGAGAAC 923
QY 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
Db 924 TTCACCATACAAAGGGATGTGGCCTTGCCCCCATACTACCAGCCGAGAGAGATGATGAG 983
QY 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
Db 984 ATGCCCTTCATCTGTCTCCCTGTGCGGCGACAAATGGGATAATGGGCTGCATGAGATCCCC 1043
QY 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 1044 CCGCTCAAGAGCAG-----GGCCGTGAGTGTGCTGCTGTCCAAGAGCAGCGTCTAC 1094
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
Db 1095 GACTTTGGGGCGGGCGCGCAGACCTCAATGCCAGCGGCTGTGTCAACTGAACCGT 1154
QY 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
Db 1155 TACTACAATGTGTGCCGCGCAGCGGCCAACCCCAACAAGGGTGCATCACTTTGAC 1214
QY 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTrpValAsp 358
Db 1215 AACATCGGTATGTGATTGTTCATCTTCCAGGTGATCACTCTGGAAGGCTGGTGAG 1274
QY 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeu 378
Db 1275 ATCATGTACTACGTGATGATGCTCACTCCTTCTACAACCTTCATCTTCACTGCTT 1334
QY 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
Db 1335 ATCATAGTGGCTCCTTCTTCATGATCAACCTGTGCTGTGTGATGCGAACCCAGTTC 1394
QY 399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
Db 1395 TCGAGAGCAACGAACGGGACACCGGCTGATGCTGAGACGCGCAGCGCTACCTGTCC 1454
QY 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys 438
Db 1455 ---TCCAGCAACGGTGGCCAGCTACGCCGAGCCTGGCGACTGTACGAGAGATCTTCCAG 1511
QY 439 TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 458
Db 1512 TATGTCTGCCACATCTGCGCAAGGCCAAGCC-----CGCGCCCTG 1553

QY 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478
Db 1554 GGCTCTACCAAGCCCTGCAGAGCCGGCCGACAGCCCTGGGC----- 1595
QY 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisIleValHisHisHis 498
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QY 499 HisHisHisHisHisIstYrHisIleuGlyAsnGlyThrLeuArgAlaProArgAlaSer 518
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QY 519 ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer 538
Db 1596 -----CCGAG 1601
QY 539 ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheThrHis 558
Db 1602 GCCCGCGCC-----CCGCGCAACCTGGGCC-----CAC 1631
QY 559 AlaAspCysHisIleuGluProValArgCysGlnAlaProProProArgSerProSerGlu 578
Db 1632 GCCAAG-----GAGCCCCGGCACTACAGCTGTGCCCGCAACATAGCCCCCTGAT 1682
QY 579 AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro 598
Db 1683 GCGAGCGCCCAACCCCTG-----GTGAGCCCATC 1712
QY 599 ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr 618
Db 1713 CCCGCCACGCTG----- 1724
QY 619 LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr 638
Db 1724 ----- 1724
QY 639 GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp 658
Db 1724 ----- 1724
QY 659 SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
Db 1725 -----GCTCCGATCCCGCCAGCTGCCCTTGCTGCCAGCATGAGAGCGCCGCGGCC 1778
QY 673 AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla 692
Db 1779 TCGGGCCTGGGCAACCGAC--TCCGGCCAGGAGGGCTCGGGCTCCGGAGCTCCGCT 1835
QY 693 ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg 712
Db 1836 GGTGGCGAG-----GACGAGGCGGATGGGAGCGGGCCCGGAGCAGCAGGACGAGACC 1889
QY 713 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu----- 726
Db 1890 TCCTCAGAACTGGGGAAGAGAGAGAGAGAGAGAGAGCGGCGGCTGTGCTG 1949
QY 727 -----AlaPheTrpArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr 744
Db 1950 TCGCGGAGATGTGTGGCGGAGACGCGCAAGCTGCGCGCATCTGTGACAGCAAGTAC 2009
QY 745 PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr 764
Db 2010 TTCAACCGGGGCATCATGATGGCCATCTGTCAACACCGTCAGCATGGCATCGAGCAC 2069
QY 765 HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784
Db 2070 CACGAGCAGCCCGGAGAGCTGACCAACATCTTGAGATCTGCAATGTGCTTACCGAGC 2129
QY 785 LeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys 804
Db 2130 ATGTTTGGCCCTGAGATGATCTGGAAGCTGGCTGCATTTGGGCTTTCGACTACCTGCGT 2189

Db 4208 TGTCTGGCATCCAAGATGGTTGGGTGAACATCATGTACAATGAGCTGGATGCTTTGC 4267
QY 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh. 1520
Db 4268 TGTGACACGACGCTGTGAACCAACCAACACCCCTGGATGCTGTGTACTTCACTTCTCCTT 4327
QY 1520 eleuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPh 1540
Db 4328 CTTGCTCATCGTCAGCTTCTTTGTGCTCAACATGTTTGTGGTGTCTGTGGAGAACTT 4387
QY 1540 eHisLysCysArgGlnHisGlnGluGluAlaArgArgArgGluGluLysArgLe 1560
Db 4388 CCACAAGTGCCTGGCAGACCAAGAGGCTGAAGAGGCACGCGCGTGAAGAGACGGCT 4447
QY 1560 uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTyrSerAspTyrSe 1580
Db 4448 GCGGCGCTGGAGAGAAAGCCGCCGAAGGCCGCGGCTGCCCTACTATGCCACCTATTG 4507
QY 1580 rArgPheArgLeuLeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleTh 1600
Db 4508 TCACACCCGCGTGTCTCATCCACTCCATGTGCACAGCCACTACCTGACATCTTCATCAC 4567
QY 1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnI 1620
Db 4568 CTTTCATCATCTGCTCAACGTTGTCACCATGTCCTGGAGCACTACAACTACGCCACGTC 4627
QY 1620 eleuAspGluAlaLeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSe 1640
Db 4628 CCTGGAAGACAGCCCTCAAGTACTGCACTATATGTTCAACCACTGTCCTTGTGCTGAGGC 4687
QY 1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe 1660
Db 4688 TGTGCTGAAGCTGTGGCTTTGTTGTTCTGAGGCGCTTCTTCAAGGACCGATGGAACCA 4747
QY 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680
Db 4748 GGACTGGCCATTGTGTACTGTCAGTCAATGGGCATCACCTGGAGAGATCGAGATCAA 4807
QY 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700
Db 4808 TCGGGCCCTGCCCATCAATCCCAACCATCATCCGATCAGGGTTCGGCATTTGCCCG 4867
QY 1700 gValleuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetG 1720
Db 4868 AGTGTGAAGCTGTGAAGATGGCCACAGAAATGGGGCCCTGCTGACACGGTGTGCA 4927
QY 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuPhePheIlePheAl 1740
Db 4928 AGCTTTGCCCCAGGTGGGCAACTGGGCCCTCTTCATGCTGCTCTTTCATCTATGC 4987
QY 1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluG 1760
Db 4988 TGTCTCTGGGGTGGAGCTCTTTGGGAAGCTGTGTCGAACGACGAGAACCCGTGCGAGGG 5047
QY 1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780
Db 5048 CATGAGCCGGCATGCCACCTTCAGAACTTCGGCATGGCTTCCTCACACTCTTCCAGGT 5107
QY 1780 lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys---AspG 1799
Db 5108 CTCACAGGGGTGAACAACGGAACGGGATCATGAAGACACGCTGCGGACTGCCACCGA 5167
QY 1799 nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa 1817
Db 5168 CGAGCCGACGCTGCTGAGCAAGCTGCAAGTTGTGTCCGGCTGTACTTCGTGAGCTTCGT 5227
QY 1817 lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLysHisLeuG 1837
Db 5228 GCTCACCGGCGAGTTCGTGCTCATCAACGTGTGTGTGTGCTCTCATGAAGCACTTGA 5287
QY 1837 uGluSerAsnLysGluAlaLysGluGluAlaGluLeuGluAlaGluLeuGluLeuGluMe 1857
Db 5288 CGACAGCAACAAGAGGCGCAGAGGAGCGCCGAGATGATGCCGAGCTCGAGCTTGAAGAT 5347

QY 1857 t---LysThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrpProG 1876
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QY 1876 yValGluGlyProAspSerProAsp----- 1884
Db 5405 C---CGAGGGCGGGAGGGGCGGGCGGGCGGACACGAGGGCGGCTTGTGCCGG 5461
QY 1885 -----SerProLysProGlyAlaLeu----- 1891
Db 5462 CTGCTACTCGCTGCCCTGCCAGAGCTCCTTGGAGGGGAGCTGACCATCATCGACAACCTGTC 5521
QY 1892 -----HisProAlaAlaHisAla----- 1897
Db 5522 GGGCTCCATCTTCCACCACTACTCCTGCTGCCCTGCCGCTGCAAGAAGTGCACCACGACA 5581
QY 1898 ----- 1901
Db 5582 GCAAGAGTGCAGCTGGCTGAGACGGAAGGCTTCTCCCTGAACCTCAGACAGTCTCTGTC 5641
QY 1901 r-----HisPheSerLeuGluHisProThrMetGlnPro----- 1912
Db 5642 CATCCTGCTGGGTGACGACCTGAGTCTGAGAGACCCCAAGCTGCCACCTGGCCGGA 5701
QY 1913 ----HisProThrGluLeuProGlyProAspLeuLeuThrValArgLysSerGly----- 1929
Db 5702 GGAACAGCAAGGTTGAGCTGGACCCCACTGAGCCCATGCGGTGTGGGAAGACCTGGGCGAATG 5761
QY 1930 -----ValSerArgThrHisSerLeuProAsn---AspSerTyrMetCysArgHis 1945
Db 5762 CTTCTTCCCCTTGTCTCTACGGCGCTGTCGCCGATCCAGAGAACTTCTGTGTGAGAT 5821
QY 1945 sGlySerThrAlaGluGlyProLeuGluHisArgGlyTyrGlyLeuProLysAlaGlnSe 1965
Db 5822 GGAGGAGATCCCATTCAACTGTC-----CGTCTGCG-----CTGAACATGACAG 5869
QY 1965 rGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyrIleLeuGlnLeuPr 1985
Db 5870 CAGTCAAGCACCCCAAGTCCCTTCTCCCGGATGCTCCAGCCCTCTGCCCCTGCGCATGCC 5929
QY 1985 oLysAspAlaProHis-----LeuLeuGlnProHisSerAlaProTh 1999
Db 5930 AGCCGAGTCTTCCACCTGCAAGTGTGTGCCAAGCAAGAAAGGCCAAGGACACTGG 5989
QY 1999 rTrpGlyThrIleProLysLeuProProProGly-----ArgSerProLe 2014
Db 5990 CACTGGAACCTTCCCAAGATTGCCGTGACAGGGCTCCTGGGCACTCTGCGGTACACCAAG 6049
QY 2014 uAlaGlnArgProLeuArgArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnG 2034
Db 6050 GGTCAACTGTACCTCTCTCGGACAGGCCACGGGAGCGACACAGCTGTGCTGAC----- 6101
QY 2034 yLeuGlySerArgGluAspLeuLeuAlaGluValSerGlyProSerProProLeuAlaAr 2054
Db 6102 -----GCCAGCCCCAGAGCTCCGGGGCAG 6127
QY 2054 gAlaTyrSerPheTrpGlyGlnSerSerThrGlnAlaGlnGlnHisSerArgSerHisSe 2074
Db 6128 CTTGCAAGACCAAGCTGAGAGACAGCTGACCTGAGCGACAGCCCGCGCTGCC----- 6182
QY 2074 rLysIleSerLysHisMetThrProProAlaProCysProGlyProGluProAsnTrpG 2094
Db 6183 -----CTGGGGCGCGCGCTGCTGCTCAGGACCCCGGGCGGCTGTG 6226
QY 2094 yLysGlyProProGluThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSe 2114
Db 6227 C-----CCCGCGCTGCGCGCGCTGAGCCTG----- 6254
QY 2114 rGlyAspLeuLeuProProGlyGlyGlnGluProProSerProAlaArgAspLeuLysLy 2134
Db 6255 -----CGCGCGCGGGGCTCTTTCAG 6274

QY 2134 sCysTyrSerValGluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluG1 2154
Db 6275 CcTGCGGGGCTGCGGGCG-----CATCA 6298
QY 2154 nArgArgHisSerIleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyTh 2174
Db 6299 GCGCAGCCACACAGCAGCGGGGGCTCC---ACCAGCCCCGGGCTGCACCCACCACTCCAT 6355
QY 2174 rAspProSerAsn-----IleuGlyGlyGlnProLeuGlyGlyProGlySerArgPr 2191
Db 6356 GGACCCCTCGGACGAGAGGGCCCGGTGGCGGGCGGGGGGGCGCGGCGCAGCA 6415
QY 2191 oLysLysLysLeuSerProProSerIleThr-----IleAspProProGluSerG1 2208
Db 6416 CTGGAGACCTCTCAGCAGCCTCTGCTCACTCCCTCTTGTGCCCGCGCC----- 6467
QY 2208 nGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaProSerSerAs 2228
Db 6468 -----CCGCCGACGCCCGGCTCTCAGCCCGCCAGGAAGTTACAGCAGCACAG 6517
QY 2228 pSer-----LysAspProLeuAlaSerGlyProProAspSerMetAlaAlase 2244
Db 6518 CAGCCTGGCGCCCGCGCGCCGCGCCGCGCCCTGGGCCACGCGCTGGCGCGGAG 6577
QY 2244 rProSerProLysLysAspValLeuSerLeuSerGlyLeuSerSerAspProAlaAsple 2264
Db 6578 CCCCTCGTGGCGCGCGAC-----CGCAGCAAGAGACCCCGCGCGCG 6619
QY 2264 uAspPro 2266
Db 6620 GGCACCG 6626

RESULT 13
US-10-425-800-1
; Sequence 1, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGiven, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 6816
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6716)
US-10-425-800-1

Alignment Scores:
Pred. No.: 0 Length: 6816
Score: 5492.50 Matches: 1236
Percent Similarity: 60.30% Conservative: 213
Best Local Similarity: 51.44% Mismatches: 506
Query Match: 46.14% Indels: 449
DB: 16 Gaps: 55

US-09-611-257A-37 (1-2266) x US-10-425-800-1 (1-6816)
QY 31 ArgProGlyProGlySerAlaGluYAspProGlySerAlaAspSerGluAlaGluGly 50
Db 264 CAGCCCGGACCCCGGAGCCCCCATCTCCCGCAGGCTGGAGAGAGCCTGTGATGGA 323
QY 51 -----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln 66
:::||||:::|||||

Db 324 GGTGATCCTCATGTCCACACCCAGACCTGGGCGCTATTGCTTCTTGCTGCGACAG 383
QY 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
Db 384 ACCACCAAGCCCCCGAAGCTGGTGATCAAGATGGTGTGCAACCCGGGTTTGAATGTGC 443
QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 444 AGCATGCTGTGATCCTGCTGAAGTGCCTGACACTTGCCATGTATACAGCCGTGCGAGAC 503
QY 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
Db 504 ATGACTGCCCTGTCCGACCGCTGCAAGATCCTGCAGGCTTGTATGACTTCACTTTATC 563
QY 127 PhePheAlaValAluMetValValLysMetValAlaLeuGlyIlePheGlyLysCys 146
Db 564 TTCCTTGCCATGAGATGGTGTCTCAAGATGGTGGCCCTGGGATTTTGGCAAGAGTGC 623
QY 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
Db 624 TACCTCGGGACACATGGAACCGCCTGATTTCTTCATGTCATGGCAGGATGTCGAG 683
QY 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 684 TACTCCCTGGACCTTCAGACATCAACCTGTGAGCCATCCGACCCGTGCGCTGTGAGG 743
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Db 804 AACTGCCCATGCTGGGGAATGCTCTGCTGCTCTTCTTGTCTTCTTCATCTTGGC 863
QY 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
Db 864 ATCATAGGTGTGAGCTGTGGCGGGCGCTGTGGTAACCGCTGCTTCTTGAGAGAGAAC 923
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Db 924 TTCACCATCAAGGGATGTGGCTTGCCCCCATTAACAGCCGAGAGGATGATGAG 983
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Db 984 ATGCCCTTCATCTGCTCCTGTGCGGCGACAAATGGGATATGGGCTGCCATGAGATCCCC 1043
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Db 1044 CCGCTCAAGAGACG-----GGCCGTGAGTGTGCTGCTGCCAAGACGAGCTTAC 1094
QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
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QY 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
Db 1155 TACTACAATGTGTGCCGACGGGCGAGCGCAACCCCAAGGGGTGCATCAACTTTGAC 1214
QY 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGlyGlyTrpValAsp 358
Db 1215 AACATCGGTATATGCTTGGATGTGTCACTTCCAGGTGATCACTTGGAAGCTGGGTGAG 1274
QY 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
Db 1275 ATCATGTAAGTGTGATGATGCTCACTCCTTCACTCAACTTCATCTCATCTGCTT 1334
QY 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
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QY 399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
Db 1395 TCGAGACCAAGCAAGGAGACACCGGTGATGTGAGCAGCGGCGGCTTACTGTCTC 1454

QY	419	AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys	438
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QY	439	TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAla	458
Db	1512	TATGTCTGCCACATCTGTGCCAAGGCCAAGCCG	1553
QY	459	GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro	478
Db	1554	GGCCTTACCAGGCCCTGCAGAGCCGGCGCCAGGCCCTGGCC	1595
QY	479	SerSerSerCysSerArgSerHisArgArgLeuSerValHisIleValHisHis	498
Db	1595	-----	1595
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Db	1595	-----	1595
QY	519	ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProProSer	538
Db	1596	-----CCGAG	1601
QY	539	ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGlnSerValHisSerPheTyrHis	558
Db	1602	GCCCCGGCC-----CCCGCAACCTGGGCC-----CAC	1631
QY	559	AlaAspCysHisLeuGluProValArgCysGlnAlaProProProArgSerProSerGlu	578
Db	1632	GCCCAAG-----GAGCCCCGGCACTACCAAGCTGTGCCCGCAACATAGCCCCCTGAT	1682
QY	579	AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro	598
Db	1683	GCGACGCCCCACACCTG-----GTGACAGCCCATC	1712
QY	599	ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr	618
Db	1713	CCCGCCACGCTG-----	1724
QY	619	LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuGluThr	638
Db	1724	-----	1724
QY	639	GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp	658
Db	1724	-----	1724
QY	659	SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg-----	672
Db	1725	-----GCTTCCGATCCCCGCCAGCTGCCCTTGCTGCCAGCATGAGACCGCGCGGCC	1778
QY	673	AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGlyAla	692
Db	1779	TCGGGCTGGGCGAGCACCAGC--TCGGGCCAGAGAGGCTCGGGCTCCGGAGCTCCGCT	1835
QY	693	ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg	712
Db	1836	GGTGGCGAG-----GACGAGCGCGATGGGGACGGGCCCGGAGCAGCAGCAGCAGCC	1889
QY	713	GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu-----	726
Db	1890	TCCTCAGAACTGGGGAAGAGAGAGAGAGAGAGAGCAGCGGATGGGGCGGTCTGCTG	1949
QY	727	-----AlaPheTyrArgLeuIleCysAspThrPheArgLysIleValAspSerLysTyr	744
Db	1950	TGCGGGGATGTGTGGCGGGAGACGCCAGCCCAAGCTGCGCGGCATCTGTGAACAGCAAGTAC	2009
QY	745	PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTyr	764
Db	2010	TTCAACCGCGGCATCATGATGCGCATCTGTGTCACACCCGTACAGATGGGCATCGAGCAC	2069

Qy	765	HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer	784
Db	2070	CACGACGACCCGAGGAGCTGACCAACATCTGGAGATCTGCAATGTGCTTCACGAGC	2129
Qy	785	LeuPheAlaLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLys	804
Db	2130	ATGTTTGCCTCGAGATGATCCTGAAGCTGGCTGCATTTGGGCTCTTCGACTACCTGCGT	2189
Qy	805	AsnProTyrAsnIlePheAspGlyValIleValValIleSerValTyrGluIleValGly	824
Db	2190	AACCCTACAACATCTTCGACAGCATCATGTCTCATCATCAGCATCTGGAGATCTGGGG	2249
Qy	825	GlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu	844
Db	2250	CAGCGGACGGTGGGCTGTGGTGTGGTGGACCTTCGGCTGTGGCGGTGTGAACCTG	2309
Qy	845	ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn	864
Db	2310	GTGCGCTTCATGCTCGCTGCGGCGGCGGACGCTCGTGTGCTCATGAAGACCATGCAAC	2369
Qy	865	ValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMet	884
Db	2370	GTGGCCACCTTGTGATGTGCTCATGTCTTTCATCTTCATCTTCAGCATCTTGGAATG	2429
Qy	885	HisLeuPheGlyCysLysPheAlaSerGluArgAsp--GlyAspThrLeuProAspArg	903
Db	2430	CATATTTTGGCTGCAAGTTCAAGCTCCGACGGAACCTGGAACACAGGTGCCGACAG	2489
Qy	904	LysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGlu	923
Db	2490	AAGAACTTCGACTCCCTGCTGTGGGCCATGCTCACTGTGTTCCAGATCCTCACCCGAG	2549
Qy	924	AspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyr	943
Db	2550	GACTGGAACGTCGTTCTTCAATGCGATGGCTCCACTTCTCCCTGGGCTCCCTCTAC	2609
Qy	944	PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeu	963
Db	2610	TTTGTCCGCTCATGACCTTCGGCAACTATGTGCTTCAACCTGTGTGGCCATCTTG	2669
Qy	964	ValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlyGlnLeuSer	983
Db	2670	GTGGAGGGCTTCCAGGCGGAG-----	2690
Qy	984	CysIleGlnLeuProValAspSerGlnGlyGlyAspAlaAsnLysSerGluSerGluPro	10033
Db	2691	-----GGTAGCGCAATCGCTCTACTCGGACGAG	2720
Qy	1004	AspPhePheSerProSer-----LeuAspGlyAsp	10133
Db	2721	GACCAGAGCTCATCCAAACATAGAAGATTGATAAGCTCAGAAAGCCTGAGACAGACG	2780
Qy	1014	GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys	10333
Db	2781	GGAGATCCCAAGCTCTGCCCAATCCCATGACCCCAATGGGAC-----	2825
Qy	1034	SerLeuLeuProProLeuIleIleHisThrAlaAlaThrPrometSerLeuProLysSer	10533
Db	2826	-----CTGGAACCC-----AGTCTCCCACTGGGT	2845
Qy	1054	ThrSerThrGlyLeuGlyGluAlaLeuGlyProAlaSerArgArgThr-----	1065
Db	2850	GGGACCTAGTCTGTGGGGTGGGAGACCTGCCGCCGACTCTCACTGCAGCCGAGC	2909
Qy	1070	-----SerSerSerGlySerAlaGluProGlyAlaAla	1080
Db	2910	CCCATGCTGTGGCTGGGCTCCGAAAGAGCAGTGTCTTCTTAGGAGAGATGAGC	2965
Qy	1081	HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla	1100
Db	2970	TATGACCAAGCGCTCCCTGTCCAGCTCCCGGAGCTCCTACTACGGGCCATGGGCGGAGC	3029
Qy	1101	SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys	1120

Db 3030 GCGGCGCTGGGCCAGCCCGTCGCTCCAGCTGGAAC-----AGCCTCAAG 3071
QY 1121 ArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyGlu--GlyGlnGluSer 1139
Db 3072 CACAAGCCCGCGTCGGCGGAGCATGAGTCCCTGCTCTTGCGGAGCGCGGCGGCGGCC 3131
QY 1140 GlnAspGluGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGGTCTGCGAGGTGTCGGCGGACGAGGGCGCGCGCGCGGCACCCCTGCACACCCCA 3191
QY 1158 His-----ArgHisArgGly 1162
Db 3192 CACGCCCAACCATTCATCACGGGCCCATCTGGCGCACCGCCACCGCCACCGCGCG 3251
QY 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182
Db 3252 ACGCTGTCCCTCGACACAGGAGCTCGGTGGACCTGGCCGAGCTGGTGCCCGCGGTGGC 3311
QY 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3312 GCCCACCCCCCGCGCGCTGGAGGGCGGCAAGCCCGCGCCCCCGGCATGAGGACTGCAAT 3371
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu-As 1220
Db 3372 GGCAGAGAT-GCCCAAGCATCGC--CAAGAAGCTTTCACCAAGATGGGGCGAGCCGGGGA 3427
QY 1220 PglyAspAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpI 1240
Db 3428 TCGCGGAGAGATGAGAGAAATGCACTACACCCCTGTGCTTCGCGTCCGCAAGATGAT 3487
QY 1240 eArgAlaArgLeuProAlaCysTrpLeuGluArgAspSerTrpSerAlaTrpIlePhePr 1260
Db 3488 CGACGTCTATAAGCCCGACTGTGTGCGAGGTCCGCGAAGACTGGTCTGTACCTCTTCTC 3547
QY 1260 oProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
Db 3548 TCCCGAGAACAGGTTCCGGGTCTGTGTCAAGACCATTAATGCCACAACACTCTTGACTA 3607
QY 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIl 1300
Db 3608 CGTCGTCTCTGGCCTTCATCTTTCTCACTGATCAATCAATCGCCCTGGAGCGGCTTCAGAT 3667
QY 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpIlePheThrAlaVa 1320
Db 3668 CGAGCGCCGGCAGCACCGAAGCATTTTCTCACCGGTGCCAATACATCTTCACGGCCAT 3727
QY 1320 lPheLeuAlaGluMetThrValLysValAlaAlaLeuGlyTrpCysPheGlyGluGlnAl 1340
Db 3728 CTTGCTGGCGGAGATGACATTGAAGTAGTCTCGCTGGCCTGTACTTCGCGCAGCAGGC 3787
QY 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360
Db 3788 GTACCTACGCAAGCACTGGAACGTGCTGGATGGCTTCTGTCTTCGTCCATCATCGA 3847
QY 1360 pIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValLe 1380
Db 3848 CATCGTGTGTCTCTGGCCTCAGCCGGGGGAGCCAAAGATCTTGGGGGTCTCCGAGTCTT 3907
QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysLe 1400
Db 3908 GCGGCTCCTGCGCACTTACGCCCCCTGCGTGTATCAGCCGGGGCGCGGGCCTGAAGCT 3967
QY 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420
Db 3968 GGTGTGAGACACTCATCTCTCCCTCAAGCCCATCGCAACATCGTCTCATCTGCTG 4027
QY 1420 sAlaPheIleIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa 1440
Db 4028 TGCCTTCTTATCATCTTTGGCATCCTGGGAGTGAGCTCTTCAAGGCAAGTTCTACCA 4087
QY 1440 lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy 1460

Db 4088 CTGTCTGGCGGTGAGACCCGCAACATCACCAACCGCTCGGACTGCATGGCCGCAACTA 4147
QY 1460 rArgTrpValArgHisLysTrpAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh 1480
Db 4148 CCGGTGGGTCCATCACAAATACAACTTGACACACTGGGCCAGGGCTGTGATGTCCCTCTT 4207
QY 1480 eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrAspGlyLeuAspAlaValG 1500
Db 4208 TGTCTGGCATCCAAAGATGGTTGGTGAACATCATGTACAATGAGTGGATGCTGTGC 4267
QY 1500 yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPh 1520
Db 4268 TGTGACACGACAGCCTGTGACCAACACACACCCCTGGATGCTGTGTACTTCATCTCTT 4327
QY 1520 eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPh 1540
Db 4328 CTTGCTCATCGTCAGCTTCTTTGTGCTCAACATGTTTGTGGGTGTGTTGGAGAAGCTT 4387
QY 1540 eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLe 1560
Db 4388 CCACAAGTCCCGGACAGCACAGAGGCTGAAGAGGCACGGCGCGTGAAGAGAAAGCGGCT 4447
QY 1560 uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrTrpSerAspTyrSe 1580
Db 4448 GCGGCGCTTGAGAAAGACCGCGGAAGCCCAAGCGGCTGCCCTACTATATGCCACTATTG 4507
QY 1580 rArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleTh 1600
Db 4508 TCACACCCGGGTGCTCATATCCATCCATGTGCAACGACCACTACCTGACATCTTCATCAC 4567
QY 1600 rGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIl 1620
Db 4568 CTTTCATCATCTGCTCAACGTGTGTACACCATGTGCTGGAGCACTACATCAAGCCACGTC 4627
QY 1620 eLeuAspGluAlaLeuLysIleCysAsnTrpIlePheThrValIlePheValLeuGluSe 1640
Db 4628 CTTGAGACAGCCCTCAAGTACTGCACACTATATGTTCACCACTGTCTTTGTCTGAGGC 4687
QY 1640 rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe 1660
Db 4688 TGTGTGAAGCTGTGTGCAATTTGGTCTGAGGCGCTTCTTCAAGGACCGATGGAACGAGCT 4747
QY 1660 uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs 1680
Db 4748 GGACTGGCCATTTGTGTAAGTGTAGTATGAGGATGAGGATGAGGATGAGATCAA 4807
QY 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700
Db 4808 TGGCGGCCCTGCCATCATATCCACCATCATCCGCATCATGAGGTTCTGCGCATTTGCCCG 4867
QY 1700 gValLeuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl 1720
Db 4868 AGTGTGAAGCTGTGTAAGATGGCCACAGGAATGCGGGCCCTGTGGACACGGTGTGCA 4927
QY 1720 nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl 1740
Db 4928 AGCTTTGCCCCAGGTGGGCAACTGGGCTCTCTTCATGTGCTCTTCTTCATCTATGC 4987
QY 1740 aAlaLeuGlyValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGl 1760
Db 4988 TGTCTCGGGGTGAGCTTTTGGGAAGCTGTGTGCAACGACGAGAACCCGTGCGAGGG 5047
QY 1760 yLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgVa 1780
Db 5048 CATGACCCGGCATGCCACCTTCGAAGACTTCGGGATGGCCTTCTTCACACTCTTCAGGT 5107
QY 1780 lSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeuArgAspCys--AspGl 1799
Db 5108 CTCCACGGGTGACAACTGGAACGGGATCATGAAGACACAGCAGCAGGACTGCACCCACGA 5167
QY 1799 nGluSerThrCysTyrAsnThrVal-----IleSerProIleTyrPheValSerPheVa 1817
Db 5168 CGAGCGCAGCTGCTGAGCAGCCTGACAGTTGTGTGCGCGCTGTACTTCTGTAGACTTCGT 5227

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QY 31 ArgProGlyProGlySerAlaGluLysAspProGlySerAlaAspSerGluAlaGluGly 50
:::|||||
Db 264 CAGCCCCGAGCCCCGGAGCCCCCATCTCCCGCCAGGCGCTGGAGAGCGCTGTGATGGA 323

QY 51 -----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln 66
:::|||||
Db 324 GCTGATCCTCATGTCCACACCCAGACCTGGCGCCTATTGCCTTCTTGTGCGCGAGACAG 383

QY 67 AspSerArgProArgSerTyrProLysLeuArgThrValCysAsnProTyrPheGluArgIle 86
:::|||||
Db 384 ACCACCAGCCCCCGGAAGTGTGCATCAAGATGTTGCAACCCGTTGTTGAATGTGTC 443

QY 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
|||||
Db 444 AGCATGCTGTGATCTCTGTGAACCTGTCACACTTGACATGTACACAGCCGTGCGACGAC 503

QY 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
:::|||||
Db 504 ATGACTGCTGTCTCCGACCGCTGCAGATCTTCAGAGTCTTGATGACTTCATCTTATC 563

QY 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys 146
|||||
Db 564 TTCTTTGCCATGGAGATGTGTCTCAAGATGTGGCCCTGGGGAATTTTGGCAAGAGTGC 623

QY 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
|||||
Db 624 TACCTCGGGACACATGGAAACCGCTGATTTCTTCATCGTCATGGCAGGGATGTGAG 683

QY 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
|||||
Db 684 TACTCCCTGGACCTTCAGAACATCAACCTGTACGCCATCCGACCGTGGCGCTGTGAGG 743

QY 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
|||||
Db 744 CCCCTCAAGCCATCAACCGCGTCCAGATATGCGATCCTGTGTAACCTGTCTCTGAGC 803

QY 207 ThrLeuProMetLeuGlyAsnValLeuLeuCysPhePheValPhePheIlePheGly 226
|||||
Db 804 ACACTGCCCATGTGGGAATGTCTGTCTGTCTTGTCTTCTTCATCTTGTGGC 863

QY 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
|||||
Db 864 ATCATAGGTGTGAGCTCTGGCGGGCTGTGCTAACCCTGTCTTCTTGAGAGAGAAC 923

QY 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
|||||
Db 924 TTCACCATACAGGGGATGTGGCCTTGGCCCCCATACTACCAAGCCGGAAGGATGATGAG 983

QY 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
|||||
Db 984 ATGCCCTTCATCTGCTCCCTGTGGCGGACAAATGGATATGGGCTGCCATGAGATCCCC 1043

QY 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
|||||
Db 1044 CCGCTCAAGAGAGCAG-----GGCCGTGAGTGTGCTGTCTCAAGAGACGAGCTCTAC 1094

QY 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
|||||
Db 1095 GACTTTGGGGCGGGCGCCAGAGCCTCAATGCGAGCGCCTGTGTCAACTGGAACCGT 1154

QY 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheGlyAlaIleAsnPheAsp 338
|||||
Db 1155 TACTACAATGTGTGCCGACGCGGACGCCCAACCCCAACAGGTTGCCATCACTTTGAC 1214

QY 339 AsnIleGlyTyrAlaTrpIleAlaIlePheGlnValIleThrLeuGluGlyTyrValAsp 358
|||||
Db 1215 AACATCGGTATGCTTGATTTGTCACTTCCAGGTGATCACTTGGAAGGCTGGGTGAG 1274

QY 359 IleMetTyrPheValMetAspAlaHisSerPheTyrAsnPheIleTyrPheIleLeuLeu 378
|||||
Db 1275 ATCATGTACTACGTGATGATGATGCTCACTCTTCTACAACCTTCATCTCATCTGCTT 1334

QY 379 IleIleValGlySerPhePheMetIleAsnLeuCysLeuValValIleAlaThrGlnPhe 398
|||||
Db 1335 ATCATAGTGGGCTCCTTCTTCATGATCAACCTGTGCTGTGTCTATAGCAGCAGGATTC 1394

QY 399 SerGluThrLysGlnArgGluSerGlnLeuMetArgGluGlnArgValArgPheLeuSer 418
|||||
Db 1395 TCGGAGACCAAGCAACGGGAGCACCAGCTGATGTCTGAGACAGCGGACTACCTGTCC 1454

QY 419 AsnAlaSerThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLys 438
:::|||||
Db 1455 ---TCCAGCACGGTGGCCAGCTACGCCGAGCCTGGCGACTGTACGAGAGATCTTCAG 1511

QY 439 TyrLeuValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaAla 458
|||||
Db 1512 TATGTCGCCACATCCTGGCGCAAGGCCAAGCGC-----CGCGCCCTG 1553

QY 459 GlyValArgValGlyLeuLeuSerSerProAlaProLeuGlyGlyGlnGluThrGlnPro 478
|||||
Db 1554 GGCTCTACCAAGGCCCTGCAGAGCCGGCCAGCCCTGGC----- 1595

QY 479 SerSerSerCysSerArgSerHisArgArgLeuSerValHisIleValHisHisHis 498

Db 1595 ----- 1595

QY 499 HisHisHisHisHisIleTyrHisIleGlyAsnGlyThrLeuArgAlaProArgAlaSer 518

Db 1595 ----- 1595

QY 519 ProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProProSer 538
|||
Db 1596 -----CCGAG 1601

QY 539 ThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPheTyrHis 558
|||||
Db 1602 GCCCGGCC-----CCGCGCAAACTGGGCC-----CAC 1631

QY 559 AlaAspCysHisLeuGlnProValArgCysGlnAlaProProProArgSerProSerGlu 578
|||||
Db 1632 GCCAAG-----GAGCCCCGGCACTACCACTGTGCCGCAACATAGCCCCCTGAT 1682

QY 579 AlaSerGlyArgThrValGlySerGlyLysValTyrProThrValHisThrSerProPro 598
|||||
Db 1683 GCGAGCCCCACACCCCTG-----GTGCAGCCCATC 1712

QY 599 ProGluThrLeuLysGluLysAlaLeuValGluValAlaAlaSerSerGlyProProThr 618
|||||
Db 1713 CCCGCCACGCTG----- 1724

QY 619 LeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHisLysLeuLeuGluThr 638

Db 1724 ----- 1724

QY 639 GlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerProCysLeuLysAlaAsp 658

Db 1724 ----- 1724

QY 659 SerGlyAlaCysGlyProAspSerCysProTyrCysAlaArg----- 672
|||||
Db 1725 -----GCTTCGATCCCGCCAGCTGCCCCCTGTGCTGCCAGCATGAGGACGCGCGGCC 1778

QY 673 AlaGlyAlaGlyGluValGluLeuAlaAspArgGluMetProAspSerAspSerGluAla 692
:::|||||
Db 1779 TCGGCGCTGGGACGACCGAC--TCGGGCCAGGAGGGCTCGGGCTCCGGAGCTCCGCT 1835

QY 693 ValTyrGluPheThrGlnAspAlaGlnHisSerAspLeuArgAspProHisSerArgArg 712
|||
Db 1836 GGTGGCGAG-----GACGAGCGGATGGGAGCGGGCCCGGAGCAGGAGCGAGGCC 1889

QY 713 GlnArgSerLeuGlyProAspAlaGluProSerSerValLeu----- 726
|||||
Db 1890 TCCTCAGAACTGGGAGAGGAGAGAGAGAGAGAGAGCGGATGGGCGGTCTGCTG 1949

QY 727 -----AlaPheTrpArgLeuIleCyAspThrPheArgLysIleValAspSerLysTrp 744
Db 1950 TCGGGGATGTGTGGCGGGAGACGGCAGCAAGCTGCGGGCATCTGACAGCAAGTAC 2009
QY 745 PheGlyArgGlyIleMetIleAlaIleLeuValAsnThrLeuSerMetGlyIleGluTrp 764
Db 2010 TTCAACCGGGGCATCATGATGGCCATCTGTGCAACACCGTCAGCATGGGCATCGAGCAC 2069
QY 765 HisGluGlnProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSer 784
Db 2070 CACGAGCAGCCGGAGAGCTGACCAACATCCTGGAGATCTGCAATGTGGTCTTCACCAGC 2129
QY 785 LeuPheAlaLeuGluMetLeuLeuLysLeuValTyrGlyProPheGlyTyrIleLys 804
Db 2130 ATGTTGGCCCTGGAGATGATCCTGAAGCTGGCTGCATTTGGGCTCTCGACTACCTGGCT 2189
QY 805 AsnProTyrAsnIlePheAspGlyValIleValIleSerValTrpGluIleValGly 824
Db 2190 AACCCCTACACATCTTCGACAGCATCATTTGTCATCATGACATCTGGAGATCGTGGGG 2249
QY 825 GlnGlnGlyGlyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeu 844
Db 2250 CAGGCGGACGGTGGCTGTGCGGTGCTGCGGACCTTCGGCTGCTGCGGTGCTGAAACTG 2309
QY 845 ValArgPheLeuProAlaLeuGlnArgGlnLeuValValLeuMetLysThrMetAspAsn 864
Db 2310 GTGGCCTTCATGCGCTGCGCTGCGGCGCAGCTCGTGTGCTCATGAAGACCATGACAAC 2369
QY 865 ValAlaThrPheCysMetLeuLeuMetLeuPheIlePheSerIleLeuGlyMet 884
Db 2370 GTGGCCACCTTCTGCATGCTGCTCATGCTCTTCATCTTCAGACATCCTTGGGATG 2429
QY 885 HisLeuPheGlyCysLysPheAlaSerGluArgAsp--GlyAspThrLeuProAspArg 903
Db 2430 CATATTTTGGCTGCAAGTTCAAGCTCCGCGCAGGACACTGGAGACACGGTGCCGACAGG 2489
QY 904 LysAsnPheAspSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGlu 923
Db 2490 AAGAACTTCGACTCCCTGTGTGGGCATGCTCACTGTGTTCAGATCTCACCCAGAG 2549
QY 924 AspTrpAsnLysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaIleLeuTyr 943
Db 2550 GACTGGAACGTGCTTCTTACAATGGCATGGCTCCACTTCTCCCTGGCCTCCCTCTAC 2609
QY 944 PheIleAlaLeuMetThrPheGlyAsnTyrValLeuPheAsnLeuValAlaIleLeu 963
Db 2610 TTTGTCCCTCATGACCTTCGGCAACTATGTGCTCTCAACCTGCTGGCCATCTCTG 2669
QY 964 ValGluGlyPheGlnAlaGluGluIleSerLysArgGluAspAlaSerGlnLeuSer 983
Db 2670 GTGGAGGGCTTCCAGGGCGAG----- 2690
QY 984 CysIleGlnLeuProValAspSerGlnGlyAspAlaAsnLysSerGluSerGluPro 1003
Db 2691 -----GGTGACGCCAATCGCTCTACTCGAGCAG 2720
QY 1004 AspPhePheSerProSer-----LeuAspGlyAsp 1013
Db 2721 GACGAGAGCTCATCCAAACATAGAAGATTGATAAGCTCCAGAGGCGCTGGACAGCAGC 2780
QY 1014 GlyAspArgLysLysCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLys 1033
Db 2781 GGAAGATCCCAAGCTCTGCCCAATCCCCATGACCCCAATGGGCAC----- 2825
QY 1034 SerLeuLeuProProLeuIleIleHisThrAlaAlaThrPrometSerLeuProLysSer 1053
Db 2826 -----CTGGACCCC-----AGTCTCCACTGGGT 2849
QY 1054 ThrSerThrGlyLeuGlyAlaLeuGlyProAlaSerArgArgThr----- 1069
Db 2850 GGGCACTAGGTCCTGCTGGGGCTGGCGGACCTGCCCGCACTCTCACTGACCGCGGAC 2909
QY 1070 -----SerSerSerGlySerAlaGluProGlyAlaAla 1080

Db 2910 CCCATGCTGTGGCCCTGGGCTCCCGAAAGACAGCATGTATGTCTTAGGAGAGATGAC 2969
QY 1081 HisGluMetLysSerProProSerAlaArgSerSerProHisSerProTrpSerAlaAla 1100
Db 2970 TATGACCAGCGCTCCCTGTCCAGCTCCCGAGCTCCTACTACGGGCCATGGGGCCGAC 3029
QY 1101 SerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyArgAlaProSerLeuLys 1120
Db 3030 GCGGCTGGCGCAGCGCTGCTCCAGCTGGAAC-----AGCTTCAAG 3071
QY 1121 ArgArgSerProSerGlyLysArgArgSerLeuLeuSerGlyGlu--GlyGlnGluSer 1139
Db 3072 CACAAGCCCGCTCGCGGAGCATGATCCCTGCTCTGCGGAGCGCGCGCGCGCC 3131
QY 1140 GlnAspGluGluGluSerSerGluGlu-----GluArgAlaSerProAlaGlySerAsp 1157
Db 3132 CGGCTGCGAGGTTGCCCGGACGAGGGCGCGCGCGCGCCACCTGCACACCCCA 3191
QY 1158 His-----ArgHisArgGly 1162
Db 3192 CACGCCACCAATTCATCACGGGCCCATCTGGCGCACCGGCCACCGCACCGCGG 3251
QY 1163 SerLeuGluArgGluAlaLysSerSerPheAspLeuProAspThrLeuGlnValProGly 1182
Db 3252 ACGTGTCCCTGCACAACAGGACTGCTGGACCTGCGCGGACTGTGCCCCGGTGCGC 3311
QY 1183 LeuHisArgThrAlaSerGlyArg-----GlySerAlaSerGluHisGlnAspCysAsn 1200
Db 3312 GCCCACCCCCCGCGCGCTGGAGGGCGGCGAGCCCGCGCGCATGAGACTGCAT 3371
QY 1201 GlyLysSerAlaSerGlyArgLeuAlaArgAlaLeuArgProAspAspProProLeu-As 1220
Db 3372 GGCAGGAT-GCCACGATCGC--CAAAGAGTCTTCAACCAAGATGGCGACCGCGGGA 3427
QY 1220 PGLysAspAlaAspAspGluGlyAsnLeuSerLysGlyGluArgValArgAlaTrpIle 1240
Db 3428 TCGCGGAGATGAGAGGAATGCACTACACCTGTGCTTCGCGCTCCGCAAGATGAT 3487
QY 1240 eArgAlaArgLeuProAlaCysTyrLeuGluArgAspSerTrpSerAlaTyrIlePhePr 1260
Db 3488 CGAGCTTATAGCCCGACTGTGTGCGAGGTCGCGAAGACTGTGTCTTACCTTTCTC 3547
QY 1260 OProGlnSerArgPheArgLeuLeuCysHisArgIleIleThrHisLysMetPheAspHi 1280
Db 3548 TCCCGAAGACAGGTTCCGGGTCTGTGTGACACCATATTATGCCCAAACTCTTCGACTA 3607
QY 1280 sValValLeuValIleIlePheLeuAsnCysIleThrIleAlaMetGluArgProLysIle 1300
Db 3608 CGTGTCTGCTTCATCTTCTCACTGCATCACCATCGCCCTGAGCGGCTCAGAT 3667
QY 1300 eAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThrAlaVal 1320
Db 3668 CGAGGCGGCGAGCACCGAAGCATCTTTCACCGTGTCCAATTAATCTTCACGGCCAT 3727
QY 1320 lPheLeuAlaGluMetThrValLysValValAlaLeuGlyTyrCysPheGlyGluGlnAl 1340
Db 3728 CTTCGTGGCGAGATGACATTGAAGGTAGTCTGCTGGGCTGTACTTCGGCGAGCAGC 3787
QY 1340 aTyrLeuArgSerSerTrpAsnValLeuAspGlyLeuLeuValLeuIleSerValIleAs 1360
Db 3788 GTAACCTACGACGAGCTGGAACGTGCTGATGGCTTCTTGTCTTCGTCCATCATCGA 3847
QY 1360 rIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLeuArgValIle 1380
Db 3848 CATCGTGTGTCTCTGCGCTCAGCCGGGGAGCAAGATCTTGGGGTCTCCGAGTCTT 3907
QY 1380 uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysIle 1400
Db 3908 GGGGCTCTCGCGACCTTACGCCCTGCGGTGTCATCAGCCGGGCGCGGCTGAAGCT 3967
QY 1400 uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy 1420

Db 3968 GGTGTGAGACACTCATCTCTCCCTCAAGCCCATCGGCAACATCGTCTCATCTGCTG 4027
QY 1420 SAIApHePheIleIlePheGIyIleuGIyValGIleuPheLySGlyLysPhePheVa 1440
Db 4028 TGCCCTTCTTCATCATCTTTGGCATCCTGGAGTGCAGCTCTTCAAGGCAAGTTCTACCA 4087
QY 1440 ICysGIInGIyGIuAspThrArGAsnIleThrAsnLySseAspCysAlaGIuAserTy 1460
Db 4088 CTGTCTGGGCGGTGGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCCGCAACTA 4147
QY 1460 rArgTrpValArGHisLySTyrAsnPhaAspAsnLeuGIyGlnAlaLeuMetSerLeuPh 1480
Db 4148 CCGCTGGTCCATCAACAATACAACTTCGACCAACCTGGGCCAGGCTCTGATGTCTCTT 4207
QY 1480 eValLeuAlaSerLySaspGIyTrpValAspIleMetTyraSpGIyLeuAspAlaValGI 1500
Db 4208 TGTCTGGCATCCAAAGATGGTGGTGAACATCATGTACAATGGAATGGAATGCTGTGC 4267
QY 1500 yValAspGIInGIProIleMetAsnHisAsnProTrpMetLeuLeuTyrrPheIleSerPh 1520
Db 4268 TGTGACACGAGCCTGTGTGACCAACCAACCCCTGGATGCTGCTACTTCACTCTCTT 4327
QY 1520 eleuLeuIleValAlaPhePheValLeuAsnMetPheValGIyValValGIuAsnPh 1540
Db 4328 CCTGCTCATCGTCAGCTTCTTGTGTCAACATGTTTGGGTGTCTGTGAGAACTT 4387
QY 1540 eHisLySAsyArGIInHisGIInGIyGlnGIuAlaArgArGIyGlnLySArgLe 1560
Db 4388 CCACAAGTGCCTGGACAGCACCAAGAGGCTGAAGAGGCACGGCGGCTGAGAGAAAGCGCT 4447
QY 1560 uArgArGIeGIuLySlySArgArGIyAlaGIInCysLySProTyrrTyrSerAspTyrSe 1580
Db 4448 GCGGCGCTGGAGAAGAAGCGCCGGAGGCCAGCGGCTGCTCTACTATGCCACTATTG 4507
QY 1580 rArgPheArgLeuLeuValHisHisLeuCysThrSerHisTyrLeuAspLeuPheIleTh 1600
Db 4508 TCACACCCGCGTGTCTCATCTCCATGTGCATGTGCACACGACCTACTGACATCTTCATC 4567
QY 1600 rGIyValIleGIyLeuAsnValValThrMetAlaMetGIuHisTyrrGIInGIProGIInI 1620
Db 4568 CTTTCATCATCTGCCTCAACGTGTGCATGTCTCCCTGGAGCACTAATCAGCCACGTC 4627
QY 1620 eleuAspGIuAlaLeuLySileCysAsnTyrrIlePheThrValIlePheValLeuGIuSe 1640
Db 4628 CCTGGAGACAGCCCTCAAGTACTGCACATATATGTTCACCACTGTCTTGTGTGAGGC 4687
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Db 4688 TGTGCTGAAGCTGTGTGCATTTGTGTGAGGCGCTTCTTCAAGAACCGATGGAACCACT 4747
QY 1660 uAspLeuAlaIleValLeuLeuSerIleMetGIyIleThrLeuGIuGIuIleGIuValAs 1680
Db 4748 GGACCTGGCCATTGTGTACTGTCACTGTGCATGGCATCACCTGGAGAGATCGAGATCAA 4807
QY 1680 nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr 1700
Db 4808 TCGGCGCCCTGCCATCAATCCACCATCATCCGATCATGAGGTTCTCGCATTGCCCG 4867
QY 1700 gValLeuLyLeuLeuLySmetAlaValGIyMetArgAlaLeuLeuAspThrValMetGI 1720
Db 4868 AGTGCTGAAGCTGTGAAGATGGCCACAGAAATGCGGCGCTGTGACACGGTGTGCA 4927
QY 1720 nAlaLeuProGIInValGIyAsnLeuGIyLeuLeuPheMetLeuLeuPhePheIlePheAl 1740
Db 4928 AGCTTTGCCCCAGGTGGGCAACCTGGGCTCTCTTCATGTCTCTTCTTCATCTATGC 4987
QY 1740 aAlaLeuGIyValGIuLeuPheGIyAspLeuGIuCysAspGIuThrHisProCysGIuGI 1760
Db 4988 TGTCTCTCGGGGTGAAGCTCTTTGGGAAGCTGTGTGCAACGACGAGAACCCGTGCGAGGG 5047
QY 1760 yLeuGIyArGHisAlaThrPheArgAsnPheGIyMetAlaPheLeuThrLeuPheArgVa 1780
Db 5048 CATGAGCCGGCATGCACTTTCGAGAACTTTCGGCATGGCTTCTTCACACTCTTCAGGT 5107

QY 1780 lSerThrGIyAspAsnTrpAsnGIyIleMetLySAspThrLeuArgAspCys---AspGI 1799
Db 5108 CTCCACGGGTGACACATGGAACGGGATCATGAAAGACACGCTGCGGGACTGCACCCACGA 5167
QY 1799 nGIuSerThrCysTyraSnThrVal-----IleSerProIleTyrrPheValSerPheVa 1817
Db 5168 CGAGCGCAGCTGCTTGAGCAGCCTGCAGTTTGTGTGCGCGCTGTACTTCTGTAGCTTCGT 5227
QY 1817 lLeuThrAlaGlnPheValLeuValAsnValValIleAlaValLeuMetLyHisLeuGI 1837
Db 5228 GCTCACCGCGCAGTTCGTCTCATCAACGTGTGTGGCTGTGCTCATGAAGCACTTGA 5287
QY 1837 uGIuSerAsnLySGluAlaLySGluGIuAlaGIuLeuGIuAlaGIuLeuGIuLeuGIuMe 1857
Db 5288 CGACAGCAACAAGAGGCGCAGAGAGACGCCGAGATGATGCCGAGCTCGAGCTGAGAT 5347
QY 1857 t---LysThrLeuSerProGIInProHisSerProLeuGIySerProPheLeuTrpProGI 1876
Db 5348 GGCCCATGGCCTGGGCGCTGGCCGAGGCTGCTACCGGCTCCCGGGGCC---CCTGG 5404
QY 1876 yValGIuGIyProAsp----- 1881
Db 5405 C---GAGGGCCGGAGGGGCGGGCGGGCGGCGGACACCGAGGGCGGCTTGTCCGGCG 5461
QY 1882 -----SerPro----- 1883
Db 5462 CTGCTACTCGCCTGCCCAGAGAACTGTGGCTGGACAGCGTCTTTAAATCATCAAGGA 5521
QY 1884 ----- 1892
Db 5522 CTCTTGAGGGGAGCTGACCATCATGCAACACTGTGCGGCTCCATCTTCCACCACTA 5581
QY 1893 -----ProAlaAla----- 1895
Db 5582 CTCTCGCCTGCGGCTGCAAGAAGTGTACACGACGAAGAAGGTGACGTGCTGA 5641
QY 1896 -----HisAlaArgSerAlaSer-----HisPh 1903
Db 5642 GACGAGGCCTTCTCCCTGAACTCAGACAGTCTCTCCATCTCTGGGTGACGACCT 5701
QY 1903 eSerLeuGIuHisProThrMetGIInPro-----HisProThrGIuLeuPr 1918
Db 5702 GAGTCTGAGGAGCCCAAGCCTGCCACCTGGCGCCAAAGACAGAGGTGAGCTGGA 5761
QY 1918 oGIyProAspLeuLeuThrValArgLySberGIy-----ValSerArgTh 1933
Db 5762 CCCACTGAGCCCATGTGTGGAGACCTGGGCGAAATGCTTCTTCCCTGTCTCTTAC 5821
QY 1933 rHisSerLeuProAsn---AspSerTyrrMetCysArgHisGIySerThrAlaGIuGIyPr 1952
Db 5822 GGCGGTCTCGCGGATGCAGAACTTCTGTGTGAGATGAGAGATCCCATTCAAACCC 5881
QY 1952 oLeuGIyHisArgGIyTrpGIyLeuProLySAlaGIInSerGIySerValLeuSerValHi 1972
Db 5882 TGTCT-----CGTCTGTG-----CTGAACAATGACAGCAGTCAAGCAACCCCAAGTCC 5929
QY 1972 sSerGIInProAlaAspThrSerTyrrIleLeuGIInLeuProLySAspAlaProHis----- 1990
Db 5930 CTTCCTCCCGGATGCTCCAGCCCTCTCTCTGCCATGCCAGCCGAGTTCTTCCACCCCTGC 5989
QY 1991 -----LeuLeuGIInProHisSerAlaProThrTrpGIyThrIleProLySLe 2006
Db 5990 AGTGTCTGCCAGCCAGAAAGGCCAGAAAGGGCACTGGCACTGGAACCTTCCCAAGAT 6049
QY 2006 uProProProGIy-----ArgSerProLeuAlaGIInArgProLeuArgAr 2021
Db 6050 TGCCTGACAGGCTCTCTGGCATCTCTGCGGTACCAAGGTCAACTGTACCTCTCTCCG 6109
QY 2021 gGlnAlaAlaIleArgThrAspSerLeuAspValGIInGIyLeuGIySerArgGIuAspLe 2041
Db 6110 GCAGGCCACCGGAGGACAGACGTGCTGAC----- 6140

Qy 2041 uLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGly 2061
Db 6141 -----GCCAGCCCCAGCAGCTCCGGCGGAGCCTGCAGACCAGCTCGAGGA 6187
Qy 2061 nSerSerThrGlnAlaGlnGlnHisSerArgSerHisSerLysIleSerLysHisMet 2081
Db 6188 CAGCCTGACCTGAGCAGACAGCCCCCGCGTGC-----CTGGG 6226
Qy 2081 rProProAlaProCyBProGlyProGlyProGluProAsnTrpGlyLysGlyProProGluThrAr 2101
Db 6227 GCCCGCCCGCGCTGCTCCAGAGACCCCGGCGGCTGTCC-----CCCGCGCTCG 6277
Qy 2101 gSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeuLeuProProG 2121
Db 6278 CCGCCGCGCTGAGCCTG----- 6293
Qy 2121 yGlyGlnGluGluProProSerProArgAspLeuLysLysCysTyrSerValGluAlaG 2141
Db 6294 -----CGCGCGCGGCGCTTTCAGCCTGCGGGGCTGCGGGCG-- 6332
Qy 2141 nSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSerIleAlaVa 2161
Db 6333 -----CATCAGCGCAGCCACAGCAGCGGGG 6358
Qy 2161 lSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn----- 2178
Db 6359 CTCC---ACCAGCCCGGCTGCACCCACACAGACTCCATGACCCCTCGGAGCAGAGAGG 6415
Qy 2179 -LeuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPr 2198
Db 6416 CCGCGGTGGCGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 6475
Qy 2198 oSerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProse 2215
Db 6476 CTGCTCACCCTCCTTCTTCTGCGCGCGCC-----CCGCGCGCAGC 6517
Qy 2215 rProGlyIleCysLeuArgArgAlaProSerSerAspSer-----LysAs 2231
Db 6518 CCGCGGCTCAGCGCGCGCAGAGTTTACAGCAGCAGCAGCCTGCGCGCGCGCGCGCGCG 6577
Qy 2231 pProLeuAlaSerGlyProProAspSerSerMetAlaAlaSerProSerProLysLysAspVa 2251
Db 6578 CCCCCAGCGCGCGCTGCGCCACAGCGCTGCGCGCGGAGCCCTCGTGGCGCGCGGAC-- 6635
Qy 2251 lLeuSerLeuSerGlyLeuSerSerAspProAlaAspLeuAspPro 2266
Db 6636 -----CGCAGCAAGACCCCGCGCGCGGCGGACCG 6665

RESULT 15
US-10-425-800-3
; Sequence 3, Application US/10425800
; Publication No. US20030180886A1
; GENERAL INFORMATION:
; APPLICANT: Dietrich, Paul S.
; APPLICANT: McGovern, Joseph G.
; TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
; TITLE OF INVENTION: AND USES
; FILE REFERENCE: R0043B-REG sequence listing
; CURRENT APPLICATION NUMBER: US/10/425,800
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US/09/404,650
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 6855
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (192)..(6755)
US-10-425-800-3

Alignment Scores:
Pred. No.: 0 Length: 6855
Score: 5484.00 Matches: 1237
Percent Similarity: 59.93% Conservative: 211
Best Local Similarity: 51.20% Mismatches: 507
Query Match: 46.07% Indels: 462
DB: 16 Gaps: 56

US-09-611-257A-37 (1-2266) x US-10-425-800-3 (1-6855)

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Db 264 CAGCCCGAGCCCGAGAGCCCCCATCTCTCCCGCAGGCTGAGAGAGCTTGTGATGGA 323
Qy 51 -----LeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGln 66
Db 324 GCTGATCCTCATGTCCACACACCACTGCGGCTATTGCTTCTTCTGCTGCGACAG 383
Qy 67 AspSerArgProArgSerTrpCysLeuArgThrValCysAsnProTrpPheGluArgIle 86
Db 384 ACCACAGCCCCCGAAGACTGTGTCAATCAAGATGTGTGCAACCCGTGTTGAATGTCTC 443
Qy 87 SerMetLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAsp 106
Db 444 AGCATCTGTGATCTGTGTAATCTGTGACACTGTGCACTGTGATGTACAGCCGTGCGAGAC 503
Qy 107 IleAlaCysAspSerGlnArgCysArgIleLeuGlnAlaPheAspAspPheIlePheAla 126
Db 504 ATGACTGCTGTGTCGACCGCTGCAAGATCTTGACGTCTTGTATGACTTTCATCTTATC 563
Qy 127 PhePheAlaValGluMetValValLysMetValAlaLeuGlyIlePheGlyLysLysCys 146
Db 564 TTCTTTGCCATGAGATGTGTCTCAAGATGTGCGCTGGGATTTTGGCAAGAGTGC 623
Qy 147 TyrLeuGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGlu 166
Db 624 TACCTCGGGACATGGAACCGCTGATTTCTTCACTGTCATGCGAGGATGTGAG 683
Qy 167 TyrSerLeuAspLeuGlnAsnValSerPheSerAlaValArgThrValArgValLeuArg 186
Db 684 TACTCCCTGACTTTCAGAACATCAACTGTCAGCATCCGACCGTGCCTGAGG 743
Qy 187 ProLeuArgAlaIleAsnArgValProSerMetArgIleLeuValThrLeuLeuLeuAsp 206
Db 744 CCCCTCAAGCCATCAACCGCGTGCAGTATGCGGATCTGTGAACTGTCTCTGAGC 803
Qy 207 ThrLeuProMetLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGly 226
Db 804 ACACTGCCCATGTCTGGGGAATGTCTGCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTT 863
Qy 227 IleValGlyValGlnLeuTrpAlaGlyLeuLeuArgAsnArgCysPheLeuProGluAsn 246
Db 864 ATCATAGTGTGCACTCTGGCGGCGCTGCTGCGTAACCGCTGCTTCTTCTGAGAGAGAC 923
Qy 247 PheSerLeuProLeuSerValAspLeuGluArgTyrTyrGlnThrGluAsnGluAspGlu 266
Db 924 TTCACCATACAGGGAGATGTGCTTGCCCCCATATACACCGGAGAGAGATGATGAG 983
Qy 267 SerProPheIleCysSerGlnProArgGluAsnGlyMetArgSerCysArgSerValPro 286
Db 984 ATGCCCTTCATCTGCTCTGCTGCGGCGCAATGGATATGGGCTGCATGATATCCC 1043
Qy 287 ThrLeuArgGlyAspGlyGlyGlyProProCysGlyLeu----- 300
Db 1044 CCGCTCAAGAGAGAG-----GGCGGTGAGTGTGCTGCTGTCCAAAGAGAGAGCTGTAC 1094
Qy 301 AspTyrGluAlaTyrAsnSerSerSerAsnThrThr-----CysValAsnTrpAsnGln 318
Db 1095 GACTTTGGGCGGCGCGCCAGAGCTCATGCGAGCGGCTGTGTCAACTGAACCGT 1154
Qy 319 TyrTyrThrAsnCysSerAlaGlyGluHisAsnProPheLysGlyAlaIleAsnPheAsp 338
Db 1155 TACTACAATGTGTGCGCAGCGGCGAGCGCCCAACCCCAAGAGGTGCATCACTTTGAC 1214

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Db	3848	CATCGTGGTGTCCCTGGCCTCAGCCCGGGGAGCCAAGATCTTGGGGGTCTCCGAGTCTT	3907
Qy	1380	uArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeuLysIle	1400
Db	3908	GGGGCTCCTGGCACCCCTACGCCCCCTGGTGTCAACGCGGGCGGCTGAAGCT	3967
Qy	1400	uValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValValIleCysCy	1420
Db	3968	GGTGGTGAGACACTCATCTCTCCCTCAAGCCCATCGGAACATCGTGTCTCATCTGCTG	4027
Qy	1420	sAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhePheVa	1440
Db	4028	TGCCTTCTTCATCATCTTTGGCATCCTGGGAGTGACAGCTCTTCAAGGGCAAGTTCAACA	4087
Qy	1440	lCysGlnGlyGluAspThrArgAsnIleThrAsnLysSerAspCysAlaGluAlaSerTy	1460
Db	4088	CTGTCTGGGCGGTGACACCCGCAACATCACCAACCGCTCGGACTGCATGGCCGCAACTA	4147
Qy	1460	rArgTrpValArgHisLysTyrrAsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPh	1480
Db	4148	CCGCTGGGTCCATCAACAATACAACCTTCGACAACCTGGGCCAGGCTCTGATGTCCCTTT	4207
Qy	1480	eValLeuAlaSerLysAspGlyTrpValAspIleMetTyrrAspGlyLeuAspAlaValGl	1500
Db	4208	TGTCTTGCCATCCAGAGATGTTGGGTGAACATCATGTACAATGAGACTGATGCTGTGC	4267
Qy	1500	yValAspGlnGlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrrPheIleSerPh	1520
Db	4268	TGTGACACGACGCTGTGACCAACCAACACCCCTGGATGCTGTGATCTTCCTCTT	4327
Qy	1520	eLeuLeuIleValAlaPhePheValLeuAsnMetPheValGlyValValGluAsnPh	1540
Db	4328	CCTGCTCATGTCAGCTTCTTGTGCTCAACATGTTTGGGTGCTGTGTGGAGAACTT	4387
Qy	1540	eHisLysCysArgGlnHisGlnGluGluGluAlaArgArgGluGluLysArgLe	1560
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Qy	1560	uArgArgLeuGluLysLysArgArgLysAlaGlnCysLysProTyrrTyrrSerAspTyrrSe	1580
Db	4448	GGGGCGCCTGGAGAGAGAGCGCCGGAAGGCCAGCGGCTGCCCTACTATGCAACCTATTG	4507
Qy	1580	rArgPheArgLeuLeuValHisIleCysThrSerHisTyrrLeuAspLeuPheIleTh	1600
Db	4508	TCACACCCGGCTGCTCATCCACTCCATGTGCACCACTA CCTGAGACATCTTCATCAC	4567
Qy	1600	rcGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrrGlnGlnProGlnIl	1620
Db	4568	CTTCATCATCTGCCTCAACGTGTGCACCATGTCCCTGGAGCACTACAATCAGCCACGTC	4627
Qy	1620	eLeuAspGluAlaLeuLysIleCysAsnTyrrIlePheThrValIlePheValLeuGluSe	1640
Db	4628	CCTGGAGACAGCCCTCAAGTA CTGCAACTATATGTTCA CCACTGTCCTTGTGTGAAGC	4687
Qy	1640	rValPheLysLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTrpAsnGlnLe	1660
Db	4688	TGTGCTGAAGCTGGTGGAATTGGTCTGAGGCGCTTCTTCAAGACCGATGGAACCAAGCT	4747
Qy	1660	uAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAs	1680
Db	4748	GGAACCTGGCCATTGTGTA CTGTCAGTCA TGCGCATCA CCGTGAGAGATCGAGATCAA	4807
Qy	1680	nAlaSerLeuProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaAr	1700
Db	4808	TGGGGCCCTGGCCCATCATCCCA CCACTCATCCGCATCATGAGGGTCTGCGCATTGCCG	4867
Qy	1700	gValleuLysLeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGl	1720
Db	4868	AGTGTCTGAAGCTGTTGAAGATGGCCACAAGAA TGCGGGCCCTGCTGGA CACGGTGGTGA	4927
Qy	1720	nAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAl	1740
Db	4928	AGCTTTGGCCCCAGGTGGGCAACTGGGGCTCTCTTTCAATGCTGCTCTTCTTCATCTATGC	4987

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2005, 17:44:07 ; Search time 14254.4 Seconds
(without alignments)
6050.997 Million cell updates/sec

Title: US-09-611-257A-37
Perfect score: 11904
Sequence: 1 MDEEDGAGAEESGQPRSFM.....PKDVLSLGSLSSDPADLDP 2266

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US09611257/runat_15092005_134301_25185/app_query.fasta_1.4878
-DB=EST -QFMT=fastap -SUFFIX=rcf -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09611257 @CGN 1 1_23209 @runat_15092005_134301_25185 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1703.5	14.3	6636 3	BC043482 Mus muscu
2	1683.5	14.1	6035 3	BC051413 Mus muscu
3	1382.5	11.6	1076 4	BM479323 AGENCOURT
4	1314.5	11.0	879 7	CF548698 AGENCOURT
5	1290.5	10.8	5666 9	AY416501 Mus muscu
6	1281.5	10.8	1064 4	BM451648 AGENCOURT
7	1257	10.6	793 6	CA319705 UI-M-FW0-
8	1223.5	10.3	5943 9	AY416499 Homo sapi
9	1216	10.2	711 5	BM950154 UI-M-EH0p

10	1215.5	10.2	771 5	BU058818 UI-M-FR0-
11	1215.5	10.2	990 4	BI905383 603167426
12	1212.5	10.2	784 7	CF742232 UI-M-HB0-
13	1187.5	10.0	810 5	BU709095 UI-M-EW0-
14	1185	10.0	736 4	BI160856 602864778
15	1183	9.9	939 4	BI736618 603361089
16	1178	9.9	973 2	BF783704 602109506
17	1174	9.9	4675 3	AK083220 Mus muscu
18	1140.5	9.6	777 6	CA945335 UI-M-FD0-
19	1136	9.5	6822 9	AY406058 Mus muscu
20	1132	9.5	715 7	CF745071 UI-M-GV0-
21	1130	9.5	676 4	BI917129 603181539
22	1130	9.5	843 5	BQ180375 UI-M-EX0-
23	1129.5	9.5	6813 9	AY406056 Homo sapi
24	1116.5	9.4	777 5	BU708898 UI-M-FI0-
25	1107.5	9.3	710 5	BU704267 UI-M-FO0-
26	1104	9.3	952 7	CF584866 AGENCOURT
27	1103.5	9.3	845 6	CA327685 UI-M-FY0-
28	1101	9.2	707 7	CN216936 RJA002G02
29	1092.5	9.2	918 6	CD557381 AGENCOURT
30	1084	9.1	647 6	CB518482 UI-M-GH0-
31	1081	9.1	693 5	BM949227 UI-M-EG0P
32	1074	9.0	708 5	BQ179746 UI-M-EW0-
33	1068.5	9.0	710 7	CR576255 CR576255
34	1065.5	9.0	727 5	BQ443110 UI-M-EV0-
35	1058.5	8.9	731 7	CN534628 UI-M-HS0-
36	1055.5	8.9	803 6	CB245297 UI-M-FY0-
37	1051	8.8	773 4	BI249987 602995228
38	1025	8.6	640 6	CB056097 NISC_jj12
39	1024	8.6	588 2	BE781203 601469131
40	1018.5	8.6	684 5	BU262763 603374462
41	1012	8.5	726 5	BQ042267 UI-M-EQ0-
42	1012	8.5	772 6	CB524438 UI-M-FY0-
43	1006	8.5	707 5	BU612176 UI-M-EW0-
44	995	8.4	1134 2	BF179657 601806048
45	993	8.3	957 4	BG298038 6023396253

ALIGNMENTS

RESULT 1	BC043482	6636 bp	musculus	musculus	calcium channel, voltage-dependent, alpha 1f subunit, mRNA (CDNA clone IMAGE:5369391), containing frame-shift errors.
LOCUS	BC043482				
DEFINITION	BC043482.1	GI:28175783			
ACCESSION	BC043482				
VERSION	BC043482.1				
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 6636)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				

JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE	22388257
PUBMED	12477932
REFERENCE	2 (bases 1 to 6636)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (09-JAN-2003) National Institutes of Health, Mammalian

REMARK	COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov	
Contact: MGC help desk	

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/RLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 86 Row: 0 Column: 1
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972
 This clone has the following problem: frame shifted.

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FEATURES
source
Location/Qualifiers
1. .6636
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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5369391"
/tissue_type="Eye, retina, mouse strain C57Bl/6"
/clone_id="NIH_MGC_94"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

```

ORIGIN

Alignment Scores:		
Pred. No.:	9.4e-107	Length: 6636
Score:	1703.50	Matches: 665
Percent Similarity:	38.49%	Conservative: 331
Best Local Similarity:	25.70%	Mismatches: 805
Query Match:	14.31%	Indels: 792
DB:	3	Gaps: 98

US-09-611-257A-37 (1-2266) x BC043482 (1-6636)

QY		1 MetAspGluGluIuaSpGIyaLaglYaLaGlutSerGIyGLnProArgSerPheMet	20
Dd		3 ATGTGGAAATCTGAAGTCGGGAAGAATACCAACCACAGGCCAAGTCCAGCCCAT-	56
QY		21 ArgLeuAsnaSplenuSerGIyaLagLyglYargProGIlyPro-----GlySeraLaGlu	38
Dd		57 -----GGGACTGGCCCCCTGGCCCCTGAATGGGGGCTCTGTCTCCT	92
QY		39 LysAspPro-----GlySeraLaaspSerGIuaLaglYleuProTYrPro-----	54
Dd		93 GGGCCTCCAACtGTggggaCTGaTaCcAgCGGGGCgtCaGGcCTGGGGACccccaGAAGA	15
QY		55 -----AlaLeuaAlaProValPhePheTYrLeu	64
Dd		153 AGGACCACGACACAACAACAAGACTGTGGCGGTGGCC-----	19
QY		65 SerGIuaSpSeratrgProArgserTrpCYsLeuaArgThrValCYsaSnPro-----	81

Db	192	AGTGCTCAGAGATCACCTCGAGCGCTTCTGCGCTCACCGCTTACTAATCCATTTCGTCGG	251
QY	82	-----Trp-----pheGluArgIleSerMetLeuValIleLeu	92
Db	252	TCCTGCATCAGCATTTGAGTGAAGCCCTTTTGATATTCTCATCTCCCTGACAAATCTTT	311
QY	93	LeuAsnCysValThrLeuGlyMetPheArgProCys--GluAsp-----	106
Db	312	GCCAACTGCGTGGCATTTGGGGTATATATCCCTTCCGTGAGACGACTCCAACACTGCT	371
QY	106	-----	106
Db	372	AACCACACTTGGTGAGGTCTACCCCATCCCAACAGACTGCAGTTCCCTTAGAGCTA	431
QY	107	---IleAlaCysAspSerGlnArg-----	113
Db	432	CAGATTAACCAACCCAGCCAGACCCCACTCCGGGGCTACCTACTTCACTTGGT	491
QY	114	-----Cys--	114
Db	492	CCTGCAAAAGCAACCCTAACCTGTGCTAGACTACCCACGCGGTCTGACCTGCCCC	551
QY	115	ArgIle-LeuGlnAlaPheAsp-----AspH	123
Db	552	GAATAATAATCGAGCGCTTACAGCGCCCGCCCTGCTCCGCCCTCAGAAACAGGTAGAATA	611
QY	123	eIlePhe---AlaPhePheAlaValGluMetValValIysMetValAlaLeuGly---Il	141
Db	612	CGTGTTCCGTGTGATTTTTCACCGTGAGACAGTGTCTCAAGATCGTAGCCTTAGGGCTGT	671
QY	141	epheGlyLysLysCysTyrLeuGlyAspThrTrpAsnArgLeuAspPheIleValIl	161
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QY	172	-----GlnAsnValSerPheSerAlaValArgThrValArgValLeuAr	186
Db	792	TACTGAGGAAGCCAGAGGCTTCGATGTAAGGCACTGCGGGCATTTAGGGTCTACG	851
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Db	852	ACCTTAAGGCTAGTGCTGCGGGTCCGAGTCTGCACATAGTGCTCAATTCCATCATGAA	911
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Db	912	GGCGCTTGCCGCTGCTGCACATTCGCCCTGTGTGCTCTTCGTCAATTATCATTTACGC	971
QY	226	ylleValGlyValGlnLeuThrPalaglyLeuLeuArgAsnArgCysPheLeuProGluAs	246
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Db	1072	-----TCTGGCTCTGGGCTTCATGCACACTGAAC-----	1101
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Db	1102	-----CATACCGAGTGCCGCGGGCG	1121
QY	326	YgluHisAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAl	346

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Db	1182	TGTGTTCCAGTGTATTAACCATGGAAGGCTGGACAGACGTCCTCTACTGATGACGATGC	1241
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Qy	385	emetIleAsnLeuCyseuValValIleAlaThrGlnPheSerGluThrLysGln----	403
Db	1302	TGTCCTCAACCTTGCTGTGGAGTCCTAAGCGGGAGTTCTCCAGGAAGAAAAAGGC	1361
Qy	404	-----ArgGluSerGlnLeuMetArgGluGlnArgVa	414
Db	1362	AAAAGCAGCAGGTGACTTTCAGAAAGCTTCGGAGAGACAGACAGATGGAAGAGACCTTCG	1421
Qy	414	lArgPheLeu-----SerAsnAl	420
Db	1422	GGGCTACCTGGACTGGATTCACACAGCGCTGAGAGTTAGACCTTCATGACCCCTCAGTAGA	1481
Qy	420	aserThrLeuAlaSerPheSerGluProGlySerCysTyrGluGluLeuLysTyrLe	440
Db	1482	CGGCAACTTGCTTCTCTTCTGAAGAGGA-----	1512
Qy	440	uValTyrIleLeuArgLysAlaAlaArgArgLeuAlaGlnValSerArgAlaIaGlyVa	460
Db	1513	-----CGGGCGGGCCA	1523
Qy	460	lArgValGlyLeuLeuSerSerProAlaProLeuGlyGly-----GlnGluTh	476
Db	1524	TGCTAGGCACTCAATTTGGCCCCGCTTCATTCCTAGCCCTGATGTGATTCCTCCTG	1583
Qy	476	rgInProSerSerSerCysSerArgSerHisArgArgLeuSerValHisIleuValHi	496
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Qy	496	SHISHISHISHISHISHISHIStyRHisLeuGlyAsnGlyThrLeuArgAlaProAr	516
Db	1630	-----GGATCAGG-----CACAG	1643
Qy	516	galASerProGluIleGlnAspArgAspAlaAsnGlySerArgArgLeuMetLeuProPr	536
Db	1644	AATCTCAACCCAGATTGAG-----ATACAAAGACTCCAACCTAGTTCC	1685
Qy	536	oProSerThrProAlaLeuSerGlyAlaProProGlyGlyAlaGluSerValHisSerPh	556
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Qy	556	eTyrHisAlaAspCysHisIleLeuGluProValArgCysGlnAlaProProProArgSerPr	576
Db	1729	-----TCTCAGTTACAAGTATCCCCCAGAGGCCACAACTG-----	1764
Qy	576	oSerGluAlaSerGlyArgThrValGly--SerGlyLysValTyrPro-----ThrVal	593
Db	1765	-TCAGAGCTGACCAATAGAGGCGCGGACGGCTGCGATGTTTCAGCCACTCTACTCGCTC	1823
Qy	594	HisThrSerProProProGluThrLeuLysGluLysAlaLeuValGluValAlaIaSer	613
Db	1824	CACACAACT-CCACCAGACGCCAG-----CCAGCC	1852
Qy	614	SerGlyProProThrLeuThrSerLeuAsnIleProProGlyProTyrSerSerMetHis	633
Db	1853	TCCAGCCAGTAGACACTGGC-TCCATGACAGACACACCCCTGGAGAT-----	1896
Qy	634	LysLeuLeuGluThrGlnSerThrGlyAlaCysGlnSerSerCysLysIleSerSerPro	653
Db	1897	-----GAGGATGAAGAGAGGGAACCATGCGTAGCTGTATACACGCTGCCTAAACAAG	1947
Qy	654	CysLeuLysAlaAspSerGlyAlaCysGlyProAspSerCysProTyrCysValaArgAla	673
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QY	674	GLYAlaGLYGLuValGLuLeuAlaAspArgGLuMetProAspSerAspSerGLuAlaVal	693
Db	1987	AACGGGGT-----	1995
QY	694	TyrGLuPheThrGLuAspAlaGLuHisSerAspLeuArgAspProHisSerArgGLu	713
Db	1996	-----CTCCGT-----GCACGCTGCC	2013
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QY	734	AspThrPheArgLysIleValAspSerLysTyrPheGLYArgGLYIleMetIleAlaIle	753
Db	2044	-----GCTGACTGTGCTGCTC-----	2061
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QY	774	AlaLeuGLuIleSerAsnIleValPheThrSerLeuPheAlaLeuGLuMetLeuLys	793
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QY	794	LeuLeuValTyrGLYProPheGLYTyrIleLysAsnProTyrAsnIlePheAsp-----	811
Db	2182	CTGTACGGCCTGGGCCCTCTGCTCTACGTTGCCCTCTTTTCAACCGCTTGACTGCTTC	2241
QY	812	-----GLYValIleValValIleSerValTrpGLuIleValGLYGLuGLuGLY	828
Db	2242	GTGGTCTGTGGGGCATCTAGAAACACTTTGGTGGAGGTGGGGCCATGCAGCTCTT	2301
QY	829	GLYLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValArgPheLeu	848
Db	2302	GGCATCTCAGTGCTCCGATGTGTACGCTCTCCACAGATCTTCAAGTCAACAGGCACTGG	2361
QY	849	ProAlaLeuGLuArgGLuLeuValValLeuMetLysThrMetAspAsnValAlaThrPhe	868
Db	2362	GCATCCCTGAGCAATCTGGTGGCATCTTGTCTCAATTCCATGAAGTCCATCGCTCTTG	2421
QY	869	CysMetLeuLeuMetLeuPheIlePheIlePheSerIleLeuGLYMetHisLeuPheGLY	888
Db	2422	CTGCTTCTCCTCTTCTCTTCATCATCATCTTCTCCCTGCTTGGCATGCAGCTGTTGGG	2481
QY	889	CysLysPheAlaSerGLuArgAspGLYAspThrLeuProAspArgLysAsnPheAspSer	908
Db	2482	GGCAAGTTCACCTTGACCAG-----ACCACACCAAGAGAGACACTTGTGATACC	2532
QY	909	LeuLeuTrpAlaIleValThrValPheGLuIleLeuThrGLuGLuAspTrpAsnLysVal	928
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QY	929	LeuTyrAsnGLYMetAlaSer-----ThrSerSerTrpAlaAlaLeu	942
Db	2593	ATGTATGATGATCATCGCTACGCTGCGCCCTTCTTCCAGGAGATGCTGTGCGGT	2652
QY	943	TyrPheIleAlaLeuMetThrPheGLYAsnTyrValLeuPheAsnLeuLeuValAlaIle	962
Db	2653	TATTTTCATCATCCTCTTCATCTGTGGCAACTACATCCTGTGAACGTGTTCTTGCCATT	2712
QY	963	LeuValGLuGLYpheGLuAlaGLuLulIleSerLysArgLysAspAlaSerGLYGLuLeu	982
Db	2713	GCCGTGATTAACCTAGCCAGC-----	2733
QY	983	SerCysIleGLuLeuProValAspSerGLuGLYGLYAspAlaAsnLysSerGLuSerGLu	1002
Db	2734	-----GGGATGCAGGCACTGCCAAA-----	2754
QY	1003	ProAspPhePheSerProSerLeuAspGLYAspGLYAspArgLysCysLeuAlaLeu	1022
Db	2755	-----GACAAAGGCGACAGAGAAGAGC-----	2775

QY	1023	ValSerLeuGluHisProGluLeuArgLysSerLeuProProLeuIleIleHis	1042
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QY	1063	GlyProAlaSerArgThrSerSerSerGlySerAlaGluProGlyAlaIaHisGlu	1082
Db	2818	-----GGTGAAGAG	2826
QY	1083	MetLysSerProProSerAlaArgSerSerProHisSerProThrSerAlaAlaSerSer	1102
Db	2827	AATGAGGACCGCAAGGTTGCAAGAAGTGAA-----	2856
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Db	2857	-----GGAGCAGCACCCAGGCATG-----	2874
QY	1123	SerProSerGlyGluArgArgSerLeuLeuSerGlyGluGlyGlnGlnSerGlnAspGlu	1142
Db	2875	-----GAGGAGGAGGAGGAGGAGAA	2898
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QY	1276	ysMetPheAspHisValValLeuValIleIlePheLeuAsnCysIleThrIleIaMetG	1296
Db	3213	ATACTTACCAAGTCTCATCTAGTGTTCATCATCTCTCAGTAGTGATGTCTCCGTGCTG	3272
QY	1296	IuArgProLysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTrpI	1316
Db	3273	AGGACCCC--ATCCGAGCTCACTCCTTCGAAACCATATTCGGATATTTTGAATTATG	3329
QY	1316	IePheThrAlaValPheLeuAlaGluMetThrValIysValAlaIaLeuGlyTrpCysP	1336
Db	3330	CCTTCACCTCATATCACTGTGAGATTCTACTCAAGATGACAGTGTGGGCGCTTCC	3389
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Db	3390	TGCACCGAGGCTCTTCTGCCGTAGCTGTTCATCTCTTGGATCTCCTTGTGTCACTG	3449
QY	1356	IeSerValIleAspIleLeuValSerMetValSerAspSerGlyThrLysIleLeuGlyM	1376
Db	3450	TGTCCCTCATCTCTTCGGCATTCAC-----TCCAGTGCATCTCAG	3491
QY	1376	etLeuArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaG	1396

D
Db

3492 TTGTGAAGATTCTCCGAGTCTCCGAGTCTCGGCCTCTCCGAGCAATCAACAGAGCCA 3551

QY 1396 lnglYleuYsLeuValValgluThrLeuMetSerSerLeuYsProIcglYAsnileV 1416

Db 3552 AGGACTCAAGCATGTGTGTCAGTGTGTGTTCTGTGGCCATCCGACCAATCGAAACATCA 3611

QY 1416 alValIlleCysCysAlaPhePheIlellePheGlYlleLeuGlYValglInleuPheLysG 1436

Db 3612 TGATTGTCAACCCTCTTGACATTCAATGTCCGCTGCATTTGGTGTGTTCAAGG 3671

QY 1436 lYlyspHePheValCysGlnGlYluAspThrArgAsnilleThrAsn----- 1451

Db 3672 GAAAATTCTACAGTTGCCACTGATGAGGCCAACACACCCTGAAGAATGCAAGGCTCCT 3731

QY 1452 -----LySeraspCysalaglualaseTYrArg-----TrpValA 1464

Db 3732 TCCTCATCTAACCTGATGAGATGTGTACGACCTTTGGTCCGGAGCGGCTGTGGGTCA 3791

QY 1464 rghIslyTYrAsnPheAspAsnleuglYalnAleuMetSerLeuPheValleuAlas 1484

Db 3792 ACAGTgATTTAActTTGACAACGTCCTTTCAGCCATGATGGCCCTGTTCACtGTCTCTA 3851

QY 1484 erLYsaSpGLYTrrValAspIleMeTYrAspGLYleuAspAlavalglYValAspGlnG 1504

Db 3852 CCTTGAAGCTGGCCTGCGCTACTATACAGCCCATAGATGCAAACGCAAGATGAGG 3911

QY 1504 lnProIIeMeTAsnHisAsnProTrpMeLeuLeuTYrPheIleSerPheLeuLeuIleV 1524

Db 3912 GCCCTATCTACAAATTACCATGTGAGATATCAGTATTCTTCATTGTCTACATCATCA 3971

QY 1524 alAlaPhePheValleuAsnMetPheValglYValValValgluAsnPheHislybCYSA 1544

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QY 1544 rgGlnHISGlnGlUGlUGlUAlaArgArgGLUGlULYSArgLeuArgArgLeuG 1564

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QY 1584 euLeuValHisIleuCYsThrsErlsTYrLeuAspLeuPheIlethrGlYValIleg 1604

Db 4143 ACCGCGTGTGGGCCACTGTGAACCTGCTGCTTGAAGTACCTCATGTTTCTCATCC 4202

QY 1604 lyLeuAsnValValThrmEtaIamETGlnHisTYrGlnGlnProGlnIleleuAspGluA 1624

Db 4203 TGCTCAACACGGGTGGCCCTAGCCATGCACCACTATGAACAGACTGCTCCCTTAACTATG 4262

QY 1624 laLeuLYsIleCYsAsnTYrIlePheThrValIlePheValleuGluservAlPheLYSL 1644

Db 4263 CCATGACATCTCTCAACATGTGTTCTACTGGCCTCTTACCATTGAGATGTGCTCAAAA 4322

QY 1644 euValAlaPheGlYPheArgArgPheGlnAspArgTrpAsnGlnleuAspLeuAlai 1664

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QY 1664 leValleuLeuSerIleMetGlYIleThrLeuGlUGlUGlUValAsnAlaSerLeu- 1683

Db 4383 TTGTAGTGGGCACTGTAGTCACATCGCCGTCACAGAAGTCAATAACGAGGCATCTTG 4442

QY 1684 -----ProIleasnProThrIleleArgIleMetArgValL 1696

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Db 4503 TGAGGCTG-----GTCAAGCTTGTGAGTAAAGGTGAGGGGATCCGACACTGCTCT 4553

QY 1716 spThrValMet-----GlnAlaLeuProGlnValglYAsnleuGlYleuLeuPheM 1733

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QY 1733 etLeuLeuPhePheIlePheAlaIaleuGlyValGluLeuPheGlyAspLeuGluCys- 1752
Db 4605 CAATGATATCTTCATCTCATGTGACAGTCAATGGCATGCAGATGTTGGCAAGGTGCTCTTC 4664
QY 1753 --AspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyM 1772
Db 4665 AGGACGGCAGCAG------ATMAATCGAAACAACAATTTCCAGACCTTCCGC 4712
QY 1772 etAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysA 1792
Db 4713 AGGCTGTGCTGCTTCTGTTCAGGTGTGCCACTGGTGAGCCCTGGCAAGATAATGCTAG 4772
QY 1792 sPThrLeu-----ArgAspCysAspGlnGluSer-----T 1802
Db 4773 CCAGCCTTCCAGGAATCGATGTGACCCCTGAGTCTGACTTTGGCCCAAGCGAGGAATTTA 4832
QY 1802 hrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValLeuThrAlaGlnP 1822
Db 4833 CCTGT--GGTAGCAGTTTGGCCATCGTCTACTCATCAGCTTCTTTATGCTCTGTGCT 4889
QY 1822 heValLeuValAsnValValIleAlaValLeuMet----- 1833
Db 4890 TCCTGATTATAATCTCTTGTGGCTGTAATCATGTGATTAACCTTGATTAACCTAACAGAG 4949
QY 1834 -----LysHisLeuGluGluSerAsnLysGluAlaLysGluAla 1847
Db 4950 ATTGCTCTATCCTGGACCCCAACCAACCTTGATGAATTC--AAGAGATCTGCTGTAAT 5006
QY 1847 laGluLeuGluAlaGluLeuGluLeuGlu-----MetLysThrL 1860
Db 5007 ATGACCCCGGAGCCCAAGGGCCGCATCAAGCAGCTTGATGTGTTGCCCTGTGAGACGCA 5066
QY 1860 euSerProGln-----ProHisSer----- 1866
Db 5067 TCCAGCCCCCATTTGGATTGGAAAGCTATGCCACACCGAGTGGCTGCAAGAGACTCG 5126
QY 1867 -----ProLeuGlySerProPhe-----LeuT 1874
Db 5127 TGGCAATGATGTGCCCCCTCAACTCAGA-TGGAACAGTGACATTCACGCTACACTCTTT 5185
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Db 5186 GCCCTGTGTGGACATCCCTGAAGATCAAGACAGAAAGGAACCTGGATCAAGCCAACCAAG 5245
QY 1894 laAla-----HisAlaArgSerAlaSerHisPheSerLeuGlu----- 1906
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QY 1907 --HisProThrMetGln-----ProH 1913
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QY 1953 eu-----GlyHisArgGlyT 1958
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QY 1958 rpGlyLeuProLysAlaGlnSerGly-----Serv 1968
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QY 1968 alLeuSerValHisSerGlnProAlaAspThrSerTyr-----Ile- 1981
Db 5594 TACAAAGACTCCATAGACTCCAGCCCAATCTCGATGAACTTAGATTTCCGCTGCT 5653

QY 1982 leuGlnLeuProLysAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGly 2001
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QY 2002 ThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuArgArg 2021
Db 5714 CTGGCTCCCACTCCAGGACGCCAGTGTGATACAGGCTGGCTCCCAACCAACAGAGAGA 5773
QY 2022 GlnAlaAlaIle-----ArgThrAspSerLeuAspValGlnGlyLeu 2035
Db 5774 AGCTCTGGGGTTTCATGTTCATCTATCCCGAAGAAGAAGTATTCAGCTCAAGGGAAT 5833
QY 2036 GlySerArgGlu-----AspLeuLeu 2042
Db 5834 CAAGGGCAGACAATCAGATGAGAACAGAAAGTCCCTGACTGGACTCCTGACTGGAT 5893
QY 2043 AlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGlyGlnSer 2062
Db 5894 GAGCAGGCCGGGACTCCTTGAACCCAGTCTTTACCA---CCTCACTGG----- 5941
QY 2063 SerThrGlnAlaGlnHisSerArgSerHisSerLysIleSerLysHisMetThrPro 2082
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Db 6032 TGTCTGCAACGCCAGGGCAGTTGTGA-----GATTTAACCATCCAGGCAAC 6079
QY 2122 -----GlyGlnGluGluProProSerProArgAspLeuLysLysCysTyrSerVal 2138
Db 6080 TACCATCGTGAGCGAAGCTCAGACCAAGC----- 6109
QY 2139 GluAlaGlnSerCysGlnArgArgProThrSerTrpLeuAspGluGlnArgArgHisSer 2158
Db 6110 -----AGGCTCAGGGTTCCTGGGACGCCCTCTCAGAAAGGTGCA 6151
QY 2159 IleAlaValSerCysLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsn 2178
Db 6152 CTGCTATATGCC-----CCCTGTTGTTGGTGAGGAATCTACA 6190
QY 2179 leuGlyGlyGlnProLeuGlyGlyProGlySerArgProLysLysLysLeuSerProPro 2198
Db 6191 GTGGGTGAAGATACCTTGGC-----AAACTTGGCGGCCCA 6226
QY 2199 SerIleThr-----IleAspProProGluSerGlnGlyProArgThrProProSer 2215
Db 6227 CTGCGTACCTTCACTGTCTGCAAGTGCCTGG-AGTCAATCCGAATCCAGCCACCGCA 6285
QY 2216 ProGlyIleCys-----LeuArgArgAlaProSer 2226
Db 6286 GAGGGCAGTGTGACAGTTGTGTGAGGCTGTGCTCATCTCCGAAGG-----CCTAGG 6339
QY 2227 SerAspSerLysAspProLeuAlaSerGlyPro-----ProAspSerMetAlaAla 2243
Db 6340 TCTCTTGGCCCAAGACCACGATTTGTGGCCCTGGCCAAAGAGAGATTTGCAGATGCATG 6399
QY 2244 SerProSerPro 2247
Db 6400 TCACCTGACCCT 6411

RESULT 2
BC051413 6035 bp mRNA linear HTC 19-NOV-2003
LOCUS
DEFINITION Mus musculus calcium channel, voltage-dependent, alpha 1F subunit,
mRNA (CDNA clone IMAGE:6493332), containing frame-shift errors.
ACCESSION BC051413
VERSION BC051413.1 GI:30802106
KEYWORDS HTC.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 6035)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257

JOURNAL MEDLINE
PUBMED 12477932
2 (bases 1 to 6035)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@hgrl.nih.gov

Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masieilo,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAK Plate: 108 Row: o Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9624972
This clone has the following problem: frame shifted.

FEATURES
source
1. 6035
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6493332"
/cissue_type="Eye, retina, mouse strain C57Bl\6"
/clone_lib="NIH MGC_94"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"

ORIGIN

Alignment Scores:
Pred. No.: 1.99e-105 Length: 6035
Score: 1683.50 Matches: 616
Percent Similarity: 38.15% Conservative: 331
Best Local Similarity: 24.82% Mismatches: 752
Query Match: 14.14% Indels: 786
DB: 3 Gaps: 86

US-09-611-257A-37 (1-2266) x BC051413 (1-6035)

QY 1 MetAspGluGluGluAspGlyAlaGlyAlaGluGluSerGlyGlnProArgSerPheMet 20
DB 18 ATGTCGGAATCTGAAGTCGGGAAAGATACACCCAGAGCCCACTCAAT----- 71
QY 21 ArgLeuAsnAspLeuSerGlyAlaGlyGlyArgProGlyPro-----GlySerAlaGlu 38
DB 72 -----GGACTGGCCCTGGCCCTGAATGGGGCTCTGTCT 107
QY 39 LysAspPro-----GlySerAlaaspSerGluAlaGluGlyLeuProTyPro----- 54
DB 108 GGGCTTCCAACCTGTGGGACTGATACCAAGCGGGCGTCAAGCCCTGGGACCCCAAGAGA 167
QY 55 -----AlaLeuAlaProValValPhePheTyLeu 64
DB 168 AGAACCACGACACAACAACAAGACTGTGGCGTGCC----- 206
QY 65 SerGlnAspSerArgProArgSerTrpCysLeuArgThrValCysAsnPro----- 81
DB 207 AGTGTCTAGAGATCACTCGAGCGCTCTTGCCTCAACCTTACTATCCCATTCGTCTCG 266
QY 82 -----Trp-----PheGluArgIleSerMetLeuValIleLeu 92
DB 267 TCCTGCATCAGCATTTGTAGAGTGAAGCCTTTGTATATTCATCTCCTGACAAATCTTT 326
QY 93 LeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleAlaCysaspSerGln 112
DB 327 GCCAAGTGGTGGCATTTGGGGGTATATATCCCTTCCCTGAGAGCAGCTCCAACACTGCT 386
QY 113 ArgCysArgIleLeuGlnAlaPheAspAspPheIlePhe--AlaPheAlaValGlu 131
DB 387 AACCAACAATTGGAACAGGTA-----GAATACGTGTCTCTGTGATTTTCACCGTGAG 440
QY 132 MetValValIysMetValAlaLeuGly--IlePheGlyLysLysCysTyLeuGlyAsp 150
DB 441 ACAGTCTCAAGATCGTAGCCTATGGCTGTGCTCCATCCAGCGCTATATTCGCAAT 500
QY 151 ThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTySerLeuAsp 170
DB 501 GCGTGAACCTGCTCGACTTCATCATCGTGTGGCTGTTCAAGCGTGTGCTGGA 560
QY 171 Leu-----GlnAsnValSer 175
DB 561 CAAGACCTGGGGCGCAGAGATGCCCGCATACTGAGGAAAGCCAGAGGCTTCGAT 620
QY 176 PheSerAlaValArgThrValArgValLeuArgProLeuArgAlaIleAsnArgValPro 195
DB 621 GTAAGGCACTGGCGGCAATTAGGGTGTACGACCTTAAGGCTAGTGTGGGTCGCCG 680
QY 196 SerMetArgIleLeuValThrLeuLeuLeuAspThrLeuProMetLeuGlyAsnValLeu 215
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QY 216 LeuLeuCysPhePheValPhePheIlePheGlyIleValGlyValGlnLeuTrpAlaGly 235
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DB 801 CGAATGCACAAGACATGCTACTTC-----CTGGGATCTGATATG 839
QY 256 GluArgTyTrpGlnThrGluAsnGluAspGluSerProPheIleCysSerGlnProArg 275
DB 840 GAA-----GCAAGAGGAGACCACTCACT----- 863

QY 276 GluAsnGlyMetArgSerCysArgSerValProThrLeuArgGlyAspGlyGlyGly 295
Db 864 -----TGTGCATCT-----TCTGGCTCTGGG 884
QY 296 ProProCysGlyLeuAspTyrGlyAlaTyrAsnSerSerSerSerAnThrThrCysValAsn 315
Db 885 CGTTCATGCACACTGAAC----- 902
QY 316 TrpAsnGlnTyrTyrThrAsnCysSerAlaGlyLuhHisAsnProPheGlyAlaIle 335
Db 903 -----CATACCGAGTGCCTGGCGGCTGGCCAGGACCCAAACGGTGGCATCAGC 950
QY 336 AsnPheAspAsnIleGlyTyrAlaTyrIleAlaIlePheGlnValIleThrLeuGlyGly 355
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Db 1191 CGG-----GAGAACGACGATGGAAGAA 1214
QY 435 GluLeuLeuLysTyrLeuValTyrIleLeuArg----- 445
Db 1215 GACCTTCGGGCTACCTGACTGATCACACAGGCTGAGAGTTAGACTTCATGACCCC 1274
QY 446 LysAlaAlaArgArgLeuAlaGlnValSer-ArgAlaAlaGlyValArgValGlyLeuLe 465
Db 1275 TCAGTAGACGGCACTGGCTTCTTGTCTGAAGAAGACGGCGGCATCGGCCACAA 1334
QY 465 UserSerProAlaProLeuGlyGlyGlnGluThrGlnProSerSerSerCysSerArgSe 485
Db 1335 CTGTCAAGAGCTGACCAATAGGAGC-----GCCGACGGCTGCCAT----- 1374
QY 485 rHisArgArgLeuSerValHisIleValHisHisHisHisHisHisHisIstY 505
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QY 505 rHisLeuGlyAsnGlyThrLeuArgAlaProArgAlaSerProGluIleGlnAspArgAs 525
Db 1375 -----GGTTCAGCCACTCTACTCGTCCACACACT----- 1404
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Db 1425 ----- 1425
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QY 585 ySerGlyLysValTyrProThrValHisThrSerProProProGluThrLeuLysGlyL 605
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QY 625 oProGlyProTyrSerSerMetHisLysLeuLeuGluThrGlnSerThrGlyAlaCysGl 645
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QY 685 tProAspSerAspSerGluAlaValTyrGluPheThrGlnAspAlaGlnHisSerAspLe 705
Db 1569 -----CT 1570
QY 705 uArgAspProHisSerArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerVa 725
Db 1571 CCGT-----GCACGCTGCCCGCGGGCCGTCAAGTCCACGCC----- 1607
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Db 1617 -----GCTGTACTGTTGCTCGTCTTCTCAACACGTTGACCATAGCTTCAGAGCACA 1669
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[illegible]

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Db	2867	GGTCAGTGTGTCCCTCATCTCTTCGGCATCCAC-----TCCAGTGC	2908
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Db	2909	CATCTCAGTTGTGAAGATTCTCCGAGTCTCCGAGTCTGCGGCTTCGAGCATCAA	2968
Qy	1393	rArgAlaGInGlyLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGI	1413
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Db	3029	AAACATCATGATTGTTCACCAACCCTCTTGCAAGTTCATGTTCCGCTGCATGGTGTTCAGCT	3088
Qy	1433	uPheLysGlyLysPhePheValCysGInGlyGluAspThrArgAsnIleThrAsn-----	1451
Db	3089	GTTCAAGGGAATAATTCTACAGTTGCACCTGATGAGGCCAACAACACCCCTGAAGAATGCAA	3148
Qy	1452	-----LysSerAspCysAlaGluAlaSerTyraArg-----	1461
Db	3149	GGGCTCCTTCCTCATCTACCTGATGAGATGTGTCAAGACCTTGGTCGGGAGCGGCT	3208
Qy	1462	-TrpValArgHisLysTyraAsnPheAspAsnLeuGIleAlaLeuMetSerLeuPheVa	1481
Db	3209	CTGGGTCAACAGTGAATTTTAACCTTGACAACAGCTCTTTCAGCCATGATGGCCCTGTTCCAC	3268
Qy	1481	IleuAlaSerLysAspGIlyTrpValAspIleMetTyraSpGIlyLeuAspAlaValGIlyVa	1501
Db	3269	TGCTCTACCTTGAAGCGCTGGCTCGCTACTATACAAGCCATAGATGCAGAAAGCAGAGA	3328
Qy	1501	IAspGInGInProIleMetAsnHisAsnProTrpMetLeuLeuTyrrPheIleSerPheLe	1521
Db	3329	AGATGAGGGCCCTATCTACAATTACCATGTGAGATATCAGTATCTTCTCATTTGCTACAT	3388
Qy	1521	uLeuIleValAlaPhePheValLeuAsnMetPheValGIlyValValGIluAsnPheHi	1541
Db	3389	CATCATCATCGCCTTCTTCATGATGAACATCTTGTGGGCTTGTATCATCATCATTC--	3446
Qy	1541	sLysCysArgGInHisGInGluGluGluAlaArgArgGluGluLysArgLeuAr	1561
Db	3447	-----CGTGCACCAGGAGAGCAGAGTACCMAAACTGTGAAGTGCAGACAAGAACCGCG	3499
Qy	1561	gArgLeuGluLysLysArgArgLysAlaGInCysLysProTyrrTyrrSerAspTyrrSerAr	1581
Db	3500	CCAGTGTGTGGAATATGCCCCGAAGCTCAGCCACTCCGCGATACATCCCTAAGAATCC	3559
Qy	1581	gPheArgLeuLeuValHisHisIleCysThrSerHisTyrrLeuAspLeuPheIleThrGI	1601
Db	3560	TCATCAGTACCCGCGTGTGGGCCACTGTGAAGTCTGCTGCCCTTGAAGTACCTCATGTTTCT	3619
Qy	1601	yValIleGlyLeuAsnValValThrMetAlaMetGluHisIleTyrrGInGInProGInIleLe	1621
Db	3620	GCTCATCTGCTCAACACGCGTGGCCCTAGCCATGACAGCACTATGAACAGACTGCTCCCTT	3679
Qy	1621	uAspGluAlaLeuLysIleCysAsnTyrrIlePheThrValIlePheValLeuGluSerVa	1641
Db	3680	TAACTATGCCATGAGCATCCTCAACATGCTTCACTGGCCCTTCAACCATGAGATGAGTGT	3739
Qy	1641	IleLysLeuValAlaPheGlyPheArgArgPhePheGluAspArgTrpAsnGInLeuAs	1661
Db	3740	GCTCAAAATCATCGCCTTTAAACCAAGACATTACTTTCAGATGCGCTGGAATACGTTTGA	3799
Qy	1661	pLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAl	1681
Db	3800	TGCTCTCATTTAGTGGGAGTGTAGTCGACATCGCCGCTC-----ACAGAGTCAATAG	3853
Qy	1681	aSerLeuPro--IleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArg	1700
Db	3854	GACAGCTCCGCGATATCTATCACGTTCTTTCGCTCTTCGAGTCAATGAGGCTG-----	3907

QY 1701 ValLeuLybLeuLeuLysMetalValGlyMetArgAlaLeuLeuAspThrValMet--- 1719
:::|||||
Db 3908 ---GTCAAGCTTCTGAGTAAGGGTGAGGGGATCCGCACACTGCTCTGACATTCATCAAG 3964
QY 1720 -----GlnAlaLeuProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhe 1737
|||||
Db 3965 TCTTTCAGGCGCTTGCCCTATGTG-----GCACCTTCTCATAGCAATGATATTTCTTC 4015
QY 1738 IlePheAlaAlaLeuGlyValGlyLeuPheGlyAspLeuGlyCys---AspGlyThrHis 1756
|||::|
Db 4016 ATCTATGACATGTCATGCGATGACAGATGTTGGCAAAGGTGCTCTTCAGACGCGACGCGAG 4075
QY 1757 ProCysGlyGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeuThr 1776
:::|
Db 4076 -----ATAATCGAACAACAATTTCCAGACCTTCCGACGGCTGTGCTGCTT 4123
QY 1777 LeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetLysAspThrLeu----- 1794
|||||
Db 4124 CTGTTCAAGGTGTGCCACTGTGAGGCGCTGGCAAGATAATGCTAGCCACTTCCAGGA 4183
QY 1795 ArgAspCysAspGlnGlySer-----ThrCysTyrrAsnThr 1806
|||
Db 4184 AATCGATGTGACCTGAGCTTGACTTGGCCGACGGAGGAATTACCTGT--GGTAGC 4240
QY 1807 ValIleSerProIleTyrrPheValSerPheValLeuThrAlaGlnPheValLeuValAsn 1826
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Db 4241 AGTTTGGCATCGTCTACTTCATCAGCTTCTTTATGCTGTGCTTCTGCTTATTAAT 4300
QY 1827 ValValIleAlaValLeuMet----- 1833
:::|
Db 4301 CTCTTGTGCTGATCATGAGTAACTTGAATTACCTAACACAGAGATTGGTCTATCCTG 4360
QY 1834 -----LysHisLeuGlyGlySerAsnLysGlyAlaLysGlyAlaGlyLeuGlyAla 1851
|||||
Db 4361 GGAACCCCAACCACTTGATGAATTC--AAGAGACTGTGCTGTAATATGACCCCGAGACC 4417
QY 1852 GlnLeuGlyLeuGlyu-----MetLysThrLeuSerProGln--- 1863
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Db 4418 AAGGGCCGCATCAAGCACTTGGATGTGTTGCCCTGCTGAGACGCATCCAGCCCATTTG 4477
QY 1864 -----ProHisSer----- 1866
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Db 4478 GGAATTGGAAAGCTATGCCACACCGAGTGCCCTGCAAGAGACTCGTGCAATGAATGTG 4537
QY 1867 ProLeuGlySerProPhe-----LeuTrpProGlyValGly 1878
|||||
Db 4538 CCCCTCAACTCAGA--TGGAAAGTAGACATTCACGCTACACTCTTGGCCTGTGTCGAGC 4596
QY 1879 GlyProAspSerProAspSerProLysProGlyAlaLeuHisProAlaAla----- 1895
|||
Db 4597 ATCCCTGAAGATCAAGACAGAGGAACTTGATCAAGCCACAGAGCTTCGGATGCT 4656
QY 1896 HisAlaArgSerAlaSerHisPheSerLeuGlyu-----HisProThrMet 1910
|||
Db 4657 CATCAAAAAGATCTGGAAGCGGATAAAGCAGAAATTGTTGATGAGGTATCCCTCCTCC 4716
QY 1911 Gln-----ProHisProThrGlyLeu 1917
:::|
Db 4717 CGATGAGAGAGAGTCACTGTGGAAATTTATGCCACATTCCTGATCCAAAGATTATTT 4776
QY 1918 ProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuPro 1937
|||
Db 4777 -----CCGAAATATCCGAGAGAAAGAAAGGGGCTACTAGGAAGAGAGC---CCC 4827
QY 1938 AsnAspSerTyrrMetCysArgHisGlySerThrAlaGlyProLeu----- 1953
|||
Db 4828 AACAGACATCTCTGCTGCTCCAGGCTGTCTAGAGAG---CCTGACAGACTTGGGTCC 4884
QY 1954 -----GlyHisArgGlyTyrrGlyLeuProLys 1962
|||
Db 4885 TGAATCCGTCAGCCCTCACTATGACACTGAGGAAGAAGAGAGAGAGAGCAGT 4944

QY 1963 AlaGlnSerGly-----SerValLeuSerValHis 1972
|||
Db 4945 GGGTCAGAGAGCTGAGGAAGAGAACTGAGAACAAACCCAGAAACCATACAAAGACTCCAT 5004
QY 1973 SerGlnProAlaAspThrSerTyrr-----Ile-LeuGlnLeuProLys 1986
|||||
Db 5005 AGACTCCAGGCCCAATCTCGATGGAACCTAGATTTCGGTGTCTTACCTGTTAAGGA 5064
QY 1986 sAspAlaProHisLeuLeuGlnProHisSerAlaProThrTrpGlyThrIleProLysLe 2006
:::|
Db 5065 GAAACTTCCAGATTCTCTCAACTGGGCGAGTGATGATGATGGGCTGCTGCCAATC 5124
QY 2006 uProProProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaAlaIle-- 2025
|||
Db 5125 CAGGACGCCAGTGTGATACAGGCTGGCTCCCAACCAACACAGAGAGAAGCTTGGGGTTT 5184
QY 2026 -----ArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGlyu-- 2039
|||
Db 5185 CATGTTACTATCCCGAAGAGAAGATTTACGCTCAAGGAACTCAAGGCGACAGCAA 5244
QY 2040 -----AspLeuLeuAlaGlyValSerGly 2047
|||||
Db 5245 TCAGATGAGGAACAGGAAGTCCCTGACTGACTCCTGACTGATGACAGAGCGCGGAC 5304
QY 2047 yProSerProProLeuAlaArgAlaTyrrSerPheTrpGlyGlnSerSerThrGlnAlaGly 2067
|||||
Db 5305 TCCTTGAACCAAGTCTTTTACCA---CCTCACTGG-----TCCCA 5343
QY 2067 nglnHisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysPr 2087
|||||
Db 5344 GCAACACGTAACGGGCAACCATGTGCCACGCCGACGTTTGTGCCCCCAGCGCTGCA-- 5401
QY 2087 oglyProGlyProAsnTrpGlyLysGlyProProGlyuThrArgSerSerLeuGlyLeuAs 2107
|||
Db 5402 -----GGTCGGAAGCCCTCCTTCAACCATCCAGTGTCTGCAACGCCA 5442
QY 2107 pThrGlyLeuSerTrpIleSerGlyAspLeuLeuProProGlyu-----GlyGly 2123
|||||
Db 5443 GGGCAGTTGTGA-----GATTTACCTATCCAGGCACTTACCATCGTGGACG 5490
QY 2123 nglyGlyProProSerProArgAspLeuLysCysTyrrSerValGlyAlaGlnSerCy 2143
|||
Db 5491 GACCTCAGACCAAGC----- 5506
QY 2143 sGlnArgArgProThrSerTrpLeuAspGlyGlnArgArgHisSerIleAlaValSerCy 2163
|||
Db 5507 ---AGGCTCAGGGTCTCTGGCAGCCCTCCTCAGAAAGGTCGACTATATGCC-- 5560
QY 2163 sLeuAspSerGlySerGlnProHisLeuGlyThrAspProSerAsnLeuGlyGlyLnp 2183
|||
Db 5561 -----CCCTGTGTTGGTGGAGGAATCTACAGTGGGTGAAGATA 5601
QY 2183 oLeuGlyGlyProGlySerArgProLysLysLysLeuSerProProSerIleThr----- 2201
|||||
Db 5602 CCTTGGC-----AAACTTGGCGGCCCACTGCGTACCTTCAAC 5637
QY 2202 ---IleAspProProGlySerGlnGlyProArgThrProProSerProGlyIleCys-- 2219
:::|
Db 5638 CTGCTCGAAGTGGCTGG--AGCTCATCCGAATCCAGCCACCGCAAGAGGGGAGTGTCTG 5696
QY 2220 -----LeuArgArgArgAlaProSerSerAspSerLysAs 2231
|||||
Db 5697 ACAAGTTGTGAGGCTGTGCTCATGTCCGAAG-----CCTAGGTTCTTTGGCCCAAG 5750
QY 2231 pProLeuAlaSerGlyPro-----ProAspSerMetAlaAlaSerProSerPro 2247
|||
Db 5751 ACCACAGATTGTGGCCCTGGCCAAAGCAGAGATTGCAAGATGCATGTCACTGACCTT 5808

RESULT 3
BM479323 1076 bp mRNA linear EST 05-FEB-2002
LOCUS BM479323
DEFINITION AGENCOURT_6418725 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5502230
5', mRNA sequence.

/db_xref="taxon:8355"
/clone="IMAGE:7018586"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC Brn1"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN

Alignment Scores:

Pred. No.:	4.47e-81	Length:	879
Score:	1314.50	Matches:	255
Percent Similarity:	94.79%	Conservative:	18
Best Local Similarity:	88.54%	Mismatches:	13
Query Match:	11.04%	Indels:	2
DB:	7	Gaps:	1

US-09-611-257A-37 (1-2266) x CF548698 (1-879)

QY 1486 ASPGIYTRPVALASPILEMETRYRASPGLYLEUASPALAVAGLYVALASPGINGINPRO 1505
|||
DB 1 GACGGATGGGTGACATCATGTATGATGACGTGCTGCGAATGTACCAAGCAGCCCA 60
QY 1506 ILEMETASNHISANPROTRPMETLEULEUYRPHELLESERPHELEULEULEVALA 1525
:::
DB 61 GTGATGATTAACAACCTTGATGCTGCTATATTTCATCTCATTTTGTGATGTGCA 120
QY 1526 PHEPHEVALLEUASNMETPHEVALGLYVALVALGLUASNPHEHISLYSCYARGGLN 1545
|||
DB 121 TTTTGTGCTCAACATGTTTGTGGGTGTGTGTGAGAACTTCCATAAGTCCCGCAG 180
QY 1546 HISGLINGLUGLUGLUALAARGARGARGGLUGLULYSARGLEUARGLEUGLULYS 1565
|||
DB 181 CATCAGAGAGAGAGAGAACGAAAGAGACGGAGAAAGAGAGAGAGAGAGAGAGAA 240
QY 1566 LYSARGARGLYSALAGINCYSLYSPROTYRYSERASPTYRSEARGPHEARGLEULEU 1585
|||
DB 241 AAGAGAAGGAAGGCCCAAGTAAACCCCTACTATTGAGATTTCTCACTTCGGCTCCTC 300
QY 1586 VALHISHISLEUCYERTHSERHISTYRLEUASPLEPHELETHRGLYVALILEGLYLEU 1605
:::
DB 301 ATCCATCAGATCTGTACAAGTCATATTGTGATTTGTTATTACTGGGGTCATTGGATTG 360
QY 1606 ASNVALVALTHRMETALAMETGLUHISTYRGLINGLINPROGLINILEUASPGLUALALEU 1625
|||
DB 361 AATGTTATCACTATGGCAATGAGCACTATCAGCAACCCAGGATTTGGTTGAAGCTCTA 420
QY 1626 LYSILECYASNTYRILEPHETHRVALILEPHEVALLEUGLUSERVALPHELYSLEUVAL 1645
|||
DB 421 AAAATCTGTAATTACATCTTTAACCTCATTTTCTGTACTGGAATCTGGGTGCAAAATGATA 480
QY 1646 ALAPHEGLYPHEARGARGPHEPHEGLNASPARGTRPASNGLINLEUASPLEUALALEVAL 1665
|||
DB 481 GCTTTTGGCTTCCGGCGAATCTTTAAAGACAGGTGGAACAGTTGATCTGGCCATCGTT 540
QY 1666 LEULEUSERILEMETGLYLETHRLEUGLUGLULEGLUVALASNALASERLEUPROILE 1685
|||
DB 541 CTTCTCTCCATCATGGGAATCACACTGGAAGAGATTGAAGTCAATGCATCACTGCCCATTT 600
QY 1686 ASNPROTHRILEILEARGILEMETARGVALLEUARGILEALARGVALLEULYSLEULEU 1705
|||
DB 601 AACCACAATCATCCGATAATGAGGGTCTTGGGATTTGCTCGGGTCTGAAGTTATTATA 660
QY 1706 LYSMETALAVAGLYMETARGALALEUASPTHRVAlMETGLNALALEUPROGLINVAL 1725
|||
DB 661 AAGATGGCAGTCCGTATGCGAGCCCTGCTGATACGGTTCTGCAAGCGCTTTCTCAAGTG 720
QY 1726 GLYASNLEUGLYLEULEUPHEMETLEULEUPHEPHELEPHEALALEUGLYVALGLU 1745
|||
DB 721 GGGAACTTCGGCCTGCTCTTATGCTGCTGTTCTTTAATTGCGCGCTTGGGAGTTGAA 780

QY 1746 LEUPHEGLYASPLEUGLUCYSASPGIUTHRHISPROCYSGLU-GLYLEUGLYARGHISAL 1765
|||
DB 781 CTTTGTGTAAGCTTAAAGACACTGGATCCCATCCCTGTGAAGGCTTTGGCAGACTTGC 840
QY 1765 ATHRPHEARGASN---PHEGLY 1771
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DB 841 CACTTTTCAAGGAATTTTCGGG 862

RESULT 5

AY416501

LOCUS

AY416501 5666 bp DNA linear GSS 17-DEC-2003

DEFINITION Mus musculus SCN8A gene, VIRUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION AY416501

VERSION AY416501.1 GI:39772461

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 5666)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering

them based on alignment.

FEATURES Location/Qualifiers

source 1..5666

gene /organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

<1..>5666

/gene="SCN8A"

/locus_tag="HCM5911"

ORIGIN

Alignment Scores:

Pred. No.:	4.47e-78	Length:	5666
Score:	1290.50	Matches:	525
Percent Similarity:	36.71%	Conservative:	305
Best Local Similarity:	23.22%	Mismatches:	713
Query Match:	10.84%	Indels:	723
DB:	9	Gaps:	77

US-09-611-257A-37 (1-2266) x AY416501 (1-5666)

QY 25 LEUSERGLYALAGLYARGPROGLYSEVALAGLULYSASPProGLYSERAla 44
|||
DB 204 CTACGGGACATCCCGCAAGCCCTGTGGCGTTCC-----CCTGAGGACTT 251
QY 45 -ASPSERGLUALAGLUGLYLEUPROTYR----- 53
|||
DB 252 TGAC-----CCGTACTATTGACGACAGAAAACCTTTGTAGTATTAA 293
QY 54 -----ProAlaLeuAlaProValValPhePh 62
|||
DB 294 CAGAGGAAAACCTCTTCAGATTTAGCGCCACTCCTGCCCTTG-----TA 338
QY 62 eTYRLEUSERGLINASPSEARArgProArgSerTRpCysLeuArgThrValCysAsnProTr 82

Db	339	CATTCTAAGTCCTTTAACTGATAGAGAATAGCTATTAAATTTTGATACATTCATT	398
QY	82	pphegluargllesermettleuvalilleuleuanscysvalthreuglymetphear	102
Db	399	CTTCAGCATGATCATCATGTGCACCATCTCGACCACTGTGTATTTCATGACTTTAGTAA	458
QY	102	gProCysgluaspilealaCysaspserglinargCysargilleuGlinalpheaspas	122
Db	459	CCCTCCCGAA-----TGTCACAGAAATGTGGA	485
QY	122	ppheillephe---AlaphephealavalGlumetValvallysmetValalaleuGlyI	141
Db	486	GTACACATTACAGAGGATTTACACATTGGAATCACTGTGAAATCATCGCCAGAGTTT	545
QY	141	epheglYlYslyscys-----TyrleuGlYAspThrTrpAsnArgLeuAs	156
Db	546	C-----TGCATAGACGGCTTCACCTTCTTACGAGACCCGTGAACCTGGTTAGA	593
QY	156	pphepheillevalillealaglYmettleuGlutYrserLeuAspleuGlInasnValSerPh	176
Db	594	CTTCAGTGTATCATGATGATGCGCTATATATACAGAGTTTGTAACCTAGGCAATGTT--	648
QY	176	eSeralavalargthrValargValleuargProleuargAlaileasnargValProse	196
Db	649	-TCAGCTACGCACCTTTCAGGGTACTGAGGGCTTGAAAACTATTTCGGTATCCACAG	707
QY	196	rMetargilleuValthrleuLeuLeuAspThrleuPrometleuGlYasnValleuLe	216
Db	708	CCTGAAGACAATCGTGGCGCCCTCATCCAGTCTGTGAAGAAAGCTGCAGACGTATGAT	767
QY	216	uLeuCysPhepheValPhepherlePheglYIleValGlYalGlIneutrpAlaglYle	236
Db	768	CCTGACGGTGTCTGCTGAGTGTCTTGCCCTGATGCGCTGCAGCTCTTCATGGGGA	827
QY	236	uLeuArgAsnArgCysPheleu--ProGlInasnPheSerleuProleuSerValasple	255
Db	828	CCTTCGAACAACAGTGTGTGTGTGGCCCATTAACCTTCAAC-----	867
QY	255	uGlUArgTyrTyrGlInthrGlInuAsnGlInuAspGluSerProphelleCysserGlInProAr	275
Db	868	-GAGAGCTATCTG-----	879
QY	275	gGlInuAsnGlYmetArgSerCysArgSerValProthrleuArgGlyaspGlyglYgl	295
Db	880	-GAGAACGGCACACAGA-----	894
QY	295	yProProCysglYleuAspTyrGlualatYr-----	305
Db	895	-----GGCTTCGACTGGAGAGATATATCAACAATAAAACAACCTTTTACATGTT	944
QY	306	-----AsnSerSerSerAsnThrThrCysValAs	315
Db	945	CCCTGGCATGCTAGAACCTTGCTCTCGCGGAACAGCTCTGACGCCGGCAATGCCAGAA	1004
QY	315	nTrpAsnGlInTyrTyrThrAsnCysSerAlaglYluHisAsnProphelysGlyAlaI	335
Db	1005	GGGGTTCAG-----TGCAATGAAGCAGAGAAATCCCACTACGGCTACAC	1052
QY	335	eAsnPheaspAsnIleGlyTyrAlatrpIleAlaIlePheGlInValIleThrleuGlInl	355
Db	1053	CAGCTTCGACACCTTCAGCTGGGCCCTTCCTGGCACATGTTCCGCCCTCATGACTCAGACTA	1112
QY	355	yTrpValAspIleMetYrPheValMetaspAlaHisSerPheTyrAsnPheIleTyrPh	375
Db	1113	CTGGAGAACTTATACCACTGACCTTACGAGCGGCTGGGAAAAAGTACATGATCTTCTT	1172
QY	375	eIleleuLeuIleIleValGlYserPhePheMetIleasnLeuCysleuValValIleAl	395
Db	1173	TGCTTGTGATCTTCGTGGTCTTCTTCTATTGTGTAACCTTGACTTGCGTGTGGC	1232
QY	395	aThrGlInPheSerGlInthrYsGlInargGluSerGlInleuMetArgGluGlInargValAr	415

[illegible]

[illegible]

Db	4630	GGATCCGACCCCTGCTCTTTGGCTTAATGATGTCGCTGCCGCCCTGTTCACATCGGCC	4689
QY	1730	euleuphamecLeuleuphetherlephelaalaLeuGlyValGlyLeuphheGlyAspL	1750
Db	4690	TCCTGCTCTTCCGTGATGTCATGTCATCTTCTCCATCTTTGGGATGTCCAATTCGCGTAGC	4749
QY	1750	eugLucysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArgAsnP	1770
Db	4750	TGAAGCACGAG-----GCCGGCATGTGACATGTTCAACTTCGAGACGT	4794
QY	1770	heGlyMetAlaPheLeuThrleuphPheArgValSerThrGlyAspAsnTPAsnGlyIleM	1790
Db	4795	TTGGCAACAGCATGATCTGCTCTGTTCAGATCACGACCTCTGCTGGATGGCTTAC	4854
QY	1790	eLysAspThrLeuArg-----AspCys-----AspGlnGlu-----	1800
Db	4855	TGCTGCCAATCCTGAACCGCCCCCTGACTGCAGCTTGAGACAAGAGCACCCAGAAAGTG	4914
QY	1801	-----SerThrCysTyrAsnThrValIleSerProIleTyrPheValSerPheValL	1818
Db	4915	GCTTCAAGGGGAGTGCGGGAACCCCTCCGTGGGCACTTCTTCTTCTGTCAGCTACATCA	4974
QY	1818	euthrAlaGlnPheValLeuValAsnValIleAlaValLeuMetLysHisLeuGluG	1838
Db	4975	TCATCTCTTCTTGATCGTGTAACATGATGATCCATCATCTTGAGAACTTCAGCG	5034
QY	1838	IuSerAsnLysGluAlaLysGlu-----GluAlaGluLeuGluAlaGluLeuGluL	1855
Db	5035	TAGCCACAGAGAAAGCGCCGATCCTTGAGCGAGGAGACTTCGAGACTTTCTATGAGA	5094
QY	1855	eugLucMetLys-ThrLeuSerProGlnProHisSerProLeuGlySerProPheLeuTrp	1874
Db	5095	TCTGGAGAAAGTTTGATCCGTGATGCCACCCAGTTCA-----TCGAGTACTGTAAGCTGG	5148
QY	1875	ProGlyValGluGlyProAspSerProAspSerPro-LysProGlyAlaLeuHisProAl	1894
Db	5149	CCGACTTTG-----CCGACGCCCTGGAGCATCCGCTCCGAG	5184
QY	1894	aAlaHisAlaArgSerAlaSerHisPheSerLeuGlnHisProThrMetGlnProHisPr	1914
Db	5185	TACCAAGCC-----CAACACCATCG	5205
QY	1914	othrGluLeuProGlyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHi	1934
Db	5206	AGCTCATCGCCATGACCT-----	5224
QY	1934	sSerLeuProAsnAspSerTyrMetCysArgHisGlySerThrAlaGluGlyPro--Le	1953
Db	5225	-----GCCCATGGTGAAGCGAGATCGAATCCACTGCT	5256
QY	1953	uGlyHis-----ArgGlyTyrGlyLeu-----Pr	1961
Db	5257	TGACATCTTCTTTCGCTTACCAAGCAGATCCTGGGAGACAGTGGGAGTTGGACATCC	5316
QY	1961	oLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTyr--	1980
Db	5317	TGCGGACAGATGAGAGAGCGGTTT--GTGGCGTCCAATCCTTCCAAGTGTCTTACGA	5374
QY	1981	-----IleLeuGln--	1983
Db	5375	GCCTATCACGACCACTTTCGCGCGCAAGCAGAAAGGTGTCTGCAGTGGTCTTGCAGCG	5434
QY	1984	-----LeuProLysAspAlaProHisLeuLeuGlnProHis-----Se	1996
Db	5435	TGCTTACAGGGGACACCTGGCTAAGCGGGCTT-CATCTGCAGAAAGATCACTTCCAACA	5493
QY	1996	rAlaProThrTrp-----GlyThrIleProLysLeuProProPr	2009
Db	5494	AGCTGAGAAATGAGAGCACCCACCGAGAGAAGAGAAGA-GCACCCTGTCACAGCCTCC	5552
QY	2009	oGlyArgSerProLeuAla-----GlnArgProLeuArgArgGlnAlaAla	2024
Db	5553	C-----TCCCTCTTACGACAGCGTGCACAAAGCCCGCAAGAGAGACGACGAGC	5601

RESULT 6
BM451648 1064 bp mRNA linear EST 05-FEB-2002
LOCUS BM451648
DEFINITION AGENCOURT_6394764 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5493169
5' mRNA sequence.
BM451648
ACCESSION BM451648.1 GI:18500688
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1064)
NIH-MGC http://mgi.nci.nih.gov/.
Natlional Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12116 row: h column: 02
High quality sequence stop: 657.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5493169"
/issue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

FEATURES
source

Alignment Scores:
pred. No.: 1.22e-78 Length: 1064
Score: 1281.50 Matches: 272
Percent Similarity: 76.36% Conservative: 9
Best Local Similarity: 73.91% Mismatches: 16
Query Match: 10.77% Indels: 71
DB: 4 Gaps: 6
US-09-611-257A-37 (1-2266) x BM451648 (1-1064)

ORIGIN
QY 1464 ArgHisIlySTyrAsnPhenAspAsnLeuGlyGlnAlaLeuMetSerLeuPheValLeuAla 1483
Db 1 CGGCACAAGTACAACTTGGACAACTTGGCCAGGCCCTGATGTCCCTGTTGGTGGCC 60
QY 1484 SerIysAspGlyTTrpValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGln 1503
Db 61 TCCAAAGATGGTGGTGACATCATGATGAGATGGCTGATGCTGTGGGCTGACACAG 120
QY 1504 GlnProIleMetAsnHisAsnProTrpMetLeuLeuTyrPheIleSerPheLeuLeuIle 1523
Db 121 CAGCCCATCATGAACACACACCCCTGGATGCTGCTGACTTCACTCGTTCCTCATTT 180
QY 1524 ValAlaPhePheValLeuAsnMetPheValGlyValValValGlyAsnPheHisIlyS 1543
Db 181 GTGGCTCTTTGTCTCTGAACATGTTTGTGGGTGTGGTGAGAGAACTTCCACAAGTGT 240
QY 1544 ArgGlnHisGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1563
Db 241 CGGCAGCACCAAG 300

QY 1564 GlnIlySlyArgArg----- 1568
Db 301 GAGAAAAAGAGAGAGAGTAAGAGAGACAGATGGCTGATCTAATGCTGGACAGATGAATT 360
QY 1569 -----LysAlaGlnCylSlySProTyrTyrSerAsp 1578
Db 361 GCTTCCGGCAGCTCAGCCAGCGCTGCTCAGAGAGCCCAAGTGAACCTTACTACTCCGAC 420
QY 1579 TyrSerArgPheArgLeuLeuValHisIleuCystrHisIleTyrLeuAspLeuPhe 1598
Db 421 TACTCCCGCTTCGGCTCCTCGTCCACCACTGTGTGACCAAGCACTAAGTGAACCTTTC 480
QY 1599 IleThrGlyValIleGlyLeuAsnValValThrMetAlaMetGluHisTyrGlnGlnPro 1618
Db 481 ATCACAGGTGTACCGGCTGAACGTGTGTACCATGAGCCATGAGCACTACACAGAGCC 540
QY 1619 GlnIleLeuAspGlnAlaLeuValIleCyAsnTyrIlePheThrValIlePheValLeu 1638
Db 541 CAGATTCTGATGAGGCTTGAAGATCTGCAACTACATCTTCACTGTTCATCTTGTCTTG 600
QY 1639 GluSerValPheIlySlyLeuValAlaPheGlyPheArgArgPhePheGlnAspArgTyrAsn 1658
Db 601 GAGTCAGTTTTCAACTTGTGGCTTGTGTTCCGTCGTTCTTCCAGAGACAGTGAAC 660
QY 1659 GlnLeuAspLeuAlaIleValLeuLeuSerIleMetGlyIleThrLeuGlnGlnIleGlu 1678
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QY 1718 lMet-GlnAlaLeuProGlnValGlyAsnLeuGly---LeuLeuPheMetLeuLeuPhe 1737
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QY 1737 he---IlePheAlaAlaLeuGlyValGlnLeuPheGlyAspLeuGlnCyAspGluThr 1756
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QY 1756 lAsProCysGlnGlyLeuGlyArgHisAlaThrPheArgAsnPheGlyMetAlaPheLeu 1776
Db 941 ----- 941
QY 1776 hrLeuPheArgValSerThrGlyAspAsnTrpAsnGlyIleMetIysAspThrLeuArg 1796
Db 942 -----GGAGAACCCTGAATGG----- 959
QY 1796 spCyAspGlnGluSerThr 1802
Db 960 -----GACAAAGAACCCACC 974
RESULT 7
CA319705 793 bp mRNA linear EST 09-JUL-2003
LOCUS CA319705
DEFINITION UI-M-FW0-cca-d-09-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
IMAGE:6816826 5', mRNA sequence.
CA319705
ACCESSION CA319705
VERSION CA319705.1 GI:24537829
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 793)
NIH-MGC http://mgi.nci.nih.gov/.
Natlional Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: PYX-5.

FEATURES

source
1. .793
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6816826"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/note="Organ: Brain; Vector: PYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into PYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemm Chin, Ph.D.,
program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 3.85e-77 Length: 793
Score: 1257.00 Matches: 241
Percent Similarity: 92.40% Conservative: 2
Best Local Similarity: 91.63% Mismatches: 2
Query Match: 10.56% Indels: 18
DB: 6 Gaps: 1

US-09-611-257A-37 (1-2266) x CA319705 (1-793)

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DB 3 CTCTTCAAGGGAAGTTCTTCGTGTGCAGGGTGAGGACACGAAACATCACTAACAAAG 62
OY 1453 SerAspCysAlaGluAlaSerTyrArgTrpValArgHisIlysTyrAsnphespaSnleu 1472
DB 63 TCCGACTGTCTGAGGCCAGTTACCGGTGGGTCCGGCACAGTACAACTTGACAACCTG 122
OY 1473 GlyGlnAlaLeuMetSerleupheValleuAlaSerIlysaSpGlyTrpValaspIleMet 1492
DB 123 GGCCAGGCTTCATGTCCCTGTTGTGCTGGCCTCCAGGATGGCTGGTTGACATCATG 182
OY 1493 TyrAspGlyLeuAspAlaValGlyValaspGlnInProIleMetAsnHisasnProTrp 1512
DB 183 TATGATGACTGGATGCTGTGGAGTGAGCACGAGCCCATCATGAACCAACCCCTTGG 242
OY 1513 MetleuLeuTyrPheIleSerPheleuLeuIleValAlaPhePheValleuAsnMetPhe 1532
DB 243 ATGCTGCTTACTTCACTCTCTCTCTCATCGTGGCCTTCTTCTGTAACAATGTTT 302
OY 1533 ValGlyValValValGluAsnphHisIlysCysArgGlnHisglnGluGluGluAla 1552
DB 303 GTGGGCGTGTGTGGAGAACTTCCATAAGTGACAGCAGACCAAGAGAGAGAGGCG 362

OY 1553 ArgArgArgGluGluLysArgLeuArgArgLeuGluLysLysArgArg----- 1568
DB 363 CGCGCGCGGAGAGAGAAAGCACTAAAGAGGCTGGAGAAAAAGAGAAATCTAATGTTG 422
OY 1569 -----LysAlaGlnCysLysPro 1574
DB 423 GACGATGTATTGCTTCGGGACAGCTCAGCCAGCGCTGCGTCAGAAAGCCAGTGCAAAACC 482
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OY 1655 AspArgTrpAsnGlnLeuAspLeuAlaIleValleuLeuSerIleMetGlyIleThrLeu 1674
DB 723 GACAGGTGGAACCAAGCTGAGCCTGGCTATTGTGCTTCTGTCATCATGGGCATCAGCTG 782
OY 1675 GluGluIle 1677
DB 783 GAAGAGATT 791
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AY416499 5943 bp DNA linear GSS 17-DEC-2003
LOCUS AY416499
DEFINITION Homo sapiens SCN8A gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY416499
VERSION AY416499.1 GI:39772459
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 5943)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarimal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITTLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1. .5943
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>5943
/gene="SCN8A"
/locus_tag="HCM5911"

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QY 1299 LysIleAspProHisSerAlaGluArgIlePheLeuThrLeuSerAsnTyrIlePheThr 1318
Db 3661 TACATTGAGCAGAGAAGAACCATCCGACCAATCCGAATATGCTGACAAAGCTTCACCC 3720
QY 1319 AlaValPheLeuAlaGluMetThrValIysValAlaLeuGlyTyrCysPheGlyGlu 1338
Db 3721 TATATCTTCATCCTGAGAGATGTTGCTCAAGTGGACAGCCTATGGCTTCGTC----- 3771
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Db 3772 ---AAGTTCCTCACCAATGCCCTGGTGGCTGGACTTCCTCATTTGTGGCTNNNNNNNNN 3828
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QY 1379 ValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnGlyLeu 1398
Db 3889 NNN 3939
QY 1399 LysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValIle 1418
Db 3940 NNNGTGGTGGAATGCGCTTGCTGGCGCCATCCCTCCATCATGAATGTGCTGCTGTG 3999
QY 1419 CysCysAlaPhePheIleIlePheGlyIleLeuGlyValGlnLeuPheLysGlyLysPhe 1438
Db 4000 TGTCTCATCTTCTGGCTGATTTTCAGCATCATGGAGTTAACTTGTTGGCGGAAGTAC 4059
QY 1439 PheValCysGlnGlyGlu-----AspThrArgAsnIleThrAsnLys 1452
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QY 1453 SerAspCysAlaGlu-----AlaSerTyrArgTyrValArgHisLys 1466
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Db 4180 ATCAACTTTGACAATGTTGGGGCAGAGATACCTGGCCCTTCTCAAGTAGCAACTTCAAA 4239
QY 1487 GlyTyrValAspIleMetTyrAspGlyLeuAspAlaValGlyValAspGlnProIle 1506
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QY 1585 LeuValHisHisLysCysThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGly 1604
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QY 1605 LeuAsnValValThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAla 1624
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QY 1625 LeuLysIleCysAsnTyrIlePheThrValIlePheValLeuGluSerValPheLysLeu 1644
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QY 1664 IleValLeuLeuSerIleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeu 1683
Db 4774 GTAGTCATCCTCTCCATTTGTGGGAATGTTCTTGGCAGATATA-----ATTGAGAAATAC 4827
QY 1684 ProIleAsnProThrIleIleArgIleMetArgValLeuArgIleAlaArgValLeuLys 1703
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QY 1704 LeuLeuLysMetAlaValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuPro 1723
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Db 4948 GCCCTGTTCAACATCGGCCCTTCTGCTGCTGTCATGTTCAATCTTCCATTTTGGG 5007
QY 1744 ValGluLeuPheGlyAspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArg 1763
Db 5008 ATGTCCAATTTTGCATATGTGAAGCAGAG-----GCTGATATCGATGAC 5052
QY 1764 HisAlaThrPheArgAsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGly 1783
Db 5053 ATGTTCACTTTGAGACATTTGGGCAACAGCATGATGCTGCCTGTTTCAAAATCACACCTCA 5112
QY 1784 AspAsnTyrAsnGlyIleMetLysAspThrLeuArg-----AspCys-----Asp 1798
Db 5113 GCTGTTGGATGGCTGCTGCTGCCATCTTAAACCGCCCCCTGACTGACGCTAGAT 5172
QY 1799 GlnGlu-----SerThrCysTyrAsnThrValIleSerProIle 1811
Db 5173 AAGGAACACCAGGAGTGGCTTTAAGGAGATTGTGGAAACCCCTCAGTGGCATCTTC 5232
QY 1812 TyrPheValSerPheValLeuThrAlaGlnPheValLeuValAsnValAlaIleAlaVal 1831
Db 5233 TTCTTTGTAAGTACATCATCATCTTCTTCTTAATGTGCGTAACATGTACATTGGCATC 5292
QY 1832 LeuMetLysHisLeuGluGluSerAsnLysGluAlaLysGlu-----GluAlaGlu 1848
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QY 1849 LeuGluAlaGluLeuGluLeuMetLysThrLeuSerProGlnProHisSerProLeu 1868
Db 5353 TTTGAGACCTTCTATGAG----- 5370
QY 1869 GlySerProPheLeuTyrProGlyValGlnGlyProAspSerProAspSerProLysPro 1888
Db 5371 -----ATCTGGGAGAAAGTTGAC---CCCGATGCCACCACTTCATTGAGTAG 5415
QY 1889 GlyAlaLeuHisProAlaHisAlaArgSerAlaSerHisPheSerLeuGluHisPro 1908
Db 5416 TGTAAGCTGGCAGACTTTCAGATGCC-----TTGAGACATCCT 5454
QY 1909 ThrMetGlnProHisProThr-----GlnLeuProGlyProAspLeuLeuThrValArg 1926
Db 5455 CTCGAGTGGCCCAAGCCAAATACCATTTGAGCTCATCGCTATGAGTCTGCCAATGTG--- 5511
QY 1927 LysSerGlyValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGly 1946
Db 5512 ---AGCGGG---GATGCGATCCACTGCTTG-----GACATCCT-TTTTGCTTCAACCA 5558
QY 1947 SerThrAlaGluGlyProLeuGluHisArgGlyTyrGlyLeuProLysAlaGlnSerGly 1966
Db 5559 GCG-----GGTCCCTGGAGATAGCGGGAGTTGACATCTCGCGGACAGCATGGA 5609

IMAGE:6413458 5', mRNA sequence.

ACCESSION BU058818
VERSION BU058818.1 GI:22499107
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 771)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pYX-5.

FEATURES
Source Location/Qualifiers

1..771
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/db_xref="taxon:10090"
/clone="IMAGE:6413458"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FRO"
/note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGCAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 2.87e-74 Length: 771
Score: 1215.50 Matches: 242
Percent Similarity: 98.38% Conservative: 1
Best Local Similarity: 97.98% Mismatches: 4
Query Match: 10.21% Indels: 2
DB: 5 Gaps: 0

US-09-611-257A-37 (1-2266) x BU058818 (1-771)

QY 1569 LysAlaGlnCysIysProTyrTyrSerAspTyrSerArgPheArgLeuValHisHis 1588
Db 31 GAAGCCAGTGCAAACCTACTACTGTGACTACTCGCGCTCCGGCTCTGCCACCAC 90
QY 1589 LeuCySThrSerHisTyrLeuAspLeuPheIleThrGlyValIleGlyLeuAsnValVal 1608
Db 91 CTGTGTACCAAGCCACTACTGGAACCTCTTCATCATCTGCTGTCATCGGGCTGAATGTGTC 150
QY 1609 ThrMetAlaMetGluHisTyrGlnGlnProGlnIleLeuAspGluAlaLeuLysIleCys 1628
Db 151 ACGATGGCCATGAACATTAACAGACGAGCCCGACATCTTGACGAGGCTCTGAAGATCTGC 210

QY 1629 AsnTyrIlePheThrValIlePheValLeuGluSerValPheLysLeuValAlaPheGly 1648
Db 211 AACTACATCTTAAACCGTCATCTTGTCTTGAGTCAGTAFTCAAACTGTGGCTTCGGC 270
QY 1649 PheArgArgPhePheGlnAspArgTyrAsnGlnLeuAspLeuAlaIleValLeuSer 1668
Db 271 TTCGCGCGGTTCTTCCAGACAGGTGAACACAGCTGAGCTGCTATTGTGCTTGTGCC 330
QY 1669 IleMetGlyIleThrLeuGluGluIleGluValAsnAlaSerLeuProIleAsnProThr 1688
Db 331 ATCATCGGATCAACGCTGGAAGATTTGAGTCAATGCTTCACTGCCATCAACCCACC 390
QY 1689 IleIleArgIleMetArgValLeuArgIleAlaArgValLeuLysLeuLeuMetAla 1708
Db 391 ATCATCCGATCATGAGGGTGTCCGCAATTGCTCGAGTTCTGAAGCTGTGAAGTGGCT 450
QY 1709 ValGlyMetArgAlaLeuLeuAspThrValMetGlnAlaLeuProGlnValGlyAsnLeu 1728
Db 451 GTGGCATGCGGCACTGTGTGACACGGTGATGACAGGCCCTGCCACAGGTGGGAACCTG 510
QY 1729 GlyLeuLeuPheMetLeuLeuPheIlePheAlaAlaLeuGlyValGluLeuPheGly 1748
Db 511 GGACTTCTCTCATGTCTATTATTTCATCTTGCAGCTCTGGGCGTGAGCTCTTGGAA 570
QY 1749 AspLeuGluCysAspGluThrHisProCysGluGlyLeuGlyArgHisAlaThrPheArg 1768
Db 571 GACCTGGAGTGTATGAGACACACCCTTGAGGGCTTGGGCGGCATGCCACCTTAGG 630
QY 1769 AsnPheGlyMetAlaPheLeuThrLeuPheArgValSerThrGlyAspAsnTyrPasnGly 1788
Db 631 AACTTGGTATGGCCTTCTTGACCTCTTCCGAGTCTCCACTGTGACAACTGGAATGCT 690
QY 1789 IleMetLysAspThrLeuArgAspCysAspGlnGluSerThrCysTyrAsnThrValIle 1808
Db 691 ATTATGAAGACACCCCTCCGGAGCTGTGACACAGAGTC-ACCTGCTACAC-ACCGTATC 748
QY 1809 SerProIleTyrPheValSer 1815
Db 749 TCACCCATCTACTTCGTGTCC 769

RESULT 11

BI905383 990 bp mRNA linear EST 16-OCT-2001
LOCUS 603167426F1 NCI_CGAP_lu33 Mus musculus cDNA clone IMAGE:5255383 5',
DEFINITION mRNA sequence.

ACCESSION BI905383
VERSION BI905383.1 GI:16167886
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 990)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: L1AM1645 row: d column: 08
High quality sequence stop: 911.

FEATURES
Source

1..990
/organism="Mus musculus"
/mol_type="mRNA"

/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5255383"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NCI CGAP Lu3"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5'. TGTACCAATCTGAAGTGGAGCGCGCCCTCTGTTTCTTTTCTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	4.32e-74	Length:	990
Score:	1215.50	Matches:	261
Percent Similarity:	83.03%	Conservative:	13
Best Local Similarity:	79.09%	Mismatches:	45
Query Match:	10.21%	Indels:	12
DB:	4	Gaps:	3

US-09-611-257A-37 (1-2266) x BI905383 (1-990)

QY	1805	AsnThrValIleSerProIle-TyrPheValSerPheValLeuThrAlaGlnPheValLe	1824
DB	1	AACACCGTCATCTCACCCCATCGTACTTCTGTCCTTCGTCTGACGCGCCAGTTTGCT	60
QY	1824	uValAsnValValIleAlaValLeuMetLysHisLeuGluGluSerAsnLysGluAlaLy	1844
DB	61	GGTCAACGTGTCATAGCCCGTGTGATGAAGCACCTGGAAGAGCAACAAGAGGCCAA	120
QY	1844	SGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerProGlnPr	1864
DB	121	GGAGAGGCGGAGTTGGAGGCGGAGCTGAGCTAGAGATGAAGACACTCAGCCGACGCC	180
QY	1864	OHISerProLeuGlySerProPheLeuTrpProGlyValGluGlyProAspSerProAs	1884
DB	181	CCACTCCCCGCTGGGACGCCCTTCTCTGGCCTGGGGTGAAGTGTCATAGCCCTGA	240
QY	1884	pSerProLysProGlyAlaLeuHisProAlaAlaHisAlaArgSerAlaSerHis--Ph	1903
DB	241	CAGCCCTAAGCCTGGGGCTCCACACACACGCGCCACATTTGAAGCAGCCTCTTCAGGCTT	300
QY	1903	eSerLeuGluHisProThrMetGlnProHisProThrGluLeuPro-----GlyPr	1920
DB	301	CTCCCTTGAGACCCCGACGATGTACTCACACTGAGAGGGGCCAGTCCCTTAGGACC	360
QY	1920	oAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnAspSe	1940
DB	361	AGACCTGTGACTGTGAGGAAGTGTGTGTCAGCCGACACACTCTCTGCCCAATGACAG	420
QY	1940	rTyrMetCysArgHisGlySerThrAlaGluGlyProLeuGlyHisArgGlyTyrGlyLe	1960
DB	421	CTACATGTGCGCAATGGAGACACTGCCGAGAGATCCCTAGGACACAGGGGCTGGGGCT	480
QY	1960	uProLysAlaGlnSerGlySerValLeuSerValHisSerGlnProAlaAspThrSerTy	1980
DB	481	CCCCAAGCCAGTCAGGCTCCATCTTGTCTGTCTCACTCCCAACGACGACACACAGCTG	540
QY	1980	rIleLeuGlnLeuProLysAspAlaProHisIleLeuLeuGlnProHisSerAlaProThrTr	2000
DB	541	CATCCTACAGCTTCCCAAGATGCACTATCTGCTCCAGCCTCATATGGGGCTCCCACTG	600
QY	2000	pGlyThrIleProLysLeuProProGlyArgSerProLeuAlaGlnArgProLeuAr	2020
DB	601	GGGCGCCATCCCTAAACTACCCCCCAGCTGGCGCTCCCTCTGGCTCAGAGGCTCTCAG	660
QY	2020	gArgGlnAlaAlaIleArgThrAspSerLeuAspValGlnGlyLeuGlySerArgGluAs	2040

DB	661	GGCCGAGGACGAATAGACTGACTCCCTTGACACTGTGACGGGCTGGTAGCCGGAGAGA	720
QY	2040	pLeuLeuAlaGluValSerGlyProSerProProLeuAlaArgAlaTyrSerPheTrpGl	2060
DB	721	CCTGTGTGACAGGTGAGTGGGCCCTCTCTGCTGACCCGCTCTCA-TCTTCTGGGG	779
QY	2060	ygln---SerSerThrGlnAlaGlnGlnHisSer-ArgSerHisSerLysIleSerLys-	2078
DB	780	GCGGGTTCGAGCATCATGTGTCAGACGGCGCTCCGGCAGCAGACGAAAGTCTCCAAAG	839
QY	2079	HisMetThrProPro-AlaProCysProGlyPro-GluProAsnTrpGlyLysGlyProp	2098
DB	840	CACATCCGGCTGCCAGGCGCCCTTGCCAGGGCCTGGAACACAGGCTGGCCCAAGACTTC	899
QY	2098	roGlu-ThrArgSerSerLeuGluLeuAspThrGluLeuSerTrpIleSerGlyAspLeu	2117
DB	900	AAGAGAACGAGAAAGCAGTTAACTTGACCGGAGCTGAAGCTGGATCAGGGAACCTC	959
QY	2118	LeuProProGlyGlyGln 2123	
DB	960	TTGGCAGAGTCCGAAAA 977	

RESULT 12	CF742232	784 bp	mRNA	linear	EST 10-OCT-2003
LOCUS	CF742232	UT-M-HB0-clk-j-06-0-UI.r1	NIH_BMAP_HB0	Mus musculus	cDNA clone
DEFINITION	IMAGE:30619901 5', mRNA sequence.				
ACCESSION	CF742232				
VERSION	CF742232.1	GI:37638571			
KEYWORDS	EST.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 784)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousef1.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5.
location/Qualifiers
1..784

FEATURES
source

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57Bl/6"
/db_xref="taxon:10090"
/clone="IMAGE:30619901"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP HB0"
/note="Organ: Eye; Vector: PYX- Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according Bonaído, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag is TTATGTGAAGT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

ORIGIN
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH). "

Alignment Scores:
Pred. No.: 4.78e-74 Length: 784
Score: 1212.50 Matches: 243
Percent Similarity: 95.40% Conservative: 6
Best Local Similarity: 93.10% Mismatches: 10
Query Match: 10.19% Indels: 2
DB: 7 Gaps: 1

US-09-611-257A-37 (1-2266) x CF742232 (1-784)

QY 937 SerSerTrpAlaAlaLeuTyrPheIleAlaLeuMetThrPheGlyAsnTyrValLeuPhe 956
Db 2 TCATCTGGGCTGCTCTTACTTCAATCGCCCTCATGACTTTGGCACTACGTGCTCTT 61
QY 957 AsnLeuValAlaIleLeuValGluGlyPheGlnAlaGluGluIleSerLysArgGlu 976
Db 62 AACCTGCTTGCGCATTTCTCGTAGAGGTTTCCAGCAGAGAAATCGCAACGGGA 121
QY 977 AspAlaSerGlyGlnLeuSerCysIleGlnLeuProValAspSerGln-GlyGlyAspAl 996
Db 122 GATACGAGTGACAGTAAAGCTGATTCAGCTGCTGTCAACTCCCAAGGNGAGATGC 181
QY 996 aAsnLysSerGluSerGluProAspPhePheSerProSerLeuAspGlyAspGlyAspAr 1016
Db 182 CACCAAGTCTGAGTCAGAGCCTGATTTCTTTCCGCCAGTGTGATGTGATGGGACAG 241
QY 1016 GlySlySlyCysLeuAlaLeuValSerLeuGlyGluHisProGluLeuArgLysSerLeu 1036
Db 242 GAAGAAAGCGCTTGCGCTGCTGCTGGGAGAACACTCGGAACCTACGAAGAAGCCTTTT 301
QY 1036 uProProLeuIleIleHisThrAlaAlaThrProMetSerLeuProLysSerThrSerTh 1056
Db 302 GCCACCTCTCATCAATCCACACAGCTGTACACCATGTCACTGCCCAAGAGCTCCAGAC 361
QY 1056 rGlyLeuGlyGluAlaLeuGlyProAlaSerArgThrSerSerSerGlySerAlaG1 1076
Db 362 AGGTGTGGGGAAGCACTGGGCTCTGCTCGCTCGCCGACAGTAGAGTGGGTCCGCTGA 421
QY 1076 uProGlyAlaAla--HisGluMetLysSerProProSerAlaArgSerSerProHis 1095
Db 422 GCCTGGAAGTCCCATATGAGATGAATCAACGCCAAGTGCAGGAGCTCCCGACAG 481
QY 1095 rProTrpSerAlaAlaSerSerTrpThrSerArgArgSerSerArgAsnSerLeuGlyAr 1115
Db 482 TCCCTGAGCGCAGCAAGCAGCTGGACCAAGCGGCTCCAGCCGGAACAGCTGGGCGC 541
QY 1115 GAlaProSerLeuLysArgArgSerProSerGlyGluArgArgSerLeuLeuSerGlyG1 1135
Db 542 GGGCCCCAGCCTGAAGCGTAGAGCCCAAGCGGAGCGGAGGTCCCTGCTGTGAGA 601
QY 1135 uGlyGlnGluSerGlnAspGluGluGluSerSerGluGluGluArgAlaSerProAlaG1 1155
Db 602 GGGTCAGAGAGACCAAGATGAGAGAGAGTTCAGAAAGAGACCGGGCCAGCCAGCAG 661
QY 1155 ySerAspHisArgHisArgGlySerLeuGluArgGluAlaLysSerSerPheAspLeuPr 1175
Db 662 CAGTGATCATCGCCACAGGGGTTCTTGAAAGTGAAGGCAAGAGTTCCTTGACCTGCC 721
QY 1175 cAspThrLeuGlnValProGlyLeuHisArgThrAlaSerGlyArgGlySerAlaSerG1 1195
Db 722 TGAACACCTGCAAGGTGCGGGGCTTCATCGAACAGCCAGCGGTCCGAGCTGCGCTTGA 781
QY 1195 u 1195
Db 782 A 782

RESULT 13
BU709095 810 bp mRNA linear EST 15-JUL-2003
LOCUS BU709095

DEFINITION
UI-M-EW0-caz-e-20-0-UI.r1 NIH_BMAP_EW0 Mus musculus cDNA clone
IMAGE:6419323 5', mRNA sequence.
BU709095
KEYWORDS
BU709095.1 GI:23642225
SOURCE
EST.
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 810)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
Seq primer: PYX-5.
Location/Qualifiers
1. 810
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6419323"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP EW0"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to
Bonaïdo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is GTGCGTGGA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 2.79e-72 Length: 810
Score: 1187.50 Matches: 244
Percent Similarity: 90.77% Conservative: 2
Best Local Similarity: 90.04% Mismatches: 6
Query Match: 9.98% Indels: 22
DB: 5 Gaps: 1

US-09-611-257A-37 (1-2266) x BU709095 (1-810)

QY 1358 ValIleAspIleLeu-ValSerMetValSerAspSerGlyThrLysIleLeuGlyMetLe 1377
Db 1 GTCATGCATCTGTGTGTCTCATGTGTTCTGACAGCGGCACCAAGATTCTCGGCATGCT 60
QY 1377 uArgValLeuArgLeuLeuArgThrLeuArgProLeuArgValIleSerArgAlaGlnG1 1397
Db 61 GAGGGTGTGCGGCTGTGCGGACCTTACGTCACACTCAGGGGTCAACGCGGCGCAGGG 120
QY 1397 yLeuLysLeuValValGluThrLeuMetSerSerLeuLysProIleGlyAsnIleValVa 1417

Db 121 GCTGAAGCTGTGGTAGAGACTGTGATGTCATCCCTCAAAACCATTGGACAATTGTGGT 180

Qy 1417 111eCyCySaLaPhePhe11e1lePheGly1leLeuGlyValGlnLeuPheLySGlyLy 1437
|||||
Db 181 CATCTGCTGTGCCCTTCTTCATCATTTTGGAAATCTTGGGGTGACGCTCTTCAAAAGGAA 240

Qy 1437 sPhePheValCysGlnGlyGluAspThrArgAsn1leThrAsnLySSerAspCysAlaG1 1457
|||||
Db 241 GTTCTTCGTGTGTCAAGGTGAGACACCAAGAACATCACTAACAAGTCCGACTGTGCTGA 300

Qy 1457 uAlaSerTyrArgTrpValArgHisLySTyrAsnPheAspAsnLeuGlyGlnAlaLeuMe 1477
|||||
Db 301 GGCCAGTTACCGGTGGTCCGGACAAGTACAACCTTGAACAACCTGGCCAGGCTTGAT 360

Qy 1477 tSerLeuPheValLeuAlaSerLySAspGlyTrpValAsp1leMetTyrAspGlyLeuAs 1497
|||||
Db 361 GTCCCTGTTGTGCTGGCTCCAGAGATGGCTGGGTTCACATCATGTATGATGGACTGGA 420

Qy 1497 pAlaValGlyValAspGlnGlnPro1leMetAsnHisAsnProTrpMetLeuLeuTyrPh 1517
|||||
Db 421 TGCTGTGGAGTGGAGCACGACGACCATCATGAACCAACCCCTTGATGCTGCTACTT 480

Qy 1517 e1leSerPheLeuLeu1leValAlaPhePheValLeuAsnMetPheValGlyValValVa 1537
|||||
Db 481 CATCTCTTCTCTCTCATCTGTGGCTTCTTCGTCCTGAACATGTTTGTGGCGGTGGTGT 540

Qy 1537 lGluAsnPheHisLySCysArgGlnHisGlnGluGluGluAlaArgArgArgGluG1 1557
|||||
Db 541 GGAGAACTTCCATTAAGTGACAGACACCAAGAGAGAGAGCGCGCGGGGAGGA 600

Qy 1557 uLySArgLeuArgLeuGluLyLySArgArg----- 1568
|||||
Db 601 GAAGCGACTAAAGAGGCTGAGAAAGAGAAATCTAATGTTGACGATGTAATTGC 660

Qy 1569 -----LysAlaGlnCysLySProTyrTyrSerAspTy 1579
:::|||||
Db 661 TTCCGGCAGCTCAGCCAGCGCTGGCTCAGAAGCCAGTGCANACCCTACTACTCTGACTA 720

Qy 1579 rSerArgPheArgLeuLeuValHis1leLeuCysThrSerHisTyrLeuAspLeuPhe1 1599
|||||
Db 721 CTGCGGCTTCCGGCTCCC-TCGTCAACACTGTGTACAGC-CACTACCTGNA-CTCTTCAT 777

Qy 1599 eThrGlyVal1leGlyLeuAsnValThr 1609
|||||
Db 778 CACTGCTGTCATCGGGCTGAATGTGTCACG 808

RESULT 14
BI160856 736 bp mRNA linear EST 05-JUL-2001
LOCUS 602864778F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019018 5',
DEFINITION mRNA sequence.
ACCESSION BI160856
VERSION BI160856.1 GI:14620857
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 736)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM1833 row: k column: 19
High quality sequence stop: 710.

FEATURES
source
location/Qualifiers
1..736
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5019018"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_42"
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
ORIGIN
Alignment Scores:
Pred. No.: 3.56e-72 Length: 736
Score: 1185.00 Matches: 236
Percent Similarity: 97.15% Conservative: 3
Best local Similarity: 95.93% Mismatches: 5
Query Match: 9.95% Indels: 2
DB: 4 Gaps: 0
US-09-611-257A-37 (1-2266) x BI160856 (1-736)
Qy 1268 LeuCysHisArg1le1leThrHisLySMetPheAspHisValValLeuVal1le1lePhe 1287
Db 2 CTGTGTCACCGGATCATCAACCCACAAGATGTTGACCACAGTGCTGCTTCATCATCTTC 61

Qy 1288 LeuAsnCys1leThr1leAlaMetGluArgProLyS1leAspProHisSerAlaGluArg 1307
Db 62 CTTAAGTGCATCACCATCGCATGAGAGCGCCCAAAATTGACCCCAAGCGCTGAACGC 121

Qy 1308 1lePheLeuThrLeuSerAsnTyr1lePheThrAlaValPheLeuAlaGluMetThrVal 1327
Db 122 ATCTTCTGACCCCTCTCCAATTACATCTTCAACGACGCTTCTTGCTGAATGACAGTG 181

Qy 1328 LySValValAlaLeuGlyTrpCysPheGlyGluGlnAlaTyrLeuArgSerSerTrpAsn 1347
Db 182 AAGTGTGGTGCACCTGGCTGTGCTTCGGGAGCAGCGGTACCTGGAGCAGTTGGAAC 241

Qy 1348 ValLeuAspGlyLeuLeuValLeu1leSerVal1leAsp1leLeuValSerMetValSer 1367
Db 242 GTGCTGGAACGGGCTGTGGTGTCTCATCTCCGTATCGACATTCTGGTGTCCATGTCTCT 301

Qy 1368 AspSerGlyThrLyS1leLeuGlyMetLeuArgValLeuArgLeuLeuArgThrLeuArg 1387
Db 302 GACAGCGGCACCAAGATCTGGGCATGTGAGGGTGTGCGGCTGTGGGACCCCTGCGC 361

Qy 1388 ProLeuArgVal1leSerArgAlaGlnGlyLeuLySLeuValValGluThrLeuMetSer 1407
Db 362 CCGCTCAGGGTGATCAGCGGGGCGCAGGGGCTGAAGCTGTGTGTGAGACGCTGATGTCC 421

Qy 1408 SerLeuLySPro1leGlyAsn1leValVal1leCysCysAlaPhePhe1le1lePheGly 1427
Db 422 TCACTGAACACCATCGGCAACATGTAGTCATCTGTGCTGCTTCTTCATCATTTTCGCG 481

Qy 1428 1leLeuGlyValGlnLeuPheLySGlyLyPhePheValCysGlnGlyGluAspThrArg 1447
Db 482 ATCTTGGGGGTGACGCTCTTCAAAAGGAAGTTTTCGTGTGCCAGGGCAGATACCAAG 541

Qy 1448 Asn1leThrAsnLySerAspCysAlaGluAlaSerTyrArgTrpValArgHisLySTyr 1467
Db 542 AACATCAACCAATAATCGGACTGTGCCGAGGCCAGTTACCGGTGGTCCGACACAAGTAC 601

Qy 1468 AsnPheAspAsnLeuGlyGlnAlaLeuMetSerLeuPheVal-LeuAlaSerLySAspG1 1487
Db 602 AACTTTGACCAACCTTGGCCAGCGCCCTGATGTCTGTCATGATATGGCTCCAAAGATGG 661

Qy	1487	YTRPVALASPILEMEtYrASpGLY-LEuAsPaLaVaLGLYValAspGLInGLInProileM	1507
Db	662	TAGGCTGACATCATGTACGATGCGCTGATGTCGTGGGGCGGTGAGCCAGACCATCA	721
Qy	1507	etAsnHisAsnPro	1511
Db	722	TGAACACACACCCT	735
RESULT 15			
LOCUS	BI736618	939 bp	mRNA linear EST 20-SEP-2001
DEFINITION	603361089F1 NIH_MGC_94	Mus musculus	CDNA clone IMAGE:5367862 5',
ACCESSION	BI736618		
VERSION	BI736618.1	GI:15713631	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 939)		
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: The Cepko Laboratory		
	CDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.llnl.gov		
	Plate: L1AM1936 row: b column: 23		
	High quality sequence stop: 853.		
FEATURES	location/Qualifiers		
Source	1..939		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/db_xref="taxon:10090"		
	/clone="IMAGE:5367862"		
	/tissue_type="retina"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_lib="NIH_MGC 94"		
	/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;		
	Site_2: SalI; Cloned unidirectionally; oligo-dT primed.		
	Average insert size 3.3 kb. Library enriched for		
	full-length clones and constructed by Life Technologies.		
	Note: this is a NIH_MGC Library."		
ORIGIN			
Alignment Scores:			
Pred. No.:	7.31e-72	Length:	939
Score:	1183.00	Matches:	247
Percent Similarity:	84.69%	Conservative:	13
Best Local Similarity:	80.46%	Mismatches:	41
Query Match:	9.94%	Indels:	9
DB:	4	Gaps:	3
US-09-611-257A-37	(1-2266) x	BI736618	(1-939)
Qy	1929	GLYValSerArgThrHisSerLeuProAsnAspSerTyrMetCysArgHisGLYSerThr	1948
Db	3	GGGTTCAGCCGGACACACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGAGCACT	62
Qy	1949	AlaGLuGLYProLeuGLYHisArgGLYTrpGLYLeuProLYsAlaGLnSerGLYSerVal	1968
Db	63	GCCGAGAGATCCCTTAGGACACAGGGGGCTGGGGGCTCCCAAGCCAGTCAGGCTCCATC	122
Qy	1969	LeuSerValHisSerGLnProAlaAspThrSerTyrIleLeuGLnLeuProLYsAsPaLa	1988
Db	123	TTGTCTGTTCACCTCCCAACGACAGACACCAAGCTGCATCCTTACAGCTTCCCAAGATGCA	182

QY	1989	ProHisLeuLeuGlnProHisSerAlaProThrTyrGlyThrIleProLysLeuProPro	2008
		:::	
Db	183	CACTATCTGCTCAGCCTCATGGGGCTCCACCTGGGGCGCCATCCCTAACTAACC	242
QY	2009	ProGlyArgSerProLeuAlaGlnArgProLeuArgArgGlnAlaIleArgThrAsp	2028
Db	243	CCTGGCGGCTCCCTCTGGCTCAGAGGCTCTCAGGCGCCAGGAGCAATAGAGACTGAC	302
QY	2029	SerLeuAspValGlnGlyLeuGlySerArgGluAspLeuLeuAlaValSerGlyPro	2048
Db	303	TCCCTGAGCGTGCAAGGCTGGTAGACCGGAAGACCTGTGTCAAGAGTGAATGGGCC	362
QY	2049	SerProProLeuAlaArgAlaTyrSerPheTyrGlyGlnSerSerThrGlnAlaGlnGln	2068
Db	363	TCCTGCCCTCTGACCCGCTCCTCATCTTCTGGGGGGGTGAGCATCCAGTGCAGACG	422
QY	2069	HisSerArgSerHisSerLysIleSerLysHisMetThrProProAlaProCysProGly	2088
Db	423	CGCTCCGGCAGCCAGAGCAAAAGTCTCCAAGACATCCGCCTGCCAGCCCTTGCCACGGC	482
QY	2089	ProGluProAsnTyrGlyLysGlyProProGluThrArgSerSerLeuGluLeuAspThr	2108
Db	483	CTGGAACCCAGCTGGGCCAAGGACCCCTCAAGAGACCAAGACAGCTTAGAGCTGACACG	542
QY	2109	GluLeuSerTyrIleSerGlyAspLeuLeuProProGlyGlyGlnGluProProSer	2128
Db	543	GAGCTGAGCTGATTCAGAGAGACCTCCTG--CCACAGTCAAGAAAGAACCCCTGTCC	599
QY	2129	ProArgAspLeuLysLysCysTyrSerValGlnAlaGlnSerCysGlnArgArgProThr	2148
Db	600	CCACGGGACTTGAAAAATGCTACAGTGTAGAGGCCAGAGCTGCCGGCGCAGGCTGGG	659
QY	2149	SerTyrLeuAspGluGlnArgArgHisSerIleAla-ValSerCysLeuAspSerGlySe	2168
Db	660	TCCTGGCTAGACGACAGAGAGACACTTCATCGCTGTGTCACTGCTGACAGCGGCTC	719
QY	2168	rglnProHisLeuGlyThrAspProSerAsnLeu-GlyGlyGlnProLeuGlyGlyProG	2188
Db	720	CCAGCCCCGCTATGTCCAAGCCCTCAAGGCTTGGGGGGCCAACTTGGGGGCCCTGG	779
QY	2188	LysArgProLysLysLysLeuSerProProSerIleThrIleAspProProGluSerG	2208
Db	780	GGAGCCGGCCTAAGAAAAAAGCTCAG-CCACCCAGATATCTTATAGACCCCGGAGACA-	837
QY	2208	InGlyProArgThrProProSerProGlyIleCysLeuArgArgAlaPro-SerSer	2227
Db	838	--GGAACCTCGGCCCCCATGCAGTCT-GGCGTGTGCC-AGGAGAGG--CCGGGCAAG	890
QY	2228	AspSerLysAspPro	2232
Db	891	GACTCGAAGGATCCT	905

Search completed: September 19, 2005, 15:16:25
Job time : 14442.4 secs

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